

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 122907

TO: Samuel W Liu

Location: 3c84 / 3c70 Tuesday, May 25, 2004

Art Unit: 1653 Phone: 272-0949

Serial Number: 09 / 880503

From: Jan Delaval

Location: Biotech-Chem Library

Rem 1A51

Phone: 272-2504

jan.delaval@uspto.gov

Search Notes		



Delaval, Jan

From:

Liu, Samuel

Sent:

Tuesday, May 25, 2004 12:43 PM

To: Subject: Delaval, Jan 09880503

Hi, Jan,

Please search amino acid sequences of SEQ ID NOs: 1, 4, 5, 6, 8 and 9 against commmerial <u>protein</u> databases for application 09880503 at least <u>50</u> printed results.

Very best,

Samue Liu AU 1653, REM 3C84 571-272-0949

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:		Examiner #:	Date:	
Art Unit:P Mail Box and Bldg Room Le	hone Number 30	Results Format Prefer	iber:PAPFI	R DISK E-MAII
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If more than one search is	submitted, please	prioritize searches in o **********	rder of need. *********	***************
Please provide a detailed statemen Include the elected species of structifity of the invention. Define an known Please attach a copy of the	ctures, keywords, synony y terms that may have a s	ms, acronyms, and registry nu special meaning. Give examp	imbers, and combine w	ath the conceptor
Title of Invention:			· · · · · · · · · · · · · · · · · · ·	
Inventors (please provide full in	imes):	<u> </u>		
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Earliest Priority Filing Date				
For Sequence Searches Only Pleappropriate serial number.	ase include all pertinent inf	formation (parent, child, division	al, or issued patent num	thers) along with the
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STAFF USE ONLY	Type of Sear NA Sequence (#		rs and cost where app	dicable
Searcher Phone #: 2	284 AA Sequence (A			
Scarcher Location	Structure (#)			
Date Searcher Picked Up:	25Bihliographic		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	
Pate Completed:	25 Litigation	I.cxis/Nexis		·
Searcher Prop & Review Time:	Fulltext	Sequence Systems		ار مستوند در این میکند.
Clerical Prop Time: 2	Patent Family	WWW/Internet		
Online time + (Other	Other (specify)		

PTG 1590 (\$ 01)

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plasmin (EC 3.4.21.7) precursor - dog (fragments)

NiAlternate names: plasminogen
C.Species: Canis lugus familiaris (dog)
C.Species: Canis lugus familiaris (dog)
C.Species: Canis lugus familiaris (dog)
C.Species: E61545
C.Accession: E61545
R.Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A.Title: Structural appects of the plasminogen of various species.
A.Reference number: A61545; MUID:89005015; PMID:3168975
A.Accession: E61545
A.Accession: E61545
A.Accession: E61545
A.Accession: E61545
A.Residues: 1-120 <SCH>
C.Superfamily: plasmin, kringle homology; plasminogen-related protein precursor >molC; Reywords: hydrolase; serine proteinase
C.Keywords: hydrolase; serine proteinase
F;37-114/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
NiAlternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
C;Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Baton, D.L.; Chen, E.Y.; Fless, C
Nature 330, 132-137, 1987
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A;Residues: 1-4548 «MCJ»
A;Residues: 1-4548 «MCJ»
A;Cross-references: GB.X06290; EMBL:X06696; NID:928619; PIDN:CAA29618.1; PID:95;
A;Cross-references: GB.X06290; EMBL:X06696; NID:928619; PIDN:CAA29618.1; PID:95;
B;Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; 1.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224, 13897
A;Title: Partial amino acid sequence of apolioporotein(a) shows that it is hom.
A;Reference number: A28017; MUID:87204109; PMID:3472206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: protein
A, Residues: 20-21, 'P', 23-34;177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200;292-314,'
X', 4396-4401 cEAT.
X', 4396-4401 cEAT.
K, Made, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A, Title: S' control regions of the apolipoprotein(a) gene and members of the r.
A, Reference number: A47277; MUID:93165698; PMID:7679504
A, Accession: A47277
                                                           1028 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHQHKRTPENHPNDDLTM-----NYCRNPDA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A;Reference number: S00657; MUID:88039109; PMID:3670400
3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 CYHGNGOSYRGTSSTTITGRKCOSWSSM1-----PHRHEKTDEHFPEAGL-TMNYCRN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CYBGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDAL----QLGLGKHNYCRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.6%; Score 156; DB 2; Length 120 ilarity 39.6%; Pred. No. 6.5e-10; Conservative 7; Mismatches 30; Indels
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A;Residues: 1-16 <RES>
A;Cross-references: GB:L07899; NID:g967973; PID:g967974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 PDNRRRPWCYVQVGLKPLV--QECMVHDCAD 86
                                                                                                                                                                     1123 DTGPWCFT----MDPSVRREYCNLTRCSD 1147
                                                                                                                              61 RRRPWCYVQVGLKPLVQE--CMVHDCAD
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hes 36; Conserv
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A; Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/
C; Complex: factor XII, prekallikrein, and HWW kininogen form a complex bound to anionic
C; Function:
                                                                                                                                                                            A; Description: factor XIIa catalyzes the proteclytic activation of plasminogen, plasma p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 22-Nov-1999 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
C;Accession: A32869; A30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Eiol. Chem. 264, 5557-5565, 1989
A;Tile: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A;Reference number: A32869; MUID:89174660; PMID:2925643
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A; Residues: 1.1420 «TON».

A; Residues: 1.1420 «TON».

A; Residues: 1.1420 «TON».

A; Csuperfamily: apolipoprotein(a); kringle homology; trypsin homology
C; Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F; So-127/Donain: kringle homology «KR1»
F; As-35.Donain: kringle homology «KR2»
F; As-35.Donain: kringle homology «KR3»
F; As-35.Donain: kringle homology «KR3»
F; So-69/Donain: kringle homology «KR5»
F; So-69/Donain: kringle homology «KR8»
F; So-60/Donain: kringle homology «KR8»
F; So-60-1145/Donain: kringle homology «KR8»
F; L191-1413/Domain: kringle homology «KR1»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDN 60
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Pred. No. 1.9e-09;
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48.5%; Pred. No. 7.8e-11;
tive 6; Mismatches 24
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40.9%; Pred. No. 1.20
... 9; Mismatches ?
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Best Local Similarity 48.5<sup>3</sup>
Matches 33, Conservative
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A,Residues: 354-3621373-615 <FUJ>
A,Residues: 354-3621373-615 <FUJ>
M,Relarris, R.J.; Ling, V.T.; Spellnan, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A,Title: O-linked fucose is present in the first epidermal growth factor domai.
A,Reference number: A44606; WUID:92184750; PMID:1544894
A,Contents: annotation; carbohydrate binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human N;Alternate names: Hageman factor (activated) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 27-Nov-1985 #sequence revision 30-Jun-1991 #text change 08-Dec-2000 C;Accession: A29411; A26814; A00930; A25191; A22248; A21037 R;Col, D.E.; MacGillivray, R.T.A.
A;Edile: Characterization of the human blood coagulation factor XII gene. Intr. A;Reference number: A29411; MUDD:88007593; PMID:2888762
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PMID:3011063
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A;Residus: 146-378, (3, 380-615 <QUE>
A;Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361
A;Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361
R;McMullen, B.A.; Fujikawa, K.
T. Biol. Chem. 2508-5344, 1985
A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (ac
A;Reference number: A22248; MUID:85182674; PMID:3886654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GB:M17466; GB:J02807; NID:g180355; PIDN:AAB59490.1; PID:g1
R;Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.
Nucleic Acids Res. 14, 3146, 1986
A;Title: CDNA sequence coding for human coagulation factor XII (Hageman).
A;Reference number: A26814; MUID:86176794; PMID:3754331
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A; Residues: 4-615 < TRIS.
A; Residues: 4-615 < TRIS.
A; Cross references: GB: M31315; NID: 9182291; PIDN: AAA70225.1; PID: 9182292
R; Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGill
A; Biol. Chem. 260, 13566-13576, 1985
A; Mitle: Characterization of human blood coaqulation factor XII cDNA. Predicti
A; Reference number: A00930; MUID: 86033830; PMID: 3877053
                                                                                                                                                                                                                                                                                                                            215 SCYEGRGVSYRGMARTIVSGAKCQRWAS----EATYRNMIAEQALRRGLGHHIFCRNPDN 270
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A, Residues: 14-332, 'S', 334-615 <CO2>
A, Residues: 16-332, 'S', 334-615 <CO2>
A, Cross-references: GB.M11723; NID:g180358; PIDN:AAA51986.1; PID:g180359
R, Que, B.G.; Davie, E.W.
Biochemistry 25, 1525-1528, 1986
A, Title: Characterization of a cDNA coding for human factor XII (Hageman A, Reference number: A25191; MUID:86216049; PMID:3011063
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                                                                       Length 603;
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A; Residues: 20-379 «MCM»
R; Pujikawa, K.; McMullan, B.A.
J. Blol. Chem. 258, 10924-10933, 1983
A; Pitle: Amino acid sequence of human beta-factor XIIa,
A; Reference number: A21037; MUID:83291041; PMID:6604055
                                                                                                         .2e-12;
es 32;
                                                                       DB 2;
                                                              Query Match
35.4%; Score 180.5;
Best Local Similarity 42.9%; Pred. No. 6.2e
Matches 36; Conservative 11; Mismatches
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A;Residues: 1-615 <COO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A26814
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C; Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C; Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
F; 1-34 / Domain: signal sequence #status predicted <SIG>
F; 108-148 / Domain: EGF homology × EGI>
F; 108-148 / Domain: EGF homology × EGI>
F; 250-237 / Domain: EGF homology × EGI>
F; 250-237 / Domain: Aringte homology × EGI>
F; 265-278 / Domain: Kringte homology × EGI>
F; 265-278 / Domain: Kringte homology × EGI>
F; 265-278 / Domain: Aringte homology × EGI>
F; 265-278 / Domain: Aringte homology × EGI>
F; 265-278 / Domain: Aringte homology × EGI>
F; 266-278 / Domain: Aringte homology × EGI>
F; 266-278 / Domain: Aringte homology × EGI × EFI × EGI × EG
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N;Alternate names: Haceman factor

S;Species: Cavia porcellus (guinea pig)

C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000

C;Accession: S28941

C;Accession: Y; Yamamoto, T; Kunisada, T; Shibuya, Y; Tanase, S; Kambara, T; Okabe, H.

Biochim: Biophys Acta 1159, 113-121, 1992

A;Title: Primary structure of guinea-pig Haceman factor: sequence around the cleavage si

A;Reference number: S28941; MUID:93003367; PMID:139917
                                                                                                                                                                                                                                 cDNA for a human serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Molecule type: mRNA

*Residues: 1-603 <SEM>.

A.SCROSS-references: EMBL:X68615; NID:949578; PIDN:CAA48600.1; PID:949579

C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;

C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: mRNA
A;Residues: 1-655 «MIV»
A;Cross-references: DDBJ:D14012; NID:g219680; PIDN:BAA03113.1; PID:g219681
A;Experimental source: 11ver (mRNA); serum (protein)
A;Note: sequence extracted from NCBI backbone (NCBIN:131227, NCBIP:131228)
A;Note: parts of the sequence, including the amino ends of the heavy and light chains, C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description: activates hepatocyte growth factor by specific proteolytic cleavage
                                                                                                                                                         z
                                                                                                                                 Miyazawa, K.; Shimomura, T.; Kitamura, A.; Kondo, J.; Morimoto, Y.; Kitamura, Biol. Chem. 268, 10024-10028, 1993
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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 25-Aug-1995 #text_change 08-Dec-2000
C;Accession: A46688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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F;134-169/Domain: fibronectin type I repeat homology <FB1>
F;177-208/Domain: EGF homology <FB1>
F;216-294/Domain: kringle homology <KRG>
F;216-294/Domain: trypein homology <TRY>
                                                                                                                                                                                                                            A,Title: Molecular cloning and sequence analysis of the d'oragination factor XII.
A,Reference number: A46688; MUID:93252878; PMID:7683665
A,Accession: A46688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:HGFAC; HGFA; HGFAP
A;Cross-references: GDB:9954514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 4p16-4p16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 RPWCYV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 RPWCYV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
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A; Molecule type: MENA
A; Residues: 1-560 < CHO>
A; Residues: 1-560 < CHO>
A; Cross-references: GB:SB3182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
A; Cross-references: GB:SB3182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
A; Cross-references: GB:SB3182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
A; Genetics:
A; Note: parts of this sequence, including the amino ends of the mature chains, rec; Genetics:
A; Genetics: GB:SB3182; HGFAL
A; Cross-references: GDB:4573962
C; Complex: a disulfide-bonded heterodimer of chains produced from the same pre resol C; Superfamily: plasma hytaluronan-binding protein; BGF homology; Kringle homolo; 10; C; Superfamily: Basma hytaluronan-binding protein; 50K chain #status predict (5); F; 77-108/Domain: EGF homology < EG1>
F; 115-147/Domain: EGF homology < EG2>
F; 115-147/Domain: EGF homology < EG3>
F; 115-147/Domain: EGF homology < EG3>
F; 114-556/Domain: kringle homology < RR:>
F; 114-556/Domain: trypsin homology < TRY>
F; 115-147-150/Domain: default by default
                F;79-158/Domain: Kringle homology «KRG»
F;173-428/Product: urokinase-type plasminogen activator chain B #status predict
F;173-446/Domain: trypsin homology «TRP»
F;172-446/Domain: trypsin homology «TRP»
F;162-296, 202-218, 210-285, 310-379, 342-358, 369-397/Disulfide bonds: #status pred
F;127,272,373/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Choi-Miura, N.H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tom J. Biochem. 119, 1157-1165, 1996
A;Title: Purification and characterization of a novel hyaluronan-binding prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasma hyaluronan-binding protein precursor - human N.Alternate names: hepatocyte growth factor activator-like protein; PHBP N.Contains: serine proteinase (EC 3.4.21.-) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Aug-1996 #text_change 19-Jul-2002 C.Species: Aug-1996 #text_change 19-Jul-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CYBGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
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                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r activator.
A,Reference number: JC4795; MUID:96425001; PMID:8827452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 37.9%; Score 193.5; DB 1; Local Similarity 41.7%; Pred. No. 2.2e-13; ne 35; Conservative 15; Mismatches 33;
                                                                                                                                                                                                                                             38.9%; Score 198.5; DB 1
54.4%; Pred. No. 4.9e-14;
tive 7; Mismatches 19
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Best Local Similarity 54.45
Matches 37; Conservative
40-71/Domain: EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 SRPWCYTK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 RRPWCYVQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: JC4795
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N;Alternate names: uPA
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
C;Accession: A35005
R;Leelle, N.D.; Kessler, C.A.; Bell, S.M.; Degen, J.L.
J. Biol. Chem. 255, 1339-1344, 1990
A;Title: The chicken urokinase-type plasminogen activator gene.
A;Accession: A35005
A;Accession: A35005
A;Status: preliminary
A;Accession: A35005
A;Status: preliminary
A;Accession: A35005
A;Cross-references: GB:J05187; NID:g212858; PIDN:AAA49131.1; PID:g212859
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C;Superfamily: urokinase-type plasminogen activator chain A #status predicted <ACH>F;22-171/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>F;22-171/Product: urokinase-type plasminogen activator chain A #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: MRNA
A, Residues: 1-558 «HAS>
C, Comment: This protein acts as serine protease.
C; Comment: This protein acts as serine protein; EGF homology; kringle homology; trypsi
C; Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsi
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 1-23/Domain: EGF homology <EG1>
F; 113-145/Domain: EGF homology <EG2>
F; 152-185/Domain: EGF homology <EG3>
F; 152-185/Domain: kringle homology <KRI>
F; 312-558/Forduct: plasma hyaluronan-binding protein small chain #status predicted <MATS
F; 312-558/Product: plasma hyaluronan-binding protein small chain #status predicted <MATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: JCS878
R;Hashimoto, K.; Tobe, T.; Sumiya, J.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, N. Biol. Pharm. Bull. 20, 1127-1130, 1997
A;Title: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyaluronan-bin A;Reference number: JCS878; MUID:98065239; PMID:9401717
A;Accession: JCS878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lasma hyaluronan-binding protein precursor - mouse
Species: Mus musculus (house mouse)
;Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYEGNGH FYRGKASTDTMGR PCL PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
                                                                                                                                                                                                                                                                  2 TCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
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                                                                                                                Length 477;
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                                                                                                                Score 213; DB 2; Length 47
Pred. No. 1.4e-15;
0; Mismatches 35; Indels
    F;225-226/Cleavage site: His-Ser (plasmin) #status predicted F;272,321,428/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.1%; Score 209.5; DB 2;
45.8%; Pred. No. 3.9e-15;
ive 13; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKPWCYVIKAGKFTSESCSVPVCS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * | | | : | : | | | | | KPWCFVKVNSEKVKWEYCDVTVC 274
                                                                                                                                                                                                                                                                                                                                                                                                                       RRPWCYVQVGLKPLVQECMVHDCA 85
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                                                                                                                                                                                             10;
                                                                                                                    41.8%;
larity 46.4%;
Conservative 10
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Best Local Similarity
Matches 39; Conserv
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1-10 sminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat C. Species: Desmouls common vampire bat)
C. Species: Desmouls rotundus (common vampire bat)
C. Species: Desmouls rotundus (common vampire bat)
C. Sacession: JS0537
C. Accession: JS057
C. Accession: JS0537
C. Accession: JS0537
C. Accession: JS0537
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A,Molecule type: protein
A,Accession: $48205
A,Molecule type: protein
A,Accession: $48205
A,Molecule type: protein
A,Accession: $48207
A,Molecule type: protein
A,Accession: $48206
A,Molecule type: protein
A,Residues: 33-37, 'X', 39-40 «LIW>
A,Residues: 309-316 «LI2>
A,Residues: 33-37, 'X', 39-40 «LIW>
A,Residues: 33-37, 'X', 39-40 «LIW>
C,Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I
C,Kayords: ibrinolysis; glycoprotein; hydrolase; Kringle; serine proteinase
C,Kayords: ibrinolysis; glycoprotein; hydrolase; Kringle; serine proteinase
F,18-29/Domain: spropeptide #status predicted «RRO>
F,18-29/Domain: propeptide #status predicted «MAT>
F,30-759/Product: t-plasminogen activator chain A #status predicted «ACH>
F,30-759/Product: t-plasminogen activator chain A #status predicted «BCH>
F,31-224/Domain: kringle homology «KR2>
F,132-24/Domain: kringle homology «KR2>
F,309-553/Domain: trypsin homology «KR2>
F,309-553/Domain: trypsin homology «TR2>
F,309-553/Domain: trypsin homology «TR3>
F,309-553/Domain: trypsin homology «TR3>
F,309-553/Domain: trypsin homology «RR3>
F,309-50/Clavage site: Arg-Ile (plasmin) trypsin homology (trypsin) #status predicted
F,305-50/Clavag
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               A;Accession: A29941
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-559 <RIC>
A;Cross-references: GB:J03520; NID:g202109; PIDN:AAA40470.1; PID:g202110
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Blochem. 224, 863.871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 LKPWCYVFKAGKYTTEFCSTPACPKGK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 40; Conserv
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A. Molecule type: manh.
A. Residues: 1-394 «RBA.
A. Residues: 1-394 «RBA.
A. Residues: 1-394 «RBA.
A. Residues: 1-394 «RBA.
A. Cross-references: GB: M63990; NID: g166078; PIDN: AA31595.1; PID: g166079
A. Cross-references: GB: M63990; NID: g166078; Find as Thr
C. Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C. Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C. Superfamily: signal sequence #status predicted «SIG»
F. 12-36 / Domain: bropeptide #status predicted «PRO»
F. 37-3-34 / Product.: plasminogen activator gamma #status predicted «PLA»
F. 45-126 / Domain: kringle homology «TRV»
F. 45-126 / Domain: trypsin homology «TRV»
F. 45-126 / Ge-108, 97-121 131-262, 174-190, 182-251, 276-351, 308-324, 341-369 / Disulfide bonds: F. 142-143 / Claevage site: His-Ser (plasmin) #status predicted
F. 189, 238, 345 / Active site: His, Asp. Ser #status predicted
F. 189, 238, 345 / Active site: His, Asp. Ser #status predicted
F. 185, Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: 56060
R;Kractzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 229-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des A;Accession: J80600
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F;124-205/Domain: kringle homology <RR1>
F;213-294/Domain: kringle homology <RR2>
F;213-294/Domain: kringle homology <RR2>
F;309-553/Pomain: trypain homology <TRN>
F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-4
F;149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;308-309/Cleavage site: Arg-11e (plasmin, trypsin) #status predicted
F;355,404,510/Active site: His, Asp, Ser #status predicted
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C;Species: Mus musculus (house mouse)
C;Accession: A29941; 848205; 548207; 848206
R;Rickles, R.J.; Darrow, A.L.; Strickland, S.
J. Biol. Chem. 263, 1183-1569, 1988
A;Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator is A;Reference number: A29941; MUID:88087303; PMID:2826484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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0
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Thes 33; Indels
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43.1%; Score 220; DB
Best Local Similarity 45.2%; Pred. No. 2e-16
Matches 38; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 VKPWCYVFKAGKYTTEFCSTPACPKG 208
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Matches 41; Conserv
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A,Rocession. A91323
A,Rocession. A91323
A,Rocession. A91323
A,Rocession. A91323
A,Bote. in the uterus, cleavage of the activation peptide may also occur after 38-Gln
A,Roce. in the uterus, cleavage of the activation peptide may also occur after 38-Gln
A,Roces in the uterus, into a 1986
A,Rocetence number: A37567; MUID:87033611; PMID:3021732
A,Contents: annotation; fibrin binding site
A,Rocetence number: A37568; MUID:87161761; PMID:3030730
A,Contents: annotation; fibrin binding site
A,Rocetence number: A37568; MUID:87161761; PMID:3030730
A,Contents: annotation; identification and pharmacokinetic properties of human tissue-type p
A,Reference number: A60902; MUID:8044681; PMID:3142086
A,Reference number: A60902; MUID:8044681; PMID:3142086
A,Rocetence number: A60902; MUID:8044681; PMID:3142086
A,Reference number: A60902; MUID:8044681; PMID:3090401
A,Reference number: A54445; MUID:8020; PMID:3090401
                                                                                                                                                                                                                                                                                                                                 A;Accession: A91143
A;Molecule type: mRNA
A;Residues: 1-38, G', 86-433, 'E', 435-562 <KAG>
A;Residues: 1-38, G', 86-433, 'E', 435-562 <KAG>
A;Residues: 1-38, G', 86-433, 'E', 435-562 <H (1) A; A;Edvarimental source: Detroit 562 cells; ATCC 138
A;Experimental source: Detroit 562 cells; ATCC 138
B;Edvard, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
A;Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ
A;Reference number: A93951; MUID:83169656; PMID:6572897
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A,Residues: 1-562 <8AS>
A,Cross-references: EMBL:X07393; NID:G37243; PIDN:CAA30302.1; PID:g37244
A,Experimental source: fetal lung cells
R,Experimental source: fetal lung cells
R,Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma FEBS Lett. 189, 145-149, 1985
A;Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen
A,Reference number: A91343; MUID:85285620; PMID:3896853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Reference number: A90488; MUID:85000468; PMID:6433976
A;Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and R;Pohl, G.; Kaplan, L.; Binarsson, M.; Wallen, P.; Jornvall, H.
FEBS Lett. 168, 29-32, 1984
A;Title: Differences between uterine and melanoma forms of tissue plasminogen activator. A;Reference number: A91322; MUID:84158956; PMID:6538514
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A;Cross-references: GB:M18182; NID:g340176; FIDN:AAA36800.1; PID:g340177
A;Cross-references: GB:M18182; NID:g340176; FIDN:AAA36800.1; PID:g340177
B;Fisher, R.; Waller, B.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
J. Biol. Chem. 260, 11223-11230, 1995
A;Title: Isolation and characterization of the human tissue-type plasminogen activator
A;Reference number: I55232; MUID:85289338; PMID:3161893
A;Accession: I55232
A;Accession: I55232
A;Accession: I55232
A;Accession: I55323
A;Accession: Dasa
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A;Accession: 160110
A;Actus: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Readdues: 251-358 < EDL>
A; Readdues: 251-358 < EDL>
Experimental souncies melanoma cells
R; Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
Biochemistry 23, 3701-3707, 1984
A; Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived
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A;Residues: 1-562 <HAR>
A;Ross-references: GB:M15518; NID:g190031; PIDN:AAA60111.1; PID:g190032
A;Ctoss-references: GB:M15518; NID:g190031; PIDN:AAA60111.1; PID:g190032
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
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A; Residues: 1-36 <RE2>
A; Residues: 1-36 <RE2>
A; Cosa-references: GB:MI1990; NID:g339837; PIDN:AAA61213.1; PID:g339839
C; Comment: Cleavage by plasmin or trypsin produces two chains held together by a c; Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val and. C; Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I c; Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I c; Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I d; C; Geneer GDB: PLAT
A; Cross-references: GDB: 119496; OMIM:173370
A; Map position: 8912-8912
A; Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 4' '3; C; Cymperfamin; signal sequence flattus predicted <SIG>C; Cymperfamin; by Lissue plasminogen activator argues experimental <ACH>E; 1-23/Domain: propebtide flattus predicted <SIG>C; Cymperfaminogen activator chain A #status experimental <ACH>E; 1-23/Domain: kringle homology <ARE>E; 1-24/Domain: EGF homology <ARE>E; 1-25/Domain: EGF homology <ARE>E; 1-25/Domain: trypsin homology <ARE>E; 11-556/Domain: trypsin h
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L.plasminogen activator (EC 3.4.21.68) precursor - rat
C;5pecies: Nattus norregicus (Norway rat)
C;Date: 10-6ep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35029, A31597
C;Accession: A35029, A31597
B;Ency P.; Ohlsson, M.; Ny. T.
J;Ency P.; Ohlsson, M.; Ny. T.
J;Ency P.; Ohlsson, M.; Ny. T.
J;Accession: A35029
A;Aitle: The structure of the TATA-less rat tissue-type plasminogen activator g
A;Accession: A35029
A;Accession: A31037
A;Accession: A31047
A;Accession
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A, Rolecule type: MRNA A, 81-559 < NVT>
A, Residues: 1-379, K', 31-559 < NVT>
A, Cross-references: GB.M2397, NID.9530159; PIDN:AAA41812.1; PID:9530160
A, Cross-references: GB.M2397, NID.9530159; Fibronectin type I C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I C, Keywords: fibrinolysis; glycoprotein; hydrolase; Kringle; serine proteinase F; 1-17Domain: aignal sequence #status predicted < SIG>
F; 1-17Domain: propeptide #status predicted < RRO>
F; 30-559/Product: t-plasminogen activator #status predicted < MAT>
F; 30-359/Product: t-plasminogen activator chain A #status predicted < ACH>
F; 38-75/Domain: fibronectin type I repeat homology < IFI>
F; 83-116/Domain: EGF homology < EGF>
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44.3%; Score 226; DB 1;
Best Local Similarity 47.7%; Pred. No. 6.2e-17;
Matches 41; Conservative 9; Mismatches 36;
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C;Keywords: alternative splicing; fibrinolysis; glycoprotein; kringle F;1-23/Domain: signal sequence #status predicted <SIG>F;24-21/Domain: propertide #status predicted <PRO.
F;34-32/Domain: propertide #status predicted <PRO.
F;31-29/Product: t-plasminogen activator, inactive endothelial splice form :P;41-78/Domain: Eibronectin type I repeat homology <1FA>F;86-119/Domain: EdF homology <EGF>F;127-208/Domain: EdF homology <EGF>F;215-229/Domain: Kringle homology <EGF>F;215-291/Domain: kringle homology #status atypical <EGF>F;215-291/Domain: kringle homology #status atypical <EGF>F;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203/Disulfide bonds:
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Matches 4
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NyAlternate names: tissue plasminogen activator
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 22-Jun-1999
C;Accession: 138098; S01678
NyAccession: 138098; B. 1086, 1990
A;Title: Variant tissue type plasminogen activator (PLAT) cDNA obtained from human endot A;Reference number: 138098; MUD:90192128; PMID:1969145
A;Accession: 138098
A;Accession: 138098
A;Accession: 1291 cSIE>
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-291 cSIE>
A;Cross-references: EMBL:X13097; NID:935282; PIDN:CAA31489.1; PID:935283
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A,Cross-references: GDB:119496; OMIM:173370
A,Map Dosition: 8p12-8p12
A,Map Dosition: 8p12-8p12
A,Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2
C,Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
                                                                                                                                                                                                                                                                                                                                                                                                              t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat NiAlternate names: tissue plasminogen activator C;Species Desmodus rotundus (common vampire bat) C;Dete: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999 C;Accession: JS0598 #sequence_revision 31-Mar-1992 #toxecschmar, J; Haandler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 229-237, 1991 A;Title: The plasminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family from the salivary gland of the vampire bat Desminogen activator family fami
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    2 TCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQOTYHAHRSDALQLGLGKHNYCRNPDNR 61
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; Pred. No. 1.2e-18;
12; Mismatches 30;
                                                                                                                                                                                 RRPWCYVQVGLKPLVQECMVHDCA 85
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Best Local Similarity 50.0°
Matches 42; Conservative
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                                                                                                                                                                                                                              2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
                                                                    44.3%; Score 226; DB 2; Length 291; 47.7%; Pred. No. 3.3e-17;
                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
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                                                                                                                                                                                                                                                                                                                                                                                   62 RRPWCYVQVGLKPLVQECMVHDCADG
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RESULT 8
A34369
L-124sminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma (ra) c.placies: Megaderma lyra
C.Species: Megaderma lyra
C.Species: Megaderma lyra
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A34369
A,Title: Isolation, characterization, and cDNA cloning of a vampire bat salivar place A,Title: Isolation, characterization, and cDNA cloning of a vampire bat salivar olas A,Reference number: A34369, MUID:90036667; PMID:2509450
A,Reference number: A34369, MUID:90036667; PMID:2509450
A,Reference number: A34369, MUID:90036667; PMID:2509450
A,Residues: 1-47 cGAR>
A,Resi
                                                                                                                                                                                                                                                                                                                     Riktaetzschmar, ususzy, thaendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon N.; Gene 105, 229-237, 1991
A.fitle: The plasminogen activator family from the salivary gland of the vampir at A; Accession. US0599
A.falle: The plasminogen activator family from the salivary gland of the vampir par A; Reference number: US0597; MUID:92039036; PMID:1937019
A.falles: 1-431 «KRA»
A.falles: 1-431 «Falles: 1-431 «KRA»
A.falles: 1-431 «KRA»
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                                            t-plasminogen activator (BC 3.4.21.68) beta precursor - common vampire bat NiAlternate names: tissue plasminogen activator Cispecies: Desmodus rotundus (common vampire bat) Cibate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999 CiAccession: US0599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.0%
Matches 42; Conservative
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C.Species Mas musculus (house mouse)
C.Species Mas musculus (house mouse)
C.Jate: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
A.Fitle: The murine urokinase-type plasminogen activator gene.
A.Residues: 1-433 cDEG
A.Rocession: A2420
A.Rolecule type: DNA
A.Residues: 1-433 cDEG
A.Rocession: A24215 MUD: Gondepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher, Eur. J. Exochem. 148, 225-232, 1988
A.Residues: 1-433 cDEG
A.Rocession: A24215 MUD: B5179474; PMID: 2985383
A.Rocession: A24215 MUD: B5179474; PMID: 2985383
A.Rocession: A24215 MUD: B5179474; PMID: 2985383
A.Rocession: A24215 MUD: B5179474; PMID: 2985311; PID: GS5128
A.Rocession: A24215 MUD: B5179474; PMID: B55128
C.Genetics:
C.Genetics:
C.Reywords: G1ycoprotein; heterodimer; hydrolase; kringle, serine proteinase
F;1-12/Domain: scringle homology cMEG>
F;2-17/8/Product: urokinase-type plasminogen activator chain B #status predicted
F;1-1-15/Domain: scringle homology cMEG>
F;10-1-12/Domain: scringle homology cMEG>
F;10-1-11-22/Domain: Scringle homology cMEG>
F;10-1-11-22/D
                                                                                                                                                                                             <ACH>
C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase P;1-20/Domain: signal sequence #starus predicted <SIG> P:21-179/Product: plasminogen activator chain A #status predicted <MAL> P;21-179/Product: plasminogen activator chain A #status predicted <AACH F;23-179/Product: urokinase-type plasminogen activator chain A #status predicted <ACH F;72-153/Domain: EXF homology <ERG> F;72-153/Domain: Extingle homology <ERG> F;181-433/Product: plasminogen activator chain B #status predicted <AMA> F;181-433/Product: plasminogen activator chain B #status predicted <AMA> F;181-431/Domain: trypsin homology <ERG> F;181-421/Domain: kringle 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 KTCYQGNGHSYRGKANRDLSGRPCLAWDSPTVLLKOYHAHRSDAIQLGLGKHNYCRNPDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 433;
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77.6%; Score 396; DB 1;
Best Local Similarity 76.1%; Pred. No. 1.3e-35;
Matches 67; Conservative 8; Mismatches 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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Best Local Similarity
Matches 64; Conserv
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A/Accession: All Accession: All Accession 67 KTCYEGNGHFYRGKASTDIMGRSCLAWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 126 9 9 NyAlternate names: upA Competica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: O4-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
Cistocession: A00922
Rinagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 9525-9541, 1984
Airtite: cDNA and gene nucleotide sequence of porcine plasminogen activator.
Airtite: cDNA and gene nucleotide sequence. 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGKHNYCRNPDN Gaps Gaps . 0 ; 0 Length 433; Query Match 82.4%; Score 420; DB 1; Length 442; Best Local Similarity 81.8%; Pred. No. 3e-38; Matches 72; Conservative 8; Mismatches 8; Indels 4; Indels - pig 93.1%; Score 475; DB 1; 94.3%; Pred. No. 2.9e-44; ive 1; Mismatches 4; u-plasminogen activator (EC 3.4.21.73) precursor 127 RRRPWCYVQVGLKQRVQECMVHNCADGK 154 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88 Query Match
Best Local Similarity 94.3
Matches 83; Conservative 61 g ð ઠે ВÞ à d à

u-plasminogen activator (EC 3.4.21.73) precursor

Concerns Reviews premaining management service; unokitase-type; utimary plasminogen civate (Concerns Reviews premaining management service) (1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1902 | 1

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esidu C.M.;

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A; Residues: 21-34 cRAB>
A; Residues: 21-34 cRAB>
R; Lii, X.; Bokman, A.M.; Lilinas, M.; Smith, R.A.G.; Dobson, C.M.
submitted to the Brookhaven Protein Data Bank, July 1993
A; Reference number: A51255; PDB: LKDU
A; Contents: annotation; conformation and disulfide bond assignments by (1) H-NMR. esistich, R.A.G.; Dobson, C.M.
B; Lii, X.; Smith, R.A.G.; Dobson, C.M.
B; Lii Sequential (1) H NMR assignments and secondary structure of the kringle analy, Contents: annotation; conformation and disulfide bond assignments by (1) H-NMR R; Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Ole assignments: annotation; conformation and disulfide bond assignments by (1) H-NMR A; Reference number: A66822; PDB: LUK
A; Reference number: A66822; PDB: LUK
A; Contents: annotation; conformation and disulfide bond assignments by (1) H-NMR A; Contents: annotation; C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobso C.R. Submitted to the Brookhaven Protein Data Bank, July 1995
A; Reference number: A66058; PDB: LLMM
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Fig. 1-62/Domain: BGF homology vEGFs.
Fig. 1-62/Domain: Kringle homology vEGFs.
Fig. 1-61/Domain: Kringle homology vEGFs.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status experimely.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status experimely.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status experiments.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status experiments.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status predicted.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status predicted.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status predicted.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status predicted.
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Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status predicted.
Fig. 1-61/Product: urokinase-type plasminogen activator chain B #status predicted.
Fig. 1-61/Producted activator chain B #status predicted.
Fig
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C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; kringle; serinc
C;Keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; kringle; serinc
C;Keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; kringle; serinc
F;1-20/Domain: signal sequence #stetus predicted <SIG>
F;21-431/Product: urokinase-type plasminogen activator; single chain form #stat
F;21-177/Product: urokinase-type plasminogen activator chain A #status experiments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 168-175; C; Comment: This enzyme is found in urine in a high molecular mass form, consist C; Comment: Urokinase-type plasminogen activator proteolytically activates plasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Reakdude: 1-433 <AND:4315; NID:438130; PIDN:CAA36200.1; PID:938131
A;Cross-references: BMEL:X51935; NID:938130; PIDN:CAA36200.1; PID:938131
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Pario cynocephalus, Papio hamadryas cynocephalus (yellow baboon) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999 C;Accession: S14687; S08651 R;Au, Y.P.T.; Wang, T.W.; Clowes, A.W. R;Au, Y.P.T.; Wang, T.W.; Clowes, A.W. A) Nucleic Acids Res. 18, 3411, 1990 A;Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type A;Reference number: S14687; WUID:90287734; PMID:2113276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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100.0%; Pred. No. 4.3e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:PLAU
A;Cross-references: GDB:119497; OMIM:191840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
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A Molecule type: protein

A Mesadacas: 188-410 < 470.

B icchem. Biophys. Res. Commun. 171, 401-406, 1990

B icchem. Biophys. Res. Commun. 171, 401-406, 1990

A Title: Carbohydrate composition and presence of a fucose-protein linkage in recombinar Aprille: Carbohydrate composition and presence of a fucose-protein linkage in recombinar Aprecession: A35689

A Accession: A35689

A Accession: A35689

A MUD: 90365737; PMID: 2393398

A Molecule type: protein

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A;Reidues: 156-176;179-193,'T',195,'T',197-224 <SCH>
A;Residues: 156-176;179-193,'T',195,'T',197-224 CCH>
R;Steffens, G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
A;Title: The complete amino acid sequence of low molecular mass urokinase from human uri
A;Reference number: A37564, MUID:83055099; PMID:6754572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Mesidues: 1-213, /1', 215-431 cNAG2>
A; Residues: 1-213, /1', 215-431 cNAG2>
A; Residues: 1-213, /1', 215-431 cNAG2>
A; Cross-references: GB: K03226; NID: 9340155; PIDN: AAC97138.1; PID: 9340158; GB: D00244; NID R; Verde, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Blasi, F.
F. Verde, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Blasi, F.
F. Verde, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Blasi, F.
A; Verde, P.; Stoppelli, M.S.A. 81, 47274731, 1984
A; Title: Identification and primary sequence of an unspliced human urokinase poly(A) + RN
A; Reference number: A37561; MUID: 84272706; PMID: 6589620
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A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of human prep
A;Reference number: 138102; MUID:85203359; PMID:3888571
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A; Residues: 1-150, W'.152-213, 'I',215-385,'C',387-429,'V',431 <JAC>
A; Residues: 1-150, W'.152-213,'I',215-385,'C',387-429,'V',431 <JAC>
B; R; Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, Biochims: Biochims: A 3-89, 1996
Biochim: Biophyse. Acta 1293, 83-89, 1996
A; Title: Characterization of single chain urckinase-type plasminogen activator with a nd
A; Reference number: S65783; MUID:96186279; PMID:8652631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 66-431 <VER>
A;Residues: 66-431 <VER>
A;Cross_references: GB:D00244; NID:g220138
A;Cross_references: GB:D00244; NID:g220138
R;Jacobs, P.; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana, P.; van Elsen,
              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 145-161 <NAG1>
A;Residues: 145-161 <NAG1>
A;Cross-references: GB:K03027; NID:g340174; PIDN:AAA61257.1; PID:g340175
K;Nogai, M.; Hiramatsu, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama, Gene 36, 183-188, 1985
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A;Residues: 21-177 <GUN>
R;Schaller, J.; Nick, H.; Rickli, E.E.; Gillessen, D.; Lergier, W.; Studer, R.O.
Bur, J. Biochem. 125, 251-257, 1982
A;Title: Human low-molecular-weight urinary urokinase. Partial characterization and ;
A;Reference number: A37563; MUID:83003608; PMID:6749491
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A; Residues: 21-140, 'L', 142-213,'I', 215-431 < YOS>
A; Cross-references: EMBL: D1143; NID: 91311467; PIDN: BAA01919.1; PID: 9119928
A; Gunzler, W.A.; Steffens, G.J.; Otting, P.; Kim, S.M.A.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1155-1165, 1982
A; Title: The primary structure of high molecular mass urokinase from human urine.
A; Reference number: A37562; MUID: 83055084; PMID: 6754569
                                                                                                                                                                                                                                                                                                                                                             Gene 36, 183-188, 1985
A,Filtle: Molecular cloning of cDNA coding for human preprourckinase.
A,Reference number: JT0102; MUID:86056954; PMID:2415429
A;Accession: JT0102
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GenCore version 5.1.6
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- protein search, using sw model OM protein

May 25, 2004, 14:47:10 ; Search time 5.09027 Seconds (without alignments) 1662.947 Million cell updates/sec Run on:

US-09-880-503-1 510 1 KTCYEGNGHFYRGKASTDTM.....QVGLKPLVQECMVHDCADGK score: Title: Perfect :

Sequence:

88

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	u-plasminogen acti		u-plasminogen acti	u-plasminogen acti	u-plasminogen acti		t-plasminogen acti	plasma hyaluronan-	u-plasminogen acti	plasma hyaluronan-	hepatocyte growth	coagulation factor	coagulation factor	apolipoprotein(a)	plasmin (EC 3.4.21	apoprotein(a) (EC	coagulation factor	(EC 3.4	(EC 3.4	plasmin (EC 3.4.21	-								
SUMMERIES	ID	UKHU	UKBAY	UKPG	818932	JN0560	UKMS	JS0599	A34369	JS0598	I38098	UKHUT	A35029	JS0600	A29941	JS0597	JC5878	A35005	JC4795	A46688	S28941	KFHU12	A32869	E61545	800657	S45281	A60140	C61545	A40522	PLBO
	DB	-	Н	Н	н	Н	н	N	Н	ď	N	н	Н	7	H	N	~	н	н	Н	7	Н	7	N	H	N	~	N	~	Н
	Length	431	433	442	432	433	433	431	477	477	291	562	559	394	559	47,7	558	434	560	655	603	615	1420	120	4548	593	89	N	169	н
%	Query Match	100.0	93.1	82.4	ø	77.6	75.9	•	47.3	47.3		44.3	44.1	43.1	42.9	41.8	41.1	38.9	37.9	37.8	35.4	33.4	31.6	30.6	30.6		30.0	29.4	29.3	29.5
	Score		475	420	406	396	387	241	241	241	226	226	225	220	219	213	209.5	198.5	193.5	193	180.5	170.5	161	156	156	155.5	153	150	149.5	149
	Result No.		7	m	4	W	φ	7	Φ	o	10	11	12	13	14	15	16	17	18	19									28	29

3.4. 3.4. 3.4. 2 rec 3.4. 3.4. 3.4.	billo ree: BC 3.44. BC 3	hypothetical proce hypothetical proce extracellular matr hypothetical prote 1,4-dichlorophenol hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote proponent sens two-component sens type II site-speci probable phage pro pectinesterase (SC probable pectinest 3-methylcrotonyl-C 3-methylcrotonyl-C 3-methylcrotonyl-C
	A48289 A60185 A50185 A35644 A35644 A401549 T181285 A40332 A40332 B1MS S33879 C15061 T181283 A55827 T1810 A77299 S10511 T15448	AF2444 AF2444 AF2444 T155094 T155094 T130723 T130723 T147974 T147974 AF2268 AB4130 AB4130 AB4130 AB4130 AB6229 T102184 AB6299 T00260
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564; 7 sminog in form
Cippecies; Homo sapiens (man)
Ciptes: 17-Dec-1982 #sequence revision 04-Dec-1986 #text change 15-Sep-2000
Ciptes: 17-Dec-1982 #sequence revision 04-Dec-1986 #text change 15-Sep-2000
Ciptes: 17-Dec-1982 #sequence revision 04-Dec-1986 #text change 15-Sep-2000
Ciptes: 17-Dec-1982 #sequence revision 04-Dec-1986 #syriates: A37562; A37563; A 564; R; Riccio, A., Grimaldid, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.
Nucleic Acids Res. 13, 2759-2771, 1985
A;Title: The human urokinase-plasminogen activator gene and its promoter.
A;Accession: A00931; MUID:85215647; PMID:2987867
A;Accession: A00931; MUID:85215647; PMID:2987867
A;Accession: A00931
A;Molecule type: DNA
A;Residues: 14-431 extra Commun.
A;Accession: A00931; MUID:85215647; PMID:2987867
A;Accession: A00931; MUID:85215647; PMID:3933505
A;Title: Exon-intron boundary Bilding in the generation of two mRNAs coding fc porc A;Reference number: 152209; MUID:86050639; PMID:3933505 RESULT 1 UKHU UPHO 19 Jesminogen activator (EC 3.4.21.73) precursor [validated] - human N'Alternate names: cellular plasminogen activator; urokinase; urokinase-type p N'Contains: urokinase-type plasminogen activator chain A; urokinase-type plasm

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plasmin (EC 3.4.21.7) precursor - chicken (fragment)
N;Alternate names: plasminogen
C;Species: Gallus gallus (chicken)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                           4122 RQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTM-----NYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TCYE - GNGHFYRGKASTDTMGRPCLPWNSATVLQQTY - HAHRSDALQLGLGKHNYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 SCYDDRDRGLSYRGWAGTTLSGAPCQSWAS----EATYWNVTAEQVLNWGLGDHAFCRNP
                                                                                                                                                                                                                                                                           1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATV--LQQTYHAHRSDALQLGLGKHNYCRNP
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                      Length 4548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
30.5%; Score 155.5; DB 2; Length Sest Local Similarity 38.4%; Pred. No. 3.3e-09;
Matches 33; Conservative 9; Mismatches 37; Indels
                                                                                                                                                                               Query Match
30.6%; Score 156; DB 1; Length 45.
Best Local Similarity 37.8%; Pred. No. 2e-08;
Matches 34; Conservative 12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                        177 DADIGPWCFT---MDPSIRWEYCNLTRCSD 4203
                                                                                                                                                                                                                                                                                                                                                                   59 DNRRRPWCYVQVGLKPLV--OECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | | | : | : | : | : | DNDTRPWCFIWKGDRLSWNYCRLAPC 287
                     F;3782-3859/Domain: kringle homology <KR34>
F;386-3973/Domain: kringle homology <KR35>
F;4010-4087/Domain: kringle homology <KR36>
F;4224-4201/Domain: kringle homology <KR37>
F;4228-4307/Domain: kringle homology <KR37>
F;4228-451/Domain: trypsin homology <TR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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Proc. AMEL. Acad. Scil. 18. Angusti. 19. Bruno. L.; Pontoglio, M.; Rocchi. M.; Sacco. ARTISE Characterization by Yests attiticial Discoses cloning of the linked apolipope Arcession and Scil. Acad. Scil. 19. Angusti. 19. Angust
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plasmin (EC 3.4.21.7) precursor - bovine
plasmin (EC 3.4.21.7) precursor - bovine
NyAlternate names: plasminogen
() forcise to be primagenius teurus (cattle)
() forcise to be primagenius teurus (cattle)
() late: 30-8ep-1987 #sequence revision 28-Apr-1995 #text_change 18-Jun-1999
() Accession: $45046; A25835; T4561; S03736
() RyBerglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A; Description: Cloning and characterizatin of the bovine plasminogen cDNA:
A; Accession: $45046
A; Molecule type: mRNA
A; Residues: 17812 -6BEA
A; Molecule type: mRNA
A; Residues: 1812 -6BEA
A; Molecule to the EMBL: X79402; NID: 9494962; PIDN: CAA55939.1; PID: 9494963
A; Residues: 1 late and the matter of the metal of the initiator
A; Molecule to the manager muller, G.A.K.; Rosselet, S.J.; Kampfer Office it is uncertain whether Met-1 or Met-8 is the initiator
A; Molecule to manager muller, G.A.K.; Rosselet, S.J.; Kampfer D.; A; Rochem. 19, 267-278, 1985
A; Mittle: Complete amino acid sequence of bovine plasminogen. Comparison with R. A; Reference number: A25835; MUID: 95203906; PMID: 3846532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: translated from GB/EMBL/DDBJ
A; Rolecule type: mRNA
A; Residues: for 743, "R, 745.812 < MAL>
A; Residues: 706-743, "R, 745.812 < MAL>
A; Residues: 706-743, "R, 745.812 < MAL>
B; Residues: 706-743, "R, 745.812 < MAL>
A; Cross-references: GB: KO2935; NID: 9163551; PIDN: AAA30714.1; PID: 9163552
B; Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, B.E.; Lergier, W.; Mann.
Bur, J. Blochem: 114, 465-470, 1981
Bur, J. Blochem: 114, 465-470, 1981
A; Title: Comparison of the primary structure of the N-terminal CNBr fragments
A; Reference number: S03735; MUID: 91212097; PMID: 7238497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c, guperfamily: plasmin, kringle homology; plasminogen-related protein precurse c, Superfamily: plasmin, fibrinolysis; glycoprotein; hydrolase; kidney; kringle; ksywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; 1-26/Domain: signal sequence #status predicted <s104 | Signal sequence #status experiments of property homology <PLPH> P; 27-812/Product: plasminogen-related protein precursor homology <PLPH> P; 27-103/Domain: activation peptide #status experimental <PRO> P; 27-103/Domain: activation peptide #status experimental <ART> P; 104-583,584-812/Product: plasmin #status experimental <ART> P; 104-583/Domain: kringle homology <RR1>
A;Cross-references: GB:MG2832; NID:g206215; PIDN:AAA1884.1; PID:g554488
A;Note: the authors translated the codon TCT for residue 76 as Ala
C;Superfamily: plasmin; kringle homology, plasminogen-related protein precurso:
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;34-112/Domain: kringle homology «KRG»
F;34-112,55-95,83-107/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Description: dissolves the fibrin of blood clots; acts as a proteolytic fact ns the walls of the graafian follicle; also activates the urokinase-type plasm A, Pathway: fibrinolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
R; Mallinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 424-4250, 1984
A; Title: Characterization of a complementary deoxyribonucleic acid coding for A; Reference number: 145961; MUID: 85023311; PMID: 6148961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 CYQGNGKSYRGISSTINIGKKQSW----VSMIPHSHSKIPANFPDSGL-EMNYCRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYEGNGHEYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQL---GLGKHNYCRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                        29; Indels
                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                ; Score 149.5; DB 2
; Pred. No. 4.6e-09;
12; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :| |||:
| NDQRGPWCFT---TDPSVRWEYCNLKRCSE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 N-RRRPWCYVQVGLKPLV--QECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                              29.3%;
37.8%;
                                                                                                                                                                                                                                                                                                                                     Query Match
Bert Local Similarity 37.84
Matches 34; Conservative
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plasmin (EC 3.4.21.7) precursor - goat (fragments)

NyAlternate names: plasminogen

C; place: 28-oct-1994 #sequence_revision 28-oct-1994 #text_change 12-May-1995

C; pate: 28-oct-1994 #sequence_revision 28-oct-1994 #text_change 12-May-1995

R; pate line for a page cts of the plasminogen of various species

A; pate not number: A61545; MulD:89005015; PMID:3168975

A; pate not number: A61545; MulD:89005015; PMID:3168975

A; pate not number: A61545; MulD:89005015; PMID:3168975

C; pate not number: A61545; MulD:89005015; PMID:3168975

C; pate number: A61545; MulD:89005015; PMID:3168975

A; pate number: A61545; PMID:3168975

A;
                   C;Accession: A60140
Biochim. Biophys. Acta 832, 326-330, 1985
Biochim. Biophys. Acta 832, 326-330, 1985
A;Title: The kringle 4 domain of chicken plasminogen.
A;Title: The kringle 4 domain of chicken plasminogen.
A;Reference number: A60140; MUD: 86077796; PMID: 4074753
A;Reference number: A60140
A;Molecule type: protein
A;Residues: 1-89 GYEs
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F;6-30,70main: kringle homology < kRGs
F;6-30,27-66,55-78/Disulfide bonds: #status predicted
F;9-83,77-66,55-78/Disulfide bonds: #status predicted
F;39/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLG--KHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYQGNGVSYRGTASFIIIGKKCQAWNS-----MSPHRHNKTESHFPNADLRQNYCRNPDA 60
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Closedes: Rattus norvegicus (Norway rat)
Cloate: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
Cloates 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
Cloates and A6522
July Biol Chem 266 10825-10829, 1991
A,Title: Identification of the rat Heymann nephritis autoantigen (GP330) as A,Reference number: A40522
A,Reference number: A40522
A,Status: preliminary
A,Nolecule type: MRNA
A,Nolecule type: MRNA
A,Nolecule type: MRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 153; DB 2; Length 89;
Pred. No. 1e-09;
7; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 DKSPWCYT---TDPRVRWEFCNLKKCSE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RRRPWCYVQVGLKPLV -- QECMVHDCAD
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Best Local Similarity 38.6%;
Matches 34; Conservative
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Matches 33
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Query Match
Best Local Similarity 44.1%
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                                                                                                                          protein precursor homology
A,Accession: $28200
A,Accession: $28200
A,Molecule type: protein
A,Residues: 118-460 <502>
C,Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C,Superfamily: plasmin; kringle homology; plasminogen fragments experimental cPRO>
F,1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental cAPT>
F,1-37,Domain: activation peptide (fragment) #status experimental cAPT>
F,18-117,118-30,231-460/Product: plasmin (fragments) #status experimental cAPT>
F,118-460/Product: miniplasminogen #status experimental cAIN>
F,118-460/Product: miniplasminogen #status experimental cBCH>
F,125-460/Domain: kringle homology cRRS>
F,226-460/Domain: kringle homology cRRS>
F,231-453/Domain: blasmin chain B #status experimental cBCH>
F,231-453/Domain: trypsin homology cRRY>
F,231-453/Domain: blasmin chain B #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine kinase-like domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYEGNGHFYRGKASTDTMGRPCLPWNSATV--LQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurotrophic receptor ror2 precursor - human
N;Contains: protein-tyrosine Kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYNGSGMDYRGTASTTKSGHOCOPW--ALQHPHSHHLSSTDFPELG-GGHAYCRNPGGQM
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A,Residues: 1-943 <MAS>
A,Residues: 1-943 <MAS>
A,Cross-references: GB:M97639; NID:g337466; PIDN:AAA60276.1; PID:g337467
A,Note: sequence extracted from NCBI backbone (NCBIP:120918)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.9%; Score 147.5; DB 2; Length ilarity 43.3%; Pred. No. 2e-08; Conservative 8; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: B45082
R;Masiakowski, P:; Carroll, R.D.
J; Biol. Chem. 267, 26181-26190, 1992
A;Title: A novel family of cell surface receptors with the Reference number: A45082; MUID:93100347; PMID:1334494
A;Accession: B45082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGPWCFTQ-NKNVRMELCDVPSCS 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRRPWCY 67
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Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
Matches 29; Conserv
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gy; pi ; tyrc ie in .; 25; plasmin (EC 3.4.21.7) precursor [validated] - human N;Alternate names: plasminogen precursor [misnomer] N;Contains: angiosteratin; microplasmin; plasminogen C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000 C;Accession: A52229; 15224-7,A5666; 162738; 184609; 803735; A00929; A04627; A(25; R;Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W. J. Biol. Chem. 265, 6104-6111, 1990 A;Accession: A35229 Auroracterization of the gene for human plasminogen, a key proenzyme i: A;Reference number: A35229; MUD: 90202879; PMID: 318848 A;Residues: 1-810 <PET-A;Residues: 1-810 <PET-A;Residues: Unit of the gene for human plasminogen, a key proenzyme i: A;Residues: 1-810 <PET-A;Residues: 1-810 <PET C. Jacesion: A45082
R. Jacession: A45082
A. Title: A novel family of cell surface receptors with tyrosine kinase-like dom. 1. A15082
A. Jacession: A45082
A. Jacession: A45082
A. Molecule type: mRNA
A. Jacession: Barranta
A. Jacession: A15082
A. Jace ņ ÷ ç 'n 9 A;Cross_references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g53613
R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FBBS Lett. 213, 254-260, 1887
A;Title: Molecular cloning and characterization of a full-length cDNA clone.
A;Reference number: A26646; MUID:87162490; PMID:3030813 neurotrophic receptor rorl precursor - human Noontains: protein-tyrosine kinase (EC 2.7.1.112) C.Species: Homo sapiens (man) C.Pote: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000 3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLG--LGKHNYCRNPDN Gaps .. 6 Length 937 28.6%; Score 146; DB 2; Length 93 44.1%; Pred. No. 5.6e-08; tive 5; Mismatches 25; Indels

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                                                                                                                   A,Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison A,Reference number: S03733
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NyAlternate names: plasminogen
NyContains: miniplasminogen
NyContains: miniplasminogen
Cypecies: Ovis orientalls aries, Ovis ammon aries (domestic sheep)
Cypecies: Ovis orientalls aries, Ovis ammon aries (domestic sheep)
Cypecies: Ovis orientalls aries, Ovis ammon aries (domestic sheep)
Cypecies: Ovis orientalls aries, Ovis ammon aries (domestic sheep)
Cypecies: Ovis orientalls aries, Ovis ammon aries (domestic sheep)
Cypecies: Ovis orientalls aries, Ovis ammon aries (domestic sheep)
Cypecies: Ovis orientalls aries, Ovis ammon aries (domestic sheep)
Cypecies (domestic sheep)
Cypecies: Ovis orientalls
Cypecies (domestic sheep)
Cypecies
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A;Residues: 1-37;38-117 <SCH>
R;Schaller, J; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A;Title: Complete amino acid sequence of ovine miniplasminogen.
A;Reference number: S28200; MUID:93149995; PMID:1492092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
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29.0%; Score 148; DB 1;
Best Local Similarity 38.2%; Pred. No. 2.9e-08;
Matches 34; Conservative 8; Mismatches 33.
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F;192-269/Domain: kringle homology F;282-369/Domain: kringle homology F;282-369/Domain: kringle homology F;284-461/Domain: kringle homology F;384-461/Domain: kringle homology F;485-564/Domain: kringle homology F;584-812/Domain: kringle homology F;584-812/Domain: trypsin homology F;584-80;60-68;110-188131-171,159-183;192-269;195-323,213-252,241-264,282-359,303-342,33
bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: Brinaceus europaeus (western European hedgehog)
C;Accession: 146260
E;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
A;Reference number: 146259; MUID:96025778; PMID:7592597
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C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology <PLPH>
F:1-56/Domain: plasminogen-related protein precursor homology <PLPH>
F:103-181/Domain: kringle homology <KR2>
F:185-262/Domain: kringle homology <KR3>
F:275-352/Domain: kringle homology <KR3>
F:379-456/Domain: kringle homology <KR3>
F:379-456/Domain: kringle homology <KR3>
F:482-561/Domain: kringle homology <KR3>
F:582-803/Domain: kringle homology <KR3>
F:582-803/Domain: kringle homology <KR3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 CYHGNGQSYRGTSSTTITGRKCQSWSS-----MTPHRHLKTPRNYPNAGL-TWNYCRNPD 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:||| || || || || 379 CYQGNOQTYRGTSSTTITGKKCQPWTSMRPHRHSKTPENYPDADLTM---NYCRNPDGDK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmin (EC 3.4.21.7) precursor - pig (fragment)
NyAlternate names: plasminogen
NyContains: miniplasminogen
NyContains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03737; A25834
F;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAH---RSDALQLGLGKHNYCRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                    F.315/Binding site: carbohydrate (Asn) (covalent) #status experimental F.35/Binding site: carbohydrate (Ser) (covalent) #status experimental F.524,667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
29.2%; Score 149; DB 1; Length 812;
Best Local Similarity 39.3%; Pred. No. 2.3e-08;
Matches 35; Conservative 8; Mismatches 32; Indels 1
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29.1%; Score 148.5; DB 2; Length Best Local Similarity 41.5%; Pred. No. 2.6e-08;
Matches 27; Conservative 7; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-810 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 ADKSPWCYT---TDPRVRWEFCNLKKCSE 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 NRRRPWCYVQVGLKPLV--QECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 GPWCY 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: 146260
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N. Chen. C. 131, R.W. 131, S.W. 130, S.W. 130, S.W. 131, S.W. 131, S.W. 131, S.W. 131, S.W. 130, S.W. 131, S.W. 130, S.W. 131, S.W. 130, S.W. 131, S.W. 131,
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A; Residues: 483-507, 'E', 509-604 < W13>
A; Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen. II. The histidine loop of human plasminogen. II. The histidine loop of human plasminogen as Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A; Title: Studies on the active center of human plasmin. Partial amino acid sequence of a A; Reference number: A92048; MID: 62234739; PMID: 4240117
A; Contents: annotation; active site
A; Texaler. M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A; Title: Structure of the onega-aminocarboxylic acid binding sites
A; Reference number: A92382; MUID: 82213905; PMID: 6919539
A; Contents: annotation; omega-aminocarboxylic acid binding sites
A; Reference number: A9288; MID: 65054994; PMID: 6094526
A; Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential A; Reference number: A92458; MID: 65054994; PMID: 6094526
A; Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
                                  A/Residues: 1-471. DZ/A/A-810 <FORD-A/Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531

A/Experimental source: 11ve.
A/Experimental source: 11ve.
B/Experimental source: 12ve.
B/Experimental source: 1
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A; Molecule type: protein
A; Residues: 20-71, E', 73-85,87-106, 'D', 108-360, 'E', 362-810 <SOT>
A; Molecule type: protein
A; Residues: 20-71, 'E', 73-85,87-106, 'D', 108-360, 'E', 362-810 <SOT>
Bur. J. Biochem. 76, 129-137, 1977
A; Title: Primary structure of the B-chain of human plasmin.
A; Reference number: A04627; MUID: 77225245; PMID: 142009
A; Accession: A04627
A; Rollente type: protein
A; Rollente type: protein
A; Residues: 581-810 <WIL>
B; Wallen, P.
Bur. J. Blochem. 50, 489-494, 1975
A; Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla
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A;Accession: A04625
A;Accession: A04625
A;Accession: A04625
A;Accession: Drotein
A;Residues: 20-50, '0,'51-71,'E',73-85,87-100 <WI2>
R;Wiman, B.; Wallen, P.
Eur. J. Blochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha A;Reference number: A04626; MUID:76043692; PMID:126863
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287 SRPWCY----SKPMGQEBYCDVPQC 307
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Best Local S
Matches 30
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                                        요
                         c; Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af c; Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor, C; Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial cond c; Comment: Stromelysin I (see PIR:KCHUSI) acts on plasminogen to produce angiostatin. TC cleanetics:

C; Gametics:
A; Gane: GDB:PLG
A; Map position: 6q26-6q27
A; Map position: 6q26-6q27
A; Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529 C; Function:
C; Function:
A; Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vant the walls of the graafian fellicle; also activates the urokinase-type plasminogen act A; Pathway: fibrinolysis inhibitor; blood; duplication; fibrinolysis; glycoprotein; by the pathway: fibrinolysis inhibitor; blood; duplication; fibrinolysis; glycoprotein; by the provate; anglogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; by the provate; plasminogen related protein precursor homology c; Keywords: anglogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr F; 1-96/Domain: signal sequence #status experimental cRA>
F; 1-19/Oomain: activation peptide #status experimental cRA>
F; 1-19/Oomain: activation peptide #status experimental cRA>
F; 1-19/Oomain: kringle homology cRR2>
F; 10-19/Domain: kringle homology cRR2>
F; 10-19/Domain: kringle homology cRR3>
F; 10-19/Domain: kringle homology cRR3>
F; 10-10/Domain: kringle homology cRR3>
F; 10-10/Domai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 CYHGDGQSYRGTSSTTTTGKKCQSWSS-----MTPHRHQKTPENYPNAGL-TMNYCRNPD 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein COIG6.8 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
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R; Berris, M.
submitted to the EMBL Data Library, August 1994
A; Reference number: 219029
A; Accession: T18840
A; Status: preliminary; translated from GB/EMBL/DDBU
A; Status: 1-806 < WILL
A; Cross-references: EMBL: 235595; PIDN: CAA84639.1; GSPDI
A; Experimental source: clone C0166
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A;Introns: 36/3; 170/3; 217/3; 636/3; 760/1
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A, Residues: 1-12, C', 14-622, 'F', 624-711 < YOS>
A, Cross-references: GB:L11924; NID:9398037; PIDN:AAA59872.1; PID:9398038
A, Cross-references: GB:L11924; NID:9398037; PIDN:AAA59872.1; PID:9398038
A, Motors authors translated the codon TTT for residue 623 as Leu; parts of this R, Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, B.; Leonard, J. Exp. Med. 173, 1227-1234, 1991
A, Title: Macrophage stimulating protein: purification, partial amino acid seque A, Reference number: A61395; MUID:91217635; PMID:1827141
A, Molecule type: protein
A, Residues: 230-247;288-291, E', 293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-3 A, Experimental source: plasma
C, Genetics:
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A; Cross-references: GDB::128833; OMIM::142408
A; Map position: 3521-3521.3
C; Complex: disulfide-bonded heterodimer of chains derived from the same precuiry position: 3521-3521.3
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology C; Superfamily: hepatocyte growth factor; kringle; plasma F; 1-18 Domain: signal sequence #status predicted <SIG> F; 1-8 Domain: signal sequence #status predicted <SIG> F; 1-8 SID Domain: signal sequence #status predicted <ACH> F; 110-186 Domain: kringle homology <KR2> F; 110-186 Domain: kringle homology <KR2> F; 370-448 Domain: kringle homology <KR3> F; 370-448 Domain: kringle homology <KR3> F; 370-448 Domain: kringle homology <KR3> F; 370-448 Domain: bringle homology <KR3> F; 370-448 Domain: kringle homology <KR3> F; 370-448 Domain: bringle homology <KR3> F; 370-448 Domain: bringle homology of KR4> F; 370-448 Domain: bringle homology of
                                              Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 103-May-1994 #sequence revision 14-Nov-1997 #text_change 18-Jun-1999
Ciscession: A40331; B40315; A61395
Rihan, S.; Stuart, L.A.; Degen, S.J.F.
Biochemistry 30, 9768-9780, 1991
A;Title: Characterization of the DNF1582 locus on human chromosome 3: identification of the DNF1582 locus on human chromosome 3: identifications. A40331; MUID:92002016; PMID:1655021
A;Reference number: A40331; MUID:92002016; PMID:1655021
A;Residues: 1-711 cHAl>
A;Residues: 1-711 cHAl>
A;Residues: GB:M74179
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F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343
F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Residues: 1-711 <HAZ
A,Cross-references: GB:M74178; NID:g183976; PIDN:AAAS0165.1; PID:g183977
R,Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
J, Biol. Chem. 268, 15461-15468, 1993
A,Reference number: A47136; MUID:93340141; PMID:8393443
A,Recession: A47136.
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33.3%; Pred. No. 1e-07;
cive 13; Mismatches 34; Indels
macrophage-stimulating protein 1 precursor - human
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A, Reference number: 148758; MUID:95122532; PMID:7822318
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A;Title: Purification and characterization of biologically active scatter fact. A;Reference number: $17173; MUID:91354223; PMID:1831975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein A;RX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377 A;Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377 R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R. Biochim. Biophys. Acta 1216, 299-303, 1993 A;Title: Molecular cloning and characterization of cDNA encoding mouse hepatoc: A;Reference number: S43416; MUID:94060105; PMID:8241272
                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatocyte growth factor precursor - mouse
NiAlternate names: hepapoietin A; scatter factor
C;Specias: Mus musculus (house mouse)
C;Specias: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence revision 26-May-1994 #text change 16-Jun-2000
C;Accession: JC2117; PC2064; Ā60185; S43416; S45521; S17<u>1</u>73; S10966; I48758; JR;Saaski, M.; Nishio, M.; Saaski, T.; Enami, J.
Biochem. Biophys: Res: Commun. 199, 772-779; 1994
A;Title: Identification of mouse mammary fibroblast-derived mammary growth fac A;Reference number: JC2117; MUID:94183257; PMID:8135822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 436-504 <SA2>
R;Rosen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990
A;Title: Purified scatter factor stimulates epithelial and vascular endothelia
A;Reference number: A60185; MUID:90377927; PMID:2144630
35 BNCYWEDGSTYRGVANVSASGKPCLRW--SWLMKEI----SDFPEL-1GQ-NYCRNPGS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: GB:D10212; NID:9220435; PIDN:BA01064.1; PID:9220436
A;Experimental source: fibroblast, COS-1 cell
A;Note: submitted to JIPID, May 1993
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A;Molecule type: protein
A;Residues: 496-507, /x',509-512, 'L',514-516,'X',518-519 <NAT>
A;Residues: 496-507, /x',509-512, 'L',514-516,'X',518-519 <NAT>
B;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, B.; Birchmeier, J. Biol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth
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A;Residues: 496-517, T',519 <COF>
R;Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A;Title: Hepatocytes and scatter factor.
A;Reference number: $10966; MUID:90326152; PMID:2142751
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A,Reference number: 845521
A,Accession: 67521
A,Status: preliminary
A,Modecule type: mRA, 856-728 <LI2>
A,Residues: 1-563, MY, 565-728 <LI2>
A,Residues: 1-563, MY, 565-728 <LI
                                                                                                                                           86
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A,Residues: 1-728 <LIU>
A,Cross-references: EMBL:X72307
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A;Residues: 1-728 <SAS2>
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A;Status: preliminary
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-810 c.TOM>
A;Residues: 1-810 c.TOM>
A;Residues: 1-810 c.TOM>
A;Residues: 1-810 c.TOM>
A;Cross-references: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Stuperfamily: plasmin; Kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; Kringle; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology cRD:
F;1-95/Domain: kringle homology cRR1>
F;103-181/Domain: kringle homology cRR3>
F;275-352/Domain: kringle homology cRR3>
F;377-454/Domain: kringle homology cRR4>
F;310-454/Domain: kringle homology cRR5>
F;381-803/Domain: kringle homology c
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C;Superfamily: Drosophilan neurotrophic receptor ror; kringle homology; protein kinase hc
C;Superfamily: Drosophilan neurotrophic receptor ror; kringle homology; protein; tyros
C;Keywords: ATP; glycoprotein; kringle homology «KRG»
F;237-310/Domain: kringle homology «KRG»
F;314-338/Domain: transmembrane #status predicted «TMI»
F;468-677/Domain: protein kinase homology «KIG»
F;468-6424/Region: protein kinase APP-binding motif
F;45,63,129,144,250/Binding site: carbohydrate (ABn) (covalent) #status predicted
                   C.Species: Macaca mulatta (rheeus macaque)
C.Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C.Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C.Accession: 32869; B30848
B.Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A.Title: Rheeus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis. A; Reference number: A32869; MUID:89174660; PMID:2925643
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NyContains: protein: tyrosine kinase (EC 2.7.1.112)
CyBecies: Drosophila melanogaster
NyMilson, C.; Goberdhan, D.C.I.; Steller, H.
RyMilson, C.; Goberdhan, D.C.I.; Steller, H.
RyMilson, C.; Goberdhan, D.C.I.; Steller, H.
And. Sci. U.S.A. 90, 7109-7113, 1993
AyTitle: Dror, a potential neurotrophic receptor gene, encodes a Drosophila
AyReference number: A48289; MUID:93348222; PMID:8394009
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A,Residues: 1-685 <WIL>
A;Cross-references: GB:L20297; NID:g348103; PIDN:AAA28860.1; PID:g348104
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         - rhesus
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Best Local Similarity 34.54
Matches 30, Conservative
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les 33; Conservative
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Matches
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A;Status: preliminary; translated from GB/EMBL/DDBJ

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KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN

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APISAS
PAISAS
PASSANTA (EC 3.4.21.7) precursor - horse (fragments)
N'Alternate names: plasminogen
N'Scherins: miniplasminogen
C'Species: Equus caballus (domestic horse)
C'Species: Equus caballus (domestic horse)
C'Species: Equus caballus (domestic horse)
C'Accession: A61545, 817527
Exymeter (a.6. 6.6.6.) 1988
A.Title: Structural aspects of the plasminogen of various species.
Brizyme (40, 63.6.6), 1988
A.Title: Structural aspects of the plasminogen of various species.
A.Reference number: A61545, MUID: 89005015; PMID: 3168975
A.Residues: 1.33,34-117, SCH>
A.Residues: 1.33,34-117, SCH>
A.Residues: 1.33,34-117, SCH>
A.Residues: 1.33,34-117, NUID: 92052077; PMID: 1946332
A.Accession: A1527
A.A
F,392-470/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: trypsin homology <TRY>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status F;295,403,569,656/Binding site: carboxydrate (Asn) (covalent) #status predicte. F;498-607/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CYEGNGHFYRGKASTDIMGRPCLPWNSATV--LQCTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYEGNGHPYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLG----KHNYCRNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 43
JH0579
JH0579
Nepatocyte growth factor precursor [validated] - human
N.Alternate names: hepapoietin A; scatter factor
C;Species: Homo sapiens (man)
C;Species: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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llarity 34.1%; Pred. No. 5.8e-07;
Conservative 13; Mismatches 33; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      07;
36; Indels
                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
26.6%; Score 135.5; DB 3
Best Local Similarity 32.0%; Pred. No. 6.2e-07,
Matches 31; Conservative 11; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 DKGPWCYT---TDPSVRWEFCNLRKCSE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 30; Conserv
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Specification: stimulates mitosis of hepatocytes and other cells

A; Description: stimulates mitosis of hepatocytes and other cells

A; Description: stimulates mitosis of hepatocytes and other cells

A; Description: stimulates mitosis of hepatocytes and other cells

C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology

C; Reywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyrections also predicted slGs

F; 3-22 Domain: signal sequence #status predicted slGs

F; 5-495, 495, 496-728 Promain: hepatocyte growth factor #status predicted slGs

F; 129-289 Domain: kringle homology skR1>

F; 106-384 Domain: kringle homology skR2>

F; 106-384 Domain: kringle homology skR3>

F; 106-384 Domain: kringle homology skR4>

F; 106-384 Do
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A35644

Mactor precursor - rat

MyAlternate names: hepapoietin A; scatter factor

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: Sa.Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000

C;Accession: A35644; S13211

R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamur

R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamur

R;Tatlle: Deduced Sci. US.A. 87, 3200-3204, 1890

A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of the A;Reference number: A35644; MUID:90222197; PMID:2139229
A,Molecule type: DNA
A,Residues: 1-30 ARES.
A,Cross-references: EMBL:X81630; NID:g673451; PIDN:CAA57286.1; PID:g673452
C,Complex: disulfide-bonded heterodimer of chains derived from the same precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 CIQGQGEGYRGTSNTIWNGIPCQRWDS-----QYPHKHDITPENFKCKDLRENYCRNP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 DNRRRPWCY----VQVGLKPLVQECMV---HDCADG 87
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Best Local Similarity 32.0%
Matches 31, Conservative
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37-386

A; Reference number: S06794; MUID: 90066676; PMID: 2531289
A; Reference number: S06794; MUID: 90066676; PMID: 2531289
A; Rocession: S06794; MUID: 90066676; PMID: 2531289
A; Molecule type: mRNA
A; Residues: 1.31, 'HK', 34-77,'N', 79-292,'V', 294-299,'M', 301-316,'A', 318-335,'K'
A; Residues: 1.31, 'HK', 34-77,'N', 79-292,'V', 294-299,'M', 301-316,'A', 318-335,'K'
A; Residues: 1.31,'HK', 34-77,'N', 79-292,'V', 294-299,'M', 301-316,'A', 318-335,'K'
A; Residues: 1.31,'HK', 34-77,'N', 79-292,'V', 294-299,'M', 301-316,'A', 318-335,'K'
A; Note: phat of this sequence, including the amino end of both the alpha and b ich R; Hartmann, G.; Naldini, L.; Weidner, K.M., Sachs, M.; Vigna, E.; Comoglio, P.; Bi Proc. Nall. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A; Title: A functional domain in the heavy chain of scatter factor/hepatocyte g th A; Reference number: 159214; MUID: 93087571; PMID: 1280830
A; Reference number: 159214; MUID: 93087571; PMID: 1280830
A; Residues: 1-288, ET'
A; Residues: 1-288, ET'
A; Residues: 1-288, ET'
A; Residues: 1-288, ET'
A; Reference number: A; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A; Title: An alternatively processed mRNA generated from human hepatocyte growt actor A; Accession. S15443; MUID: 91200041; PMID: 1826653 A;Pescription: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily; hepatocyte growth factor; kringle homology; trypsin homology
C;Superfamily; hepatocyte growth factor; heterodimer; kr jle,
F;1-31/Domain: alternative splicing; glycoprotein; growth factor; heterodimer; kr jle,
F;22-494/Domain: algran sequence #status predicted <SIG>F;22-494/Domain: alpha chain #status experimental <ACH>F;22-494/Domain: alpha chain #status experimental <ACH>F;22-494/Domain: kringle homology <KR2>F;21-288/Domain: kringle homology <KR2>F;31-469/Domain: kringle homology <KR2>F;31-469/Domain: beta chain #status experimental <BCH>F;39-469/Domain: trypsin homology <FR2>F;39-469/Domain: trypsin homology <FR2>F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status
F;294,402,566,653/Binding site: carboxylacate (Asn) (covalent) #status predicte.
F;487-604/Disulfide bonds: #status predicted A,Accession: S15443
A,Accession: S15443
A,Accession: S15443
A,Accession: preliminary
A,Accession: breathinary
A,Accession: 1-288, 'ET' < MIY2>
A,Accession: S154, 'ET' < MIY2>
B,Accession: S154, 'ET' < MIY2>
B,Accession: S154, 'ET' < MIXAGO, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A,Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblast.
A,Reference number: 152253; MUID:92062058; PMID:1835383
A,Accession: 152253
A,Accession: 152553
A,Ac CIQGQGGGYRGTVWTIWNGIPCQRWDS-----QYPHBHDMTPENFKCKDLRENYCRNPDG 359 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH--RSDALQLGLGKHNYCRNPDN A;Gene: GDB:HGF A;Cross.references: GDB:127524; OMIM:142409 A;Map position: 7q21.1-7q21.1 A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; C;Complex: disulfide-bonded heterodimer of chains derived from the same C;Function: Length 728; Indels Query Match 26.2%; Score 133.5; DB 1; Best Local Similarity 34.7%; Pred. No. 1e-06; Matches 33; Conservative 10; Mismatches 37; SESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRG 394 61 RRRPWCY-----VQVGLKPLVQEC-MVH--DCADG 87 360 Best Loca Matches 원 à à 셤 C;Accession: JH0579; JU0333; A41140; B36677; A35627; A35906; PH0114; A37796; S06 Green 102. 213-219, 1991
Green 102. 213-219, 1991
A;Reference number: JH0579; MUID:91340155; PMID:1831432
A;Reference number: JH0579; MUID:91340155; PMID:1831432
A;Recession: JH0579
A;Recession: JH0579
A;Recession: JH0579
A;Residues: 1-728 <SEXA;Recession: JH0579
A;Recession: JH140; MUID:91334393; PIDN:AAA64239-1; PID:9337936
A;Recession: A41140; MUID:9133493; PIDN:AAA64239-1; PID:9337936
A;Recession: JH078
A;Recession: JH078
A;Recession: A41140; MUID:91337935; PIDN:AAA64239-1; PID:9337936
A;Recession: JH078
A;Recession: JH078
A;Recession: A41140; MUID:91337935; PIDN:AAA64239-1; PID:9337936
A;Recession: JH078
A;Recession: JH078
A;Recession: JH078
A;Recession: A41140; MUID:91337935; PIDN:AAA64239-1; PID:9337936
A;Recession: JH078
A;Re A; Rolecule type: mRNA
A; Residues: 1-161,167-728 <SE4>
A; Residues: 1-161,167-728 <SE4>
A; Residues: 1-161,167-728 <SE4>
A; Cross references: EMBL:XX533
A; Cross references: EMBL:XX533
A; Experimental source: leukcoyte
B; Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
B; Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
B; Minchalar Cloning and sequence analysis of cDNA for human hepatocyte growth fac
A; Reference number: A33512; MUID:89392017; PMID:2528952
A; Reture: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-728 <MIY.
A; Cross-references: GB:M29145; NID:g184041; PIDN:AA525550.1; PID:g306846
B; Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
Broc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A; Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
A; Accession: A39006; WUID:91110540; PMID:1824873 A;Accession: A37796 A;Molecule type: protein A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',5 R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashi Nature 342, 440-443, 1989 epi Molecule type: mRNA; ROBS (RUB) (ROBS) (ROBS ō A/Accession: PH0114
A/Rolecule type: protein
B/Weidner, K.M.; Behrens, U.; Vandekerckhove, U.; Birchmeier, W.
A/Rolecule 111, 2097-2108, 1990
A/Title: Scatter factor: molecular characteristics and effect on the invasiveness
A/Reference number; A37796; MUID:91035621; PMID:2146276 ,Molecule type; mRNA ;Residues: 1-728 <5E3> ;Cross. references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032 ;Accession: A36677

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Gaps

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PLMSS
plasmin (EC 3.4.21.7) precursor - mouse
N'Contains: angiostatin; plasminogen
N'Contains: angiostatin; plasminogen
N'Contains: angiostatin; plasminogen
N'Contains: angiostatin; plasminogen
C'Species: Mus musculus (house mouse)
C'Date: 20-Sep-1991 #sequence=revision 01-Nov-1996 #text_change 18-Jun-1999
R'Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
A'Recence number: A38514; MUD: 9184812; PMID: 2081600
A'Residues: 1-812 CBG3
A'Molecule type: mRNA
A'Residues: 1-812 CBG3
A'Molecule type: protein
A'Recence number: 848202; MUD: 95010076; PMID: 7523120
Bir. J. Biochem. 224, 863-871, 1994
A'Accession: 848202
A'MOlecule type: protein
A'Recence number: 848202
A'Molecule type: protein
A'Residues: 20-25 CLIJ>
A'Molecule type: protein
A'Residues: 20-25 CLIJ>
A'Molecule type: protein
A'Residues: 20-27 CLIJ>
C'Comment: Plasminogen is converted into plasmin by plasminogen activators, bo mediately after talssociation from the clot. In the presence of the inhibitor, the activation involves also removal of the activation involves also removal of the activation peptide.
C'Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angio cinuminose.
C'Punction:
C'Punction:
A'Description: dissolves the fibrin of blood clots; acts as a proteolytic fact in A'Description:
Biochemistry 30, 9781-9791, 1991

A, Title: Characterization of the mouse cDNA and gene coding for a hepatocyte g; A, A, A, Cacsaion: A40332; MUID:92002017; PMID:1832957

A, Accession: A40332

A, Molecule type: DNA

A, Residues: 1-716 cDEG3-
A, Accession: B40332

A, Molecule type: DNA

A, Residues: 1-716 cDEG3-
A, Accession: B40332

A, Molecule type: MRNA
A, Residues: 1-18, 7P', 20-716 cDEG2-
A, Accession: B40332

A, Molecule type: MRNA
A, Residues: 1-18, 7P', 20-716 cDEG2-
A, Accession: B40332

A, All Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
A, Residues: 1-18, 7P', 20-716 cDEG2-
A, ACCES-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
A, Residues: 1-18, 7P', 20-716 cDEG2-
A, Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
C, Genetics: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
C, Gomplex: disulfide-bonded heterodimer of chains dector; kringle homology crowning tringle homology crowning acceptance flatual and flatues experimental contain kringle homology crowning residence flatual and flatues experimental contain kringle homology crowning residence flatue experimental contain kringle homology crowning covalent; E392-370/Domain: kringle homology crowning covalent; E392-370/Domain: tringle homology crowning covalent; E392-370/Domain: tringle contain flatues experimental covalent; F; 7948-703/Domain: trypsin homology crowning covalent; E592-703/Domain: trypsin hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQTYHAHR-----SDALQLGLGKHNY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.9%; Score 132; DB 1; Length 716; Best Local Similarity 33.8%; Pred. No. 1.5e-06; Matches 27; Conservative 11; Mismatches 22; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 CRNPDGSEAPWCFTSRPGLR 360
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                                                                                   hepatocyte growth factor/scatter factor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: 151285
C;Accession: 151286
C;Accession: 151286
Development 121, 813-824,1958
A;Attle: A role for HGF/6F in neural induction and its expression in Hensen's node durin A;Accession: 151285, MUID:95237013; PMID:7720585
A;Accession: 151285, MUID:95237013; PMID:7720585
A;Accession: 151285
A;Accession: 151286
A;Accession: 151286
A;Accession: 151287
A;Accession: 151286
A;Coss-references: GB:877480; NID:9998675; PID:9998676
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
F;124-197/Domain: kringle homology <RR2>
F;202-279/Domain: kringle homology <RR2>
F;206-374/Domain: kringle homology <RR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polipoprotein(a) - western European hedgehog (fragment)

(Species: Brinaceus europaeus (western European hedgehog)

(Species: Brinaceus europaeus (western European hedgehog)

(Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999

(Shacesion: T18518

(Shiawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong A; Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot A; Reference number: 146259; MUID:96025778; PMID:7592597

A; Reference record in RNA

A; Reference in RNA

A; Residues: 1-2869 cLAM

A; Residues: 1-2869 cLAM

A; Residues: 1-2869 cLAM

A; Residues: EMBL:U33170; NID:gl046358; PID:gl046359; PIDN:AAC48522.1

C; Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con ent apolipoprotein(a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2591 CLEGNGENYQGNWAITVSGOPCQGWRKQTPHRHEYTPENYPSKNL-FG--NYCRNPDGEI 2647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCIQGQGEGYRGTVNTIWSGIQCQRWDS-----QFFHQENITPENFKCKDLRENYCRNPD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHR--SDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     macrophage-stimulating protein 1 precursor - mouse
N;Alternate names: hepatocyte growth factor-like protein
C;Species: Mus musculus (house mouse)
C;Date: 17-7ul-1992 #sequence_revision 17-7ul-1992 #text_change 18-Jun-1999
C;Accession: A40332; B40332
R;Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.0%; Score 132.5; DB 2; Length 411; Best Local Similarity 32.3%; Pred. No. 7.7e-07; Matches 31; Conservative 12; Mismatches 38; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 NRRRPWCY----VQVGLKPLVQECMV---HDCADG 87
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C;Species: Rattus norvegicus (Norway rat.)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
R;Obshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Biochem. Biophys. Res. Commun. 227, 273-280, 1996
A;Title: Molecular voloning of rat macrophage-stimulating protein and its invol. A;Reference number: JC5061, MUD:97011126; PMD:8858136
A;Accession: JC5061
A;Abccules: L716 <OHS
A;Residues: L716 <OHS
A;Residues: L716 <OHS
A;Residues: L716 <OHS
A;Cross-references: EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PID:g1669719
C;Complex: disulfided-bonded heterodimer of chains derived from the same precur: C;Superfamily: hepatocyte growth factor; kringle homology
C;Keywords: duplication; glycoprotein; growth factor; kringle
F;131-Damin: signal sequence #status predicted <C;Csuperfamily: hepatocyte growth factor; kringle homology <KRII>
F;32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted
F;101-266/Domain: kringle homology <KRII>
F;292-370/Domain: kringle homology <KRII>
F;292-370/Domain: macrophage-stimulating protein 1 beta chain #status predicted
F;489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted
F;280-716/Domain: trypsin homology <KRII>
F;72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted
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plasmin precursor - lamprey (fragments)
c;Species: Petromyzontidae gen. sp. (lamprey)
c;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 07-Nov-1997
c;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 07-Nov-1997
c;Date: 02-Dec-1993 #sequence_revision of-sep-1995 #text_change 07-Nov-1997
c;Affolter, M.; Schaller, J.; Rickli, E.E.
Protein Seq Data Anal. S, 207-211, 1993
A;Attles: Isolation, characterization and partial amino acid sequence of lamprey plasminc
A;Reference number: S33879
A;Accession: S33879
A;Accession: S33879
A;Accession: S34979
A;Molecule type: protein
A;Residues: 1-15;16-34;35-44;45-59;60-76;77-111;111-138;139-158;159-178;179-216;217-236;
C;Superfamily: plasmin; kringle homology <Rm3>
F;81-146/Domain: kringle homology <Rm3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 336;
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25.7%; Score 131; DB 2; Length 336;
Best Local Similarity 32.9%; Pred. No. 9.2e-07;
Matches 28; Conservative 5; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels
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macrophage-stimulating protein 1 precursor
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Length 710;

DB 1;

Score 127.5;

25.0%;

	52	33		
Gaps	LGLGKH	SE		
27; Gaps	-SPALQ	CKDL		
Best Local Similarity 30.1%; Pred. No. 4.5e-06; Matches 31; Conservative 10; Mismatches 35; Indels	1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKH 52	287 KDCMKGGGEGYRGSVSTTYNGIQCQRWDSQFPHLHNFTPENYKCKDLSE 33	53 NYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCADG 87	336 NYCRNPDGSESPWCFTTDPNIRIGHCSQIKKCQASNQQECYYG 378
-06; 35;	QTYHAH	 Огрици	HDC	SNOOEC
. 4.5e	SATVLO		/QECMV	KKCOA
ed. No Mismat	CLPWNS	CORWDS	GLKPL	IRIGHCSQIKKCQAS
; Pre	DIMGRI	TYNGIC	.OA	DPNIR
30.1% tive	RGKAST	RGSVST	PWCY	PWCFTT
rity nserva	GNGHFY	GQGEGY	PDNRRR	PDGSES
mila Co	TCYE	- MX	YCRN	YCRN
31;	ન	7- X-	κ 2-	-Z 9
ocal s		28		33
Best Local Similarity 30.1%; Pred. No. 4.5e-06; Matches 31; Conservative 10; Mismatches 35.	οχ	Db	٥y	QQ

Search completed: May 25, 2004, 14:58:28 Job time: 7.09027 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 25, 2004, 14:43:40 ; Search time 3.39351 Seconds (without alignments) 1350.274 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-880-503-1 510 1 KTCYEGNGHFYRGKASTDTM.....QVGLKPLVQECMVHDCADGK 88

Scoring table:

141681 segs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	P00749 homo sapien	papic /		~	Q05589 bos taurus	mus	P98121 desmodus ro						P98119 desmodus ro	Q28198 bos taurus	P15120 gallus gall	Q04756 homo sapien	Q9r098 mus musculu			P14417 macaca mula			Q90y90 xenopus lae		P08519 homo sapien		Q01177 rattus norv	P06868 bos taurus		85	Sus	974 homo	138 mus n
SUMMARIES	ΩI	UROK HUMAN	UROK_PAPCY	UROK_PIG	UROK RAT	UROK_BOVIN	UROK_MOUSE	URTB_DESRO		TPA HUMAN	TPA_RAT	URIG DESRO	TPA_MOUSE	URT1_DESRO	TPA BOVIN	UROK_CHICK	HGFA HUMAN	HGFA_MOUSE	FA12_CAVPO	FA12_HUMAN	APOA MACMU	KRM1_MOUSE	KRM1_RAT	KRM1_XENLA	KRM1 HUMAN	APOA_HUMAN	FA12_BOVIN	PLMN_RAT	PLMN BOVIN	KRM2 HUMAN	PLMN_ERIEU	PLMN_PIG	ROR2 HUMAN	ROR2_MOUSE
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	Score	510	475	420	406	396	387	241	241	226	225	220	219	213	209	198.5	193	Н	180.5	5	161	159	159	158	156	156	S	149.5	149	4	148.5	148	147.5	4,
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KRM2_MOU ROR1_HUM ROR1_MOU PLMN_HUM HGFL_HUM PLMN_CAN PLMN_MAC	HGF HGF HGF HGF HGF PLM PLM ROLM ROLM THRI PLM NETI	RHSD_ECOLI LNT_CHLMU AD28 HUMAN PRH_PECR FBNI_BOVIN GSRI_BRAJU NOTC_XENLA RTO7 MARPO PIP1_YEAST MANNE_PIRSP LNT_CHLRR GLNT_CHLRR GLNT_CHLRR GLNT_CHLRR GLNT_CHLRR GLNT_VIBPA
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ALIGNMENTS

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MEDINE-2238825; PubMed=12477932;

MEDINE-2238825; PubMed=12477932;

MEDINE-2238825; PubMed=12477932;

MISCHISE-238825; PubMed=12477932;

MISCHISE-238825; PubMed=12477932;

MISCHISE, Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

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MEDLINE-83055099; PubMed-6754572;
Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe L.;
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MEDLINE-83055084; PubMed-6754569;
Gunzler W.A., Steffens G.J., Otting F., Kim S.-M.A., Frankus
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MEDLINE=83003608; PubMed=6749491;
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Studer R.O.;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
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VARIANT LEU-141.
MEDLINE-96186279; PubMed-8652631;
Yoshimoto M., Ushiyama Y., Sakai M., Tamaki S., Hara H., Takahashi K., Sawagaki Y., Hanada K.;
                                                                                                                                                                                                                                                                                                                                                        X-AXY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 159-411.
MEDIJINE-20266327; Pubmed=10805774;
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"Sequential 1H NMR assignments and secondary structure of the kringle
domain from urokinase.";
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Li X., Bokman A.M., Llinas M., Smith R.A.G., Dobson C.M.;
"Solution structure of the kringle domain from urokinase-type
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                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=$600858; PubMed=$631045;
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"The crystal structure of the catalytic domain of human
urokinase-type plasminogen activator.";
structure 3:681-691(1995).
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MEDLINE=89127526; PubMed=2536903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97218551; PubMed=9065988;
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Thromb. Haemost. 77:434-435(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 67-155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 67-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 337:579-582(1989).
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48595 MW, 816D22DFEDDC8792 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.1%; Score 475; DB 1; Length 433; 94.3%; Pred. No. 2.7e-47; ive 1; Mismatches 4; Indels
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REGE-LIKE

REINGLE

CONGCING PEPTIDE.
SSRINE PROTESSE.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
            -!- SIMILARITY: Belongs to peptidase family :-!- SIMILARITY: Contains 1 EGF-like domain. -!- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                      EMBL; X51935; CAA36200.1; -.
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es 83; Conservative
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MEROPS; S01.231; -.
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of two chains, A and B. The high molecular mass form contains a long chain A. Cleavage occurs after residue 155 in the low molecular mass form to yield a short Al chain.

-!- PHARMACEUTICAL: Available under the name Abbokinase (Abbott). Used in PULMOARTY Eablongs to peptidase family SI.
-!- SIMILARITY: Contains I EGF-like domain.
-!- SIMILARITY: Contains I Kringle domain.
-!- SIMILARITY: Contains I I Kringle domain.
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01-A2R-1990 (Rel. 14, Last sequence update)

01-APR-1990 (Rel. 14, Last sequence update)

01-APR-1990 (Rel. 41, Last annotation update)

Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (UPA)

(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecines, Papio.
NCBI_TaxID=9556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 510; DB 1; Length 431; 100.0%; Pred. No. 2.4e-51; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 RRRPWCYVQVGLKPLVQBCMVHDCADGK 155
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EMBL; M15476; AAA61253.1;
EMBL; D10143; BAA0115.1;
EMBL; D11143; BAA01919.1;
EMBL; X02760; CAA65355.1;
EMBL; AR377330; AAK53822.1;
EMBL; K03226; AAR13575.1;
EMBL; X03226; AAA13575.1;
EMBL; X03226; AAA61252.1;
EMBL; X02286; AAA61252.1;
EMBL; A21571; CAA01590.1;
PIR; A00931; UKHU.
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Best Local Similarity 100.
Matches 88, Conservative
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                                                                                                                                                                                                                                                     TISSUE-Kidney;
MEDLINE-88087954; PubMed=6096832;
MSDLINE-8087954; PubMed=6096832;
Magamine Y., Pearson D., Altus M.S., Reich E.;
"CDMA and gene nucleotide sequence of porcine plasminogen activator.";
Nucleic Acids Res. 12:9525-9541(1984).
                                                                                                             28-FEB-2003 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uph)
PLAU.
                                                                                                                                                                                  Sus scrofa (Pig).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activation; Hydrolase; Serine protease; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                     Nagamine Y.;
Submitted (DEC-1986) to the PIR data bank.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in plasmingen to form plasmin.
-!- SIMILARITY: Belongs to peptidase family SI.
-!- SIMILARITY: Contains 1 EGP-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
                       RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; SO1.231,
InterPro; IPR000003; Cys_Ser_trypsin.
InterPro; IPR000509; Gys_Gsr_trypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR0000124; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR00134; Peptidase_S1.
InterPro; IPR00134; Frypsin; 1.
PERS; PIRSF001144; Vir plasm act; 1.
PRNINTS; PR00722; CHYMOTEXPSIN.
PRINTS; PR00129; KRINGIE.
PROPOM: PR00130; KRINGIE.
PROPOM: PR00130; KRINGIE.
PROPOM: PR00130; KRINGIE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO0021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X01648; CAA25806.1; -.
EMBL; X02724; CAA26511.1; -.
PIR; A00932; UKPG.
HASSP, PO0749; 1KDU.
MEROPS; S01.231; -.
                                                                                        STANDARD;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          REVISION TO 241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kefford R.F., Transcriptional and posttranscriptional activation of urokinase plasminogen activator gene expression in metastatic tumor cells."; Cancer Res. 52:2489-2496(1992).
domain; Zymogen; Signal.
20 BY SIMILARIPE.
442 CHAIN A (BY SIMILARITY).
188 CHAIN B (BY SIMILARITY).
442 CHAIN B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 420; DB 1; Length 442;
Pred. No. 6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=FISCHER 199; PubMed=1568219;
MEDIJINE=92233409; PubMed=1568219;
Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                      KRINGLE,
CONNECTING PEPTIDE.
                                                                                                                                      SERINE PROTEASE.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 81.8%; Pred. No. 6e-4
es 72; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 QRRPWCYVQVGLKQLVQECMVPNCSGGE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 EMBL, X65434; CAA45601.1; -...

EMBL, X65651; CAA46601.1; -...

RRSP, P00749; IKUU.

RROPS; S01.231; -...

RROPS; S01.231; -...

InterPro; IPR000209; EGF-like.

RICEPTO; IPR000209; EGF-like.

RICEPTO; IPR000209; EGF-like.

RICEPTO; IPR000209; FGF-like.

RICEPTO; IPR000209; FGF-like.

RICEPTO; IPR000209; FGF-like.

RICEPTO; IPR00134; Peptidase_S1.

RRAPT; SR00134; Peptidase_S1.

RRAPT; SR00139; KRINGLE.

RRAPT; SR00139; KRINGLE.

RRAPT; SR00139; KRINGLE.

RRAPT; SR00139; RRINGLE.

RRAPT; RRAPT; RRAPSIN-JERE.

RRAPT; SR00139; RRINGLE.

RRAPT; RRAPT; RRAPSIN-JERE.

RRAPT; RRAPT; RRAPT; RRAPT; RRAPT;

RRAPT; RRAPT; RRAPT;

RRAPT; RRAPT; RRAPT;

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RRAPT; RRAPT;

RRAPT; RRAPT;

RRAPT; RRAPT;

RRAPT; RR
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CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1) (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
EGF-LIKE.
KRINGLE.
CONNECTING PEPTIDE.
SPERINE PROTEASE.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
molecular mass form to yield a short Al chain (By similarity).
-!- SIMILARITY: Belongs to peptidase family Sl.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> H (IN REF. 2).
-> G (IN REF. 2).
-> N (IN REF. 2).
4EBIB96C716244C8 CRC64;
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DOMAIN
DISULEID
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DISULEID
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DISULEID
ACT-SITE
ACT-SITE
CONFLICT
CONFLICT
SEQUENCE
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Gaps

0;

79.6%; Score 406; DB 1; Length 432; 79.5%; Pred. No. 2.4e-39; ive 5; Mismatches 13; Indels

Conservative

Similarity

Query Match Best Local Simi Matches 70;

RESULT 6
UROK_MOUSE STANDARD; PRT; 433 AA.

AC PO6669;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28 FEBS-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-plasminogen activator).

GN PLAU.

SN Mus musculus (Mouse).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
C Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

R SEQUENCE FROM N.A.

RX MEDIINE=85179474; PubMed=2985383;
RA Reich B., Kocher H.P., Duvoisin R.M.;
RA Reich B., Kocher H.P., Duvoisin R.M.;
RA Reich B., Magamine Y.,
RT Mouse urokinase-type plasminogen activator.";
RT Mouse urokinase-type plasminogen activator.";
RN SEQUENCE FROM N.A.

RR MEDLINE=88163489; PubMed=2831940;

The maintain uncidinate type plaeminged activator gene.",

"The maintain uncidinate type plaeminged activator gene.",

"Colemniator Carry Static (Cleavage of Arg-[-Val bond in Cleavage o

us-09-880-503-1.rsp

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                                                                                                                   69 KTCYHGNGDSYRGKANTDTKGRPCLAMNAPAVLQKPYNAHRPDAISLGLGKHNYCRNPDN 128
                                                                                                1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!- FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Probable potent thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
MEDLINE=93393059; PubMed=1309059; Schleuring W.-D., Alagon A., Boidol W., Bringmann P., Petri T., Schleuring W.-D., Alagon A., Langer G., Baldus B., Witt W., Donner P., Ponner P., "Plasminogen activators from the saliva of Desmodus rotundus (common
                                                                                                                                                                                                                                             URTB_DESRO STANDARD; PRT; 431 AA.
P98121;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA beta):
                                                                                                                                                                                                                                                                                                                                                      Desmodus rotundus (Vampire bat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE-Salivary gland;

MEDLINE-92039036; PubMed=1937019;

Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;

"The plasminopen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";

Gene 105:229-237(1991).
                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SUBUNIT: Monomer.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGP-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
                                        ch 75.9%; Score 387; DB 1; Length 433; l Similarity 72.7%; Pred. No. 3.8e-37; 64; Conservative 10; Mismatches 14; Indels
 378 378 CHARGE RELAY SYSTEM.
433 AA; 48268 MW; A99C35F6250443F9 CRC64;
                                                                                                                                                                         129 QKRPWCYVQIGLRQFVQECMVHDCSLSK 156
                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M63989; AAA31594.1; -.
PIR; 780589; 130589.
HSSP, P98119; 1A51.
MEROPS; S01.239; -.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9430;
ACT SITE
SEQUENCE
                                       Query Match
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                                                                     Matches
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2 TCYECNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
R InterPro; IPR000001; Kringle.
R InterPro; IPR001254; Peptidase S1.
R InterPro; IPR001254; Peptidase S1.
R Pfam; PF00008; EGF; 1.
Pfam; PF00008; Kringle; 1.
R PRINTS; PR00722; CHPMOTRYPSIN.
R PRINTS; PR007018; KRINGLE.
R PRODOM; PR00018; KRINGLE.
R PRODOM; PR00181; EGF; 1.
SMART; SM00181; EGF; 1.
SMART; SM00180; KRINGLE; 1.
R PROSTITS; PS0020; EGF; 1.
R PROSTITS; PS0020; EGF; 1.
R PROSTITS; PS0020; KRINGLE; 1.
R PROSTITS; PS00186; EGF; 2.
R PROSTITS; PS00186; EGF; 3.
R PROSTITS; PS00187; KRINGLE; 1.
R PROSTITS; PS00187; MALNGLE; 1.
R PROSTITS; PS00187; M
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SALIVARY PLASMINOGEN ACTIVATOR BETA.
EGF-LIKE.
KRINGLE
SERINE PROTEASE.
CHARGE RELAY SYGTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 31, Last semoreation update)
Salivary polasminogen activator alpha 2 precursor (EC 3.4.21.68) (I alpha-2) (BAT-PA) (T-plasminogen activator).
Desmodus rotundus (Vampire bat).
Bukaryotas Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria, Chiroptera; Microchiroptera; Phyllostomidae; NCBI_TAXID=9430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 N-
48221 MW;
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CARBOHYD
SEQUENCE
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ACT_SITE
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DISULFID
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URT2 DESRO
ID URT2 DES
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                                                                                                                                                                                                                                                                                                                                                                                                              agent.
-!-CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- ENZAME REGULATION: Activity toward plasminogen is stimulated in the presence of fibrin I.
-!- SUBUNIT: Monomer.
-!- DOWAIN: The fibronectin type-I domain mediates binding to fibrin, and the kringle domain apparently mediates fibrin-induced activity.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains I EGF-like domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
-!- SIMILARITY: Contains I kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: JPR009003; Cys Ser trypsin. InterPro: JPR009003; Cys Ser trypsin. InterPro: JPR0006209; EGF like. InterPro: JPR0006209; EGF like. InterPro: JPR0006210; IEGF. InterPro: JPR000601; Kringle. InterPro: JPR001814; Peptidase_S1. InterPro: JPR001814; Peptidase_S1. InterPro: JPR001814; Peptidase_S1. Ffam; PP000081; Kringle; 1. Ffam; PP00081; Kringle; 1. Ffam; PP00081; Kringle; 1. FRINTS; PR00181; Kringle; 1. FRINTS; PR00181; Kringle; 1. SMART; SM00181; EGF; 1. SMART; SM00088; KN1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M63988; AAA31533.1; --
EMBL; J05082; AAA31596.1; --
PIR; A34369; A44369.
PIR; J30598; US0598.
HSSP; P98119; I351.
MEROPS; S01.232; --
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R SMART; SM00130; KR; 1.

R PROSITE; PS00022; EGF_1; 1.

R PROSITE; PS00022; EGF_1; 1.

R PROSITE; PS00026; EGF_3; 1.

R PROSITE; PS00026; EGF_3; 1.

R PROSITE; PS00021; KRINGLE 1; 1.

R PROSITE; PS00021; KRINGLE 2; 1.

R PROSITE; PS00013; KRINGLE 2; 1.

R PROSITE; PS00135; TRYPSIN_DOW; 1.

R PROSITE; PS00135; TRYPSIN_DOW; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                  SALIVARY PLASMINOGEN ACTIVATOR ALPHA FIBRONECTIN TYPE-I. EGF-LIKE. KRINGLE.
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Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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900750; Q15103;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
11-SSUE-type plasminogen activator precursor (EC 3.4.21.68) (LPA) (L-plasminogen activator) (Alteplase) (Reteplase).
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Y -> H (IN REF. 2).
M -> R (IN REF. 2).
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ses 42; Conservative
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TISSUE=Melanoma;
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--- FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Probable potent thrombolytic
[1]
SEQUENCE FROM N.A.
TISSUE-Salivary gland;
TISSUE-Salivary gland;
MEDLINE-92039036; PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Salivary gland;
MEDLINE=90036867; PubMed=2509450;
Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
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"Isolation, characterization, and cDNA cloning of a vampire bat salivary plasminogen activator.";
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MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
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us-09-880-503-1.rsp

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MEDLINE=22388257, PubMed=12477932;

MEDLINE=22388257, PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ridusner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Blotchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Pahey J., Helton E., Ketteman M., Nadan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schentz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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SEQUENCE FROM N.A.
MEDLINE=88054470; PubMed=2824147;
MEDLINE-88054470; PubMed=2824147;
Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J.,
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MEDLIKE-90192129; PubMed=2107528;
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"Variant tissue-type plasminogen activator (FLAT) cDNA obtained from human endothelial cells.";
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MEDLINE=86284200, PubMed=3090401;
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Codenakker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
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MEDLINE=83115262; PubMed=6337343; Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A., Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A., Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L., Goeddel D.V., Collen D., "Cloning and expression of human tissue-type plasminogen activator CDNA in E. coli."; Anture 301:214-221(1983).
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MEDLINE-88262579; PubMed=3133640;
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J. Biol. Chem. 261:6972-6985(1986),
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SEQUENCE OF 31-552 PROM N.A.
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
Purification and characterization of tissue plasminogen activator
"Purification and characterization of tissue plasminogen activator
Agric. Biol. Chem. 55:1225-1232(1991).
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MEDITNE=96200985; PubMed=8613982;
Banda D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
Bode W.;
"The 2.3 A crystal structure of the catalytic domain of recombinant
"The 2.3 A crystal structure of the catalytic domain of secombinant
Two-chain human tissue-type plasminogen activator.";
J. Mol. Biol. 258:117-135(1996).
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MEDLINE=91244765; PubMed=1645336;
Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.;
"Disulfide pairing of the recombinant kringle-2 domain of tissue plasminogen activator produced in Escherichia coli.";
J. Biol. Chem. 266:10070-10072(1991).
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Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
"Tissue plasminogen activator has an O-linked fucose attached threonine-61 in the epidermal growth factor domain.";
Biochemistry 30:2311-2314(1991).
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MEDIATE=9092112; PubMed=2513186;
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"Carbohydrate structure of recombinant human uterine tissue plasminogen activator expressed in mouse epithelial cells.";
Els. J. Biochem. 186:273-286 (1989).
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MEDLINE-83169656; PubMed=6572897;
JOSEPHNOT T., Ny T., Raanby M., Heden L.-O., Palm Josephson S.;
"Isolation of CDNA sequences coding for a part
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Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983).
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Eur. J. Biochem. 132:681-686(1983).
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TISSUE=Melanoma;
MEDLINE=85000468; PubMed=6433976;
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7:671-677(1988)
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MEDLINE=97449126; PubMed=9305622;
Bendaus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
Bode W.;
"Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
crystal structure of single-chain human tPA.";
[19]
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MEDLINE-90122799; PubMed-2558718;
Byeon I.-J.L., Kelley R.F., Llinas M.;
Byeon I.-T.L., Kelley R.P., Llinas M.;
HIN MR structural characterization of a recombinant kringle 2 domain from human tissue-type plasminogen activator.";
Biochemistry 28:9350-9360(1989).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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MEDLINE=92106329; PubMed=1762144;
Byeon I.-J.L., Llinas M.;
"Solution structure of the tissue-type plasminogen activator kringle
2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF KRINGLE 2.

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MEDLINE=92118803; PubMed=1310033;
MEDLINE=92118803; PubMed=1310033;
Med Vos A., Ultsch M.H., Kalley R.F., Padmanabhan K., Tulinskly A., Westbrook M.L., Kossiaka A.A., "Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4-A resolution.";
Biochemistry 31:270-279(1992).
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P19637;
01-F8191 (Rel. 17, Created)
01-F8191 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA) (t-PA) (t-Pasminogen activator).
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186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
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J. Mol. Biol. 222:1035-1051(1991).
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TPA_RAT
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REPLYINGS FROW N. WY. T.

REPLY. COLUMN N. WY. T.

REPLY P., Otherwise PROW N. WY. T.

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Desmodontinae; Desmodus.
NCBI_TaxID=9430;
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CHARACTERIZATION.
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| R PROSITE; PS01062; EGF 1; 1. | R PROSITE; PS01166; EGF 2; 1. | PROSITE; PS01025; EGF 3; 1. | PROSITE; PS01025; FIBEON 2; 1. | PROSITE; PS01025; FIBEON 2; 1. | PROSITE; PS01025; FIBEON 2; 2. | PROSITE; PS01013; TRYBIN 2; 2. | PROSITE; PS01034; TRYPSIN DOM; 1. | PROSITE; PS01034; TRYPSIN DOM; 1. | PROSITE; PS01034; TRYPSIN DOM; 1. | PROSITE; PS01035; TRYPSIN SER; 1. | PROSITE; PS01035; TRYPSIN SER; 1. | Plasma; Kringle; EGF-like domain; Repeat; Signal. | PROBABLE. | R PROSITE; PS01035; TRYPSIN SER; 1. | PROBABLE. | PROBABLE. | PROSITE; PS01035; TRYPSIN SER; 1. | PROBABLE. | PROSITE; PS01035; TRYPSIN SER; 1. | PROBABLE. | PROSINOGEN ACTIVATOR A TISSUE-TYPE PLASMINOGEN ACTIVATOR A TISSUE-TYPE ACTIVATOR A TISSUE-TYPE ACTIVATOR A TISSUE-TYPE ACTIVATOR A TISSUE-TYPE ACTIVATOR A T
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URTG DESRO
AC P49150;
DT O1-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 34, Last aequence update)
DT 01-FEB-2003 (Rel. 41, Last annotation update)
DE Salivary plasminogen activator gamma precursor (BC 3.4.21.68) (DSPA DE Salivary plasminogen activator gamma precursor (BC 3.4.21.68) (DSPA DE Salivary plasminogen activator gamma precursor (BC 3.4.21.68) (DSPA OS Desmodus rotundus (Vampire bat).
OS Bukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
OC Bukaryota, Metazoa; Chiroptera, Microchiroptera, Phyllostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-LIKE

KRINGLE 1.

KRINGLE 1.

KRINGLE 1.

CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SI
                                                                                                                                                                                                                                                                                                                  TISSUE-TYPE PLASMINOGEN ACTIVATOR.
TISSUE-TYPE PLASMINOGEN ACTIVATOR A
TISSUE-TYPE PLASMINOGEN ACTIVATOR B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.1%; Score 225; DB 1; Length 559; 47.7%; Pred. No. 2.4e-18; ive 10; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN.
FIBRONECTIN TYPE-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RRPWCYVQVGLKPLVQECMVHDCADG 87
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559 AA;
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                                                                                                                                                                                                                                                                                  TISSUE-Salivary gland;
MEDLINE-20203036; PubMed=1937019;
Kraetzschmar J., Haendlar B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agent.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SUBUNT: Monomer.
-!- SUBUNT: Monomer.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 kringle domain.
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REDILINE_25282825; PubMed=12477932;

KR SEQUENCE FROM N.A.

KR SEQUENCE FROM N.A.

KR STEAUSDERGE R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alterbul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alterbul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heish F.,

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heish F.,

RA Sigleton M., Soarse M.B., Bonaldo M.F., Carrinci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Tochiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Basak S.A., McEwan P.J., McKernan K.J., Mahake J.A., Gunarathe P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Girmwood J., Schwarthen V., Bouffard G.G.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Girmwood J., Schwartz J., Wyers R.M.,

RA Schrerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schrerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schrerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schrerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

C. - FUNCTING: Converts the abundant, but hacking an important controlling plasmin-mediated proteolysis, it plays an important controlling plasmin-mediated proteolysis, it plays an important many other physiopathological events.

C. CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in many other physiopathological events.

C. - CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in blasminogen to form plasmin.

C. - Submin A. A. Schein J
                                                                                                                                                                                 0
                                                                                                                                                                                                                                                         2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPA_MOUSE STANDARD; PRT; 559 AA.
P11214, Q91VP2;
01-UTU-1969 (Rel. 11, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Tissue-type plasminogen activator precursor (BC 3.4.21.68) (tPA)
(t-PA) (t-PA) (t-PA)
308 324 BY SIMILARITY.
341 369 BY SIMILARITY.
315 N-LINKED (GLCNAC. . ) (POTENTIAL)
394 AA, 44105 MW, 9CCD6F52F3D81FCD CRC64;
                                                                                                                                                                                 .;
0
                                                                                                                              Length 394;
                                                                                                                      43.1%; Score 220; DB 1; Length 39 45.2%; Pred. No. 6.2e-18; Ative 13; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                          104 SKPWCÝVIKARKFTSESČSVPVCS 127
                                                                                                                                                                                                                                                                                                                            62 RRPWCYVQVGLKPLVQECMVHDCA 85
                                                                                                                                                                           38; Conservative
                                                                                                                   Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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DISULFID
DISULFID
CARBOHYD
                                                                        SEQUENCE
                                                                                                                                                                           Matches
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AD DT TIPA MOUSE

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-!- FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Potent thrombolytic agent.
-!- CATALYTIC ACTIVITY. Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin paraminogen to form plasminogen is stimulated in the presence of fibrin I.
-!- ENZYME REGIZATION: Activity toward plasminogen is stimulated in the presence of fibrin I.
-!- SUBUNT: Monomer.
-!- DOWALN: The fibronectin type-I domain mediates binding to fibrin, and the kringle domain apparently mediates fibrin-induced stimulation of activity.
-!- SIMILARITY: Contains I EGF-like domain.
-!- SIMILARITY: Contains I EGF-like domain.
-!- SIMILARITY: Contains I kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it: use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M65986; AAA1592.1; -

EMBCOS; 601.232, -

EMBCOS; 61.232, -

EMBCOS; EMBCS; EMBCS; EMBCS; EMBCS; EMBCS; EMBCS; EMBCS; EMBCS; EMBCOS; EMBCS; EMBCS;
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FIBRONECTIN TYPE-I.
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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DOMAIN
DOMAIN
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DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
ACT_SITE
DISULPID
           TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
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01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA alpha-1).
Desmodus roundus (Vampire bat).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ๗
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TISSUB=Salivary gland;
MEDLINE=98022741; PubMed=9354616;
Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
Schleuning W.D., Bode W.;
Grallytic domain structure of vampire bat plasminogen activator:
molecular paradigm for proteolysis without activation cleavage.";
Biochemistry 36:13483-13493(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MISSUB-Salivary gland;

MEDLINE=92039036, PubMed=1937019;

Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,

Alagon A., Donner P., Schleuning W.D.;

The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";

Gene 105:229-237(1991).
BY SIMILARITY.
BY SIM
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CHARACTERIZATION.
CHARACTERIZATION.
MBDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 219; DB 1; Length 559;
; Pred. No. 1.2e-17;
11; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8CCEE2BDB94514D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                63122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 46.0%
Les 40; Conservative
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     DESRO
DISULPID
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
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ID URTI DES
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TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGKHNYCRNPDNR 61
                                                                                                                                                    0; Gaps
                                                                                                                                               Query Match 41.8%; Score 213; DB 1; Length 477; Best Local Similarity 46.4%; Pred. No. 4.8e-17; Matches 39; Conservative 10; Mismatches 35; Indels
                                                                                                                                          53616 MW; AA06FD1739C10E5E CRC64;
                    N-LINKED (GLCNAC. .).
/FIId=CAR_000027.
N-LINKED (GLCNAC. .).
/FIId=CAR_000028.
SIMILARITY.
SIMILARITY.
BY
     345
243
243
443
404
103
103
                              149
1880
2214
2257
3359
3359
153
DISULFID
DISULFID
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SEQUENCE
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TISSUE Addrey;

TISSUE Addrey;

TISSUE Addrey;

TISSUE Extension of the bovine plasminogen activators upa many p., Berglund L., Petersen T.E.;

Tand tPA.";

Int. Dairy J. 5:605-617(1995).

T. FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events.

C. --- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

C. --- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide

Bos taurus (Bovine). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator)

PLAT.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL; X85800; CAAS3795.1; -
HSSP; P00750; IRTF.
HSROPS; S01.22.3; -
INTERPRO; IPRO09003; Cys Ser_trypsin.
INTERPRO; IPRO06209; EGF_like.
INTERPRO; IPRO00639; EGF_like.
INTERPRO; IPRO001254; Peptidase_S1.
INTERPRO; IPRO01254; Peptidase_S1.
INTERPRO; IPRO01254; Peptidase_S1.
INTERPRO; IPRO0134; Peptidase_S1.
INTERPRO; IPRO0134; Peptidase_S1.
INTERPRO0139; ENT.
INTERPRO0139; ENT.
PRON15; PRO00139; KINGLE.
PRONTS; PRO0139; KINGLE.
PRODOM; PRO00130; KRINGLE.
PROMITS; PRO0130; KRINGLE.
SWART; SMO0130; KRINGLE.
SWART; SMO0130; KRINGLE.
PROSITE; PSO0022; EGF_1; I.
PROSITE; PSO0021; EGF_1; I.
PROSITE; PSO0021; EGF_1; I.
PROSITE; PSO0021; KRINGLE.
PROSITE; PSO0021; KRINGLE.
PROSITE; PSO0021; KRINGLE.
PROSITE; PSO0021; KRINGLE.
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PRT;

STANDARD;

TPA BOVIN Q28198;

RESULT 14 TPA BOVIN ID TPA B AC Q2819

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219 CYTGNGLAYRGTRSHTKSGASCLPWNSVFLTSKIYTAWKSNAPALGLGKHNHCRNPDGDA 278
3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
NCBI _TaxID=9031;
                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                          ch 41.0%; Score 209; DB 1; Length 566; 1 Similarity 47.6%; Pred. No. 1.7e-16; 39; Conservative 9; Mismatches 34; Indels
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SEQUENCE FROM N.A.
MEDLINE=90110185; Pubmed=2295632;
Leslie N.D., Kessler C.A., Bell S.M., Degen J.L.;
"The chicken urokinase-type plasminogen activator gene.";
                                                                                                                                                                                                                                                                                                                                                           279 QPWCHVWKDRQLTWEYCDVPQC 300
                                                                                                                                                                                                                                                                                                                                                   63 RPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           UROK_CHICK
ID UROK_CHICK
AC P15120;
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The Boll, Chem 266:1399 140(1990)

The Boll, Chem 267:1399 140(1990)

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The SHISS-PROOF act y; Specific cleavage of Arg-|val bond in plasmings to form plasmings to form plasmings to form plasmings to pepidase family St.

This SHISS-PROOF entry; Specific cleavage of Arg-|val bond in the Boll of State of State
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                 79 CYSGNGEDYRGMAEDP----GCLYWDHPSVIRWGDYHADLKNALQLGLGKHNYCRNPNGR 134
61
3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ-QTYHAHRSDALQLGLGKHNYCRNPDNR
                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUB=Liver, and Serum;
MEDLINE=9322878; PubMed=7681865;
Miyazawa K., Shimomura T., Kitamura A., Kondo J., Morimoto Y.,
Kitamura N.;
"Molecular cloning and sequence analysis of the cDNA for a human
serine protease reponsible for activation of hepatocyte growth
factor. Structural similarity of the protease precursor to blood
coagulation factor XIII.;
'), Biol. Chem. 268:10024-10028(1993).
                                                                                                                                                                           HGFA HUMAN STANDARD; PRT; 655 AA.

004756; Q14726;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF
activator) (HGFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 604552; -...
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0004252; F:serine-type endopeptidase activity; TAS.
GO:0004582; F:serine-type endopeptidase activity; TAS.
GO; GO:006508; P:proteolysis and peptidolysis; TAS.
InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_1ike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, D14012; BAA03113.1; -.
EMBL, Z69923; -; NOT ANNOTATED_CDS.
PIR; A46688.
HASSP, P00763; 1DPO.
MEROPS; S01.228; -.
Genew; HGNC:4894; HGPAC.
                                                            62 RRPWCYVQ 69
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135 SRPWCYTK 142
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HGFA_HUMAN
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                             ö
                                                                                                         62
                                                                                      3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       various.

J. Biol. Chem. 276:15099-15106 (2001).

J. Biol. Chem. 276:15099-15106 (2001).

J. Biol. Chem. 276:15099-15106 (2001).

J. FUNCTION: Activates hepatocyte growth factor (HGF) by converting it from a single chain to a heterodimeric form (By similarity).

J. SUBGNIT: Dimer of a short chain and a long chain linked by a disulfide bond (By similarity).

J. SUBCELLIULAR LOCATION: Secreted as an inactive single-chain precursor and is then activated to a heterodimeric form (By cimilarity).
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                 HGFA_MOUSE STANDARD; PRT; 653 AA.

OPR059; OSUKV4;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

15-MAR-2004 (Rel. 43, Last annotation apdate)

4 Epatocyte growth factor activator precursor (RC 3.4.21.-) (HGF HGFAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
MEDLINE=21226753; PubMed=11032833;
van Adelsberg J.S., Sehgal S., Kukes A., Brady C., Barasch J.,
Yang J., Huan Y.;
"Activation of hepatcoyte growth factor (HGF) by endogenous HGF
activator is required for metanephric kidney morphogenesis in
                                                             ö
                            Query Match 37.8%; Score 193; DB 1; Length 655; Best Local Similarity 54.5%; Pred. No. 1.4e-14; Matches 36; Conservative 4; Mismatches 26; Indels
                                                          26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Itoh H., Kataoka H., Koono H.; "Mouse hepatocyte growth factor activator."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70681 MW; 2CF72F1E1B862ED7 CRC64;
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EMBL, AF224724, AAF34712.1; -.
HSSP, P00763; 1DP0.
MEROPS; S01.228; -.
MGD; MG:1859281; Hgfac.
InterPro; IPR009003; Cys. Ser_trypsin.
InterPro; IPR000742; EGF_2.
InterPro; IPR000742; EGF_2.
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
 655 AA;
                                                                                                                                                                          346 RPWCYV 351
                                                                                                                                               63 RPWCYV 68
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SEQUENCE FROM N.A.
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2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSD-ALQLGLGKHNYCRNPDN
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Best Local Similarity 42.9%
Matches 36; Conservative
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TISSUELINE=3003367; PubMed=1390917;

A Sembara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S., Kambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S., Kambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S., Kambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S., Kambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S., Kambara T., Okabe H.; Kunisada H.; Shibara T., Contains I fibronectin that participates in the intitation of blood coagulation, fibrinolysis, and the CATIVITY: Cleaves selectively Arg-|-Ile bonds in factor VII to form factor VII and factor XI to form factor XII, prekallikrein, and HWW kininogen form a Complex bound to an amionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XII and then to beta-factor XII activates factor XII to form kallikrein, which then cleaves factor XII is similakiii surivates factor XII to form sallikrein to beta-factor XII surivates factor XII to form sallikrein to SIMILAKIIY: Contains I fibronectin type I domain.

SIMILAKIIY: Contains I fibronectin type I domain.

SIMILAKIIY: Contains I kringle domain.
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                                                                                                  CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi; Caviidae, Cavia.
                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Coagulation factor XII precursor (BC 3.4.21.38) (Hageman factor)
                          Query Match
36.9%; Score 188; DB 1; Length 653;
Best Local Similarity 53.0%; Pred. No. 5.1e-14;
Matches 35; Conservative 6; Mismatches 25; Indels
  653 AA; 70567 MW; 88B4B20255DF7FDC CRC64;
                                                                                                                                                                                                                                     603 AA
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EGF_2.
EGF_Ca.
EGF_like.
Fibrnctn1.
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InterPro; IPR006209; EGF_11ke.
InterPro; IPR000083; Fibrnch11.
InterPro; IPR000562; FN Type_II
InterPro; IPR000510; IEGF.
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HSSP; P00763; 1DPO.
MEROPS; S01.211; -.
                                                                                                                                                                                                                                    STANDARD;
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InterPro; IPR000742;
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                                                                                                                                      63 RPWCYV 68
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Q04962;
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Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease; Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal. SIGNAL <1 18
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EGF-LIKE 1.

FIBRONECTIN TYPE-I.

FIBRONECTIN TYPE-I.

KRINGLE.

PRO-RICH.
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48DC6B946FB9ED59 CRC64;
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BY SIMILARITY.
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                                                              PR001254; Peptidase_S1.
PR001314; Peptidase_S1A.
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IPR000001; Kringle
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Gaps

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SCYEGRGVSYRGMARTTVSGAKCQRWAS----EATYRNMTAEQALRRGLGHHTFCRNPDN 270
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Nucleic Acids Res. 14:3146-3146(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-86033830; PubMed=3877053; MEDLINE-86033830; PubMed=3877053; Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D., McGillivray R.T.A.; "Characterization of human blood coagulation factor XII cDNA. Prediction of the primary structure of factor XII and the tertiary structure of beta-factor XIIa."; J. Biol. Chem. 260:13666-13676(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 20-379,
MEDLINE=85182674; PubMed=3886654;
McMullen B.A., Fujikawa K.;
"Amino acid sequence of the heavy chain of human alpha-factor XIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (2)
SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605.
SEQUENCE FROM M.A., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (AUG-2002) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-88007593; PubMed=2888762;
Cool D.E., McGillivray R.T.A.;
"Characterization of the human blood coagulation factor XII gene."
Intron/exon gene organization and analysis of the 5'-flanking
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
VCBI_TaxID=9606;
                                                                                                                                                                               FA12_HUMAN STANDARD; PRT; 615 AA.
P00748, P78132,
21_UUL-1986 (Rel. 01, Created)
01_OCT-1989 (Rel. 12, Last sequence update)
28_FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human factor XII (Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 4-615 FROM N.A.
MEDLINE-86176794; PubMed-3754331;
Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
Cortese R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 354-362 AND 373-615.
MEDLINE=82291041, PubMed6604055;
Fujikawa K., McMullen B.A.;
"Amino acid sequence of human beta-factor XIIa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region.";
J. Biol. Chem. 262:13662-13673(1987).
                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 258:10924-10933(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5]
SEQUENCE OF 146-615 FROM N.A.
MEDLINE=86216049; PubMed=3011063;
Que B.G., Davie E.W.;
"Characterization of a cDNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (activated Hageman factor).";
J. Biol. Chem. 260:5328-5341(1985).
                                                               ||||:| :| : | : | DIRPWCFVWMGNRLSWEYCDLAQC
                                       RRRPWCYVQVGLKPLVQECMVHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 25:1525-1528(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 561-615 FROM N.A.
TISSUE=Blood;
215
                                       61
                                                                            271
                                                                                                                                          RESULT 19
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REPLIES 9613029 : pubMeds22225;

REPLIES 6610028 W., Fofferbers S., Bartz U., Lutse G., Lammle B., Engel W.;

RIT proper decuses a truncated transcript in cross-reacting material in the invest acceptor splice ste materion 11396 (G--A) in the factor XII gene causes a truncated transcript in cross-reacting material in the construction of the cons
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18-03-660-505-T.TED
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||||:| 272 DIRPWCFV 279

q

RESULT 20

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Score 170.5; DB 1; Length 615;
Pred. No. 5e-12;
6; Mismatches 24; Indels 5,
                                                                                                                                                                                 ALPHA-FACTOR XIIA HEAVY CHAIN.
ALPHA-FACTOR XIIA LIGHT CHAIN.
BETA-FACTOR XIIA PART 1.
BETA-FACTOR XIIA PART 2.
FIBRONECTIN TYPE-II.
FIBRONECTIN TYPE-II.
FIBRONECTIN TYPE-I.
                                                                                                                                                                                                                            O-LINKED (FUC).

N-LINKED (GLONAC. .).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).
                                                                                                                                                                                                                KRINGLE.
PRO-RICH.
SERINE PROTEASE.
                                                                                                                                                                                                                                                           33.4%;
                                                                                                                                                                                                                        DOMAIN
CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
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SCYDGRGLSYRGLARTTLSGAPCQPWAS----EATYRNVTAEQARNWGLGGHAFCRNPDN 271

61 RRRPWCYV 68

216

2 TCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDN

Local Similarity 48.5 les 33; Conservative

Matches

ò 셤 8

9

5;

Transus monkey apolipopiocein(a). Sequence, evolution, and sites or synthesis."

5. Spid. Chem. 264:5957-5965(1989).

6. FONCTION: Apoli is the main constituent of lipoprotein(a) autoproteolysis. Inhibits tissue-type plasminogen activator 1.

1.p(a) may be a ligand for megalin/Gp 330.

1.p(a) may be a ligand for megalin/Gp 330.

2. SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and decorin (By similarity).

3. Subvated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with atherospenicity of the protein, because the tragment are competing with plasminogen kringles IV and V is naturally occurring proteolytic fragments are correlated with plasminogen kringles IV and V is naturally occurring proteolytic fragments are competing with plasminogen for fibrin(ogen) binding.

3. MSCELLANBOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of a promote thrombogenesis. Oglycosylation may limit the extent of proteolytic fragmentation (By similarity).

5. SIMILARITY: Belongs to peptidase family SI. Plasminogen subfamily.

6. SIMILARITY: Contains at least 10 kringle domains. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it was by non-profit institutions as long as its content is in no was endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@lsb-sib.ch) LPA.
Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9544; SEQUENCE FROM N.A. MEDLINE-89174660; PubWed=2925643; Tomlinson J.E., McLean J.W., Lawn R.M.; "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites PRT; 1420 AA InterPro; PR000001; Kringle.
InterPro; IPR000001; Kringle.
InterPro; IPR001201; Kringle.
InterPro; IPR001201; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
Pfam; PR00051; Kringle; 11.
Pfam; PR00051; Kringle; 11.
PRINTS; PR000121; CHIMOTRYPSIN.
PRNDTS; PR000122; CHIMOTRYPSIN.
PRNDTS; PR000130; KRINGLE.
PRODCM; PR000130; KRINGLE.
PROSITE; PS00021; KRINGLE_1; 10.
PROSITE; PS00021; KRINGLE_1; 10.
PROSITE; PS00021; KRINGLE_1; 10.
PROSITE; PS000131; KRINGLE_1; 10.
PROSITE; PS000131; KRINGLE_1; 10.
PROSITE; PS000131; KRINGLE_1; 10.
PROSITE; PS000131; KRINGLE_2; 10.
PROSITE; PS00131; TRYPSIN DOM; 11. EMBL, J04635; AAA36833.1; -. PIR; A32869; A22869. HSSP; P00747; 2PK4. MEROPS; S01.226; -. STANDARD; APOA MACMU P14417;

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61 RRRPWCYV 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                           CHAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
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                                                                                                                                                                                                                                                                                                             1068 CYHGNGQSYRGTESTTVTGRTCQSWSSMTPHQHKRTPENHPNDDLTM-----NYCRNPDA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.

TISSUE-Brain, and Kidney,

MEDLINE-2116732; Bubmed-11267660;

MEDLINE-2116732; Bubmed-11267660;

MARAMURA T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,

MARAMURA T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,

MARAMURA T.,

MARAMURA T.,

MORCHILA Cloning and characterization of Kremen, a novel

Kringle-containing transmembrane protein.";

Biochim. Biophys. Acta 1518:63-72(2001).

T. FUNCTION: Receptor for Dickkopf protein. (Coperates with Dickkopf to block Wart Deta-catenin signaling (By similarity).

T. SUBCELLULAR LOCATION: Type I membrane protein (Potential).

T. SIMILARITY: Contains I CUB domain.

T. SIMILARITY: Contains I Lange domain.

T. SIMILARITY: Contains I Kingle domain.
                                                                                                                                                                                                                                                                                          3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (bickkopf receptor).
 protease; Lipid transport; Plasma; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                 31.6%; Score 161; DB 1; Length 1420; 40.9%; Pred. No. 1.5e-10; ative 9; Mismatches 31; Indels 12
                                      49 127 KRINGLE 1.
163 241 KRINGLE 2.
277 355 KRINGLE 3.
391 469 KRINGLE 3.
505 583 KRINGLE 5.
619 697 KRINGLE 6.
725 803 KRINGLE 6.
725 803 KRINGLE 6.
727 1145 KRINGLE 8.
1191 1420 SERINE PROTEASE.
1420 AA; 158367 MW; BE102949E03C5B0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                   1123 DTGPWCFT----MDPSVRREYCNLTRCSD 1147
                                                                                                                                                                                                                                                                                                                                                   61 RRRPWCYVQVGLKPLVQE--CMVHDCAD 86
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 36, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRM1 MOUSE
Q99N43;
STILLERITAR
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(See http://www.isb-sib.ch/announce,
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28-FEB-2003 (Rel. 41, Last sequence update)
10-077-2003 (Rel. 42, Last annotation update)
Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 CFTANGADYRGTQSWTALQGGKPCLFWNE--TFQHPYNTLKYPNGEGGLGEHNYCRNPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura T., Nakamura T.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Wnt/beta-catenin signaling (By similarity).
-!- SUBCELJULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Contains 1 CUB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 210 WSC.
214 321 CUB.
59 8-N-LINKED (GLCNAC. .) (POTENTIAL).
259 257 N-LINKED (GLCNAC. .) (POTENTIAL).
255 258 N-LINKED (GLCNAC. .) (POTENTIAL).
293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
343 N-LINKED (GLCNAC. .) (POTENTIAL).
345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.2%; Score 159; DB 1; Length 473; Best Local Similarity 45.6%; Pred. No. 8.1e-11; Matches 31; Conservative 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Transmembrane, Kringle.
POTENTIAL.
KREMEN PROTEIN 1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
KRINGLE.
                                                                                                                                           MSSP; VOU/44; LLEA.

MGD; MGI:1933988; Kremen.

GO; GO:0016021; C:integral to membrane; NAS.
InterPro; IPR000859; CUB.
InterPro; IPR00081; Kringle.
InterPro; IPR0001; Kringle.
InterPro; IPR001; Kringle.
InterPro; IPR001; Kringle.
Ffam; PF0041; CUB.
Pfam; PF0041; Kringle: 1.
Pfam; PF0041; Kringle: 1.
Pfam; PF00182; WSC; 1.
Pfam; PF00182; WSC; 1.
PROSITE; P801180; CUB; 1.
PROSITE; P801180; CUB; 1.
PROSITE; P801180; CUB; 1.
PROSITE; P801180; CUB; 1.
PROSITE; P801040; KRINGLE 1; 1.
PROSITE; P801040; KRINGLE 2; 1.
PROSITE; P801041, TANDAMAN POTENTIAL.
entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                            EMBL, AB059617; BAB40968.1; -.
HSSP; P00747; 1CBA.
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C the European Bloinformatics Institute. There are no restrictions on its monitoring of the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/corsential removed a license agreement (See http://www.isb-sib.ch/announce/corsend as mail to license@isb-sib.ch).

EMBL: AB065009; BAB62003.1; DR GO; GO:0016021; C:integral to membrane; ISS.

BR InterPro; IPRO0080; Kringle.

BR InterPro; IPRO0080; Kringle.

BR PETRY, SMO0015; Kringle; I.

BR PETRY; SMO0015; Kringle; I.

BR PETRY; SMO0015; Kringle; I.

BR PETRY; SMO0015; Kringle; I.

BR PROSITE; PSSO002; KRINGLE; I.

BR PROSITE; PSSO002; KRINGLE; I.

FT CHAIN

BR PROSITE; PSSO007; KRINGLE; I.

FT CHAIN

C STEAL STANDER CHAIN CHAIN CHAIN COUNTIAL).

FT DOWAIN

THE STANDER CHAIN -!- SIMILARITY: Contains 1 WSC domain

GRT.T-000-000-00-

3 CYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60 Query Match 31.2%; Score 159; DB 1; Length 473; Best Local Similarity 45.6%; Pred. No. 8.1e-11; Matches 31; Conservative 7; Mismatches 26; Indels 4; Gaps 61 RRRPWCYV 68 90 DVSPWCYV 97 ò d ò

KRNI XENLA STANDARD; PRT; 452 AA.

G90Y907

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor)

KREMENI. RESULT 23
KRM1_XENLA

Xenopus laevis (African clawed frog).
Mekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.

[1] SEQUENCE FROM N.A. Nakamura T.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
to block Mar/Derea-catenin signaling (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

-1- SIMILARITY: Contains 1 CUB domain.

-1- SIMILARITY: Contains 1 WSC domain.

-1- SIMILARITY: Contains as Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no was entities requires a license agreement (see http://www.isb-sib.ch/announce, or send an email to license@lsb-sib.ch). 139 CTB.
143 N-LINKED (GLCNAC. .) (POTENTIAL).
157 N-LINKED (GLCNAC. .) (POTENTIAL).
158 N-LINKED (GLCNAC. .) (POTENTIAL).
1591 N-LINKED (GLCNAC. .) (POTENTIAL).
1591 N-LINKED (GLCNAC. .) (POTENTIAL).
150188 MM; ED248CD1AF4564E2 CRC64; Query Match 31.0%; Score 158; DB 1; Length 452; Best Local Similarity 44.1%; Pred. No. 1e-10; Matches 30; Conservative 9; Mismatches 25; Indels 4; POTENTIAL. KREMEN PROTEIN 1. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). KRINGLE. WSC. ENEL; ABO70851; BAB64294.1; InterPro; IPR000801; Kringle.
InterPro; IPR000801; Kringle.
InterPro; IPR000801; Kringle.
Ffam; PF00131; CUB; 1.
Ffam; PF00135; Kringle; 1.
Fram; PF001395; Kringle; 1.
FrankT; SM001395; Kringle; 1.
SWART; SM00131; WSC; 1.
FROSITE; FS01180; CUB; 1.
FROSITE; FS010021; KRINGLE 1; 1.
FROSITE; FS010021; KRINGLE 2; 1.
FROSITE; FS00021; KRINGLE 2; 1 SOLUTION STATEMENT OF STATEMENT g

61 RRRPWCYV 68 ð

88 DVSPWCYI 95

RESULT 24

KRM1 HUMAN STANDARD; PRT; 475 AA.

AC Q96NŪ8; Q9BY70; Q9UGS5; Q9UGU1;

DT 28-FFBE-2003 (Rel. 41, Created)

DT 10-OCT-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Kreman protein 1 precursor (Kringle-containing protein marking the on the nose) (Dickkopf receptor).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. SEQUENCE FROM N.A. (ISOFORM 1). Homo sapiens (Human) NCBI_TaxID=9606;

Tashiro H., Yamazaki M., Watenabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamaten A., Ishii S. Yamamoto J. Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Nakamura T., Nakamura T.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. (ISOFORM 2)

REDURANCE FROM N.A.

REDURANCE C.P. Grant N. Ainscough R. N. Baces K. N. Beasaly O. P.

REDURANCE C.P. Balley S. E. Barddemar.A. M. Baces K. N. Beasaly O. P.

REDURANCE C.P. Carder C. Collier R.E., Connor R. Connor R. Connor N. Carder C. Collier R.E., Connor R. Connor N. Carder C. Collier R.E., Connor R. Carder C. Collier R.E., David C. B. Carder C. Collier R.E., Connor R. Carder C. Collier R.E., Connor R. Carder C. Sandley S. Morthure S. Morthure S. Carder C. Sandley S. Smith M. L., Rockelling C. B. Schaff H.K. Steward C. A. Sandley S. Smith M. L., Milliams C. L. Williams C. M. Williams C. C. Hubbard T. Bantley D. M. Williams C. L. Williams C. A. Williams C. C. Milliams C. C. Milliams C. C. Milliams C. Carder C. D. Georges S. Lad H. Carder C. Carder C. D. Carder S. Lad H. Word C. Carder C. Carde

Nature 402:489-495(1999)

-1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Wht/bera-catenin signaling (By similarity).
-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

IsoId=096MU8-1; Sequence=Displayed;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no war modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch) N-LINKED (GLCNAC. . .) (POTENTIAL). VSD -> AIQDSEVTSLIWSQGQPRSI (in isoform (POTENTIAL) : (POTENTIAL) : (POTENTIAL) : 4 ; (POTENTIAL) 30.6%; Score 156; DB 1; Length 475; 44.1%; Pred. No. 1.8e-10; arive 8; Mismatches 26; Indels 29 30 Mrssing (IN REF. 1).
206 206 I -> V (IN REF. 2).
475 AA, 51898 MW, B7E86FD80F96A0A4 CRC64; PRINTS, PROSES, KRINGLE.
PRODOM, PROSES, KRINGLE.
PRODOM, PROSES, KRINGLE.
SWART; SMOO130; KR; 1.
PROSITE; PSO1180; CUB; 1.
PROSITE; PSO5021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 1; 1.
Wht signaling pathway; Signal; Transmembrane; Kringle; SIGNAL EXTRACELLULAR (POTENTIAL) POTENTIAL) CYTOPLASMIC (POTENTIAL). KRINGLE, IsoId=Q96MU8-2; Sequence=VSP 003900; Note=No experimental confirmation available; -!- SIMILARITY: Contains 1 CUB domain. -!- SIMILARITY: Contains 1 kringle domain. -!- SIMILARITY: Contains 1 WSC domain. EMBL, AB059618; BAB40969.1; EMBL, AR056425; BAB71180.1; EMBL, AL021393; CAB62952.1; EMBL, AL021393; CAB62959.1; Genew, HGNC:17550; KREMENI.
GO; GO:0016021; C:Infegral to membrane; ISS.
GO; GO:0005624; C:membrane fraction; TAS.
Interpro; IPR000859; CUB.
Interpro; IPR000895; CUB.
Interpro; IPR0019; Kringle.
Interpro; IPR0019; Kringle.
From: PF00431; CUB.
Pfam; PF00431; CUB.
Pfam; PF00431; CUB.
Pfam; PF00451; Kringle; I.
Pfam; PF00451; Kringle; I. (GLCNAC. (GLCNAC. (GLCNAC. POTENTIAL. KREMEN PROTEIN N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED Query Match
Query Match
Best Local Similarity 44.11,
Best Local 30; Conservative CONFLICT CONFLICT SEQUENCE DOMAIN TRANSMEM DOMAIN DOMAIN DOMAIN DOMAIN CARBOHYD CARBOHYD CARBOHYD VARSPLIC CARBOHYD CARBOHYD CARBOHYD

3 CYEGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60 91 d

61 RRRPWCYV 68 DVSPWCYV ò

25 RESULT

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CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.

MEDLINE=2103595, PubMed=11294842;

Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;

"Structural elucidation of the N- and O-glycans of human apolipoprotein(a): role of o-glycans in conferring protease resistance.";

J. Biol. Chem. 276:22200-22208(2001).

K. SAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.

MEDLINE=96217891; PubMed=8642595,

M Mixol. V. Lograsso P.V., Boetrcher B.R.;

"Crystal structures of apolipoprotein(a) kringle IV37 free and complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic J. Mol. Biol. 256:751-761(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTM: N- and O-glycosylated. The N-glycans are complex biantennary structures present in either a mono- or disialylated state. The O-glycans are mostly (80%) represented by the monosialylated core type I structure, NeuMacalpha-36albetal-36alMac, with smaller amounts of disialylated and non-sialylated O-glycans also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95002201; PubMed=7918682;
MEDLINE=95002201; PubMed=7918682;
Scanu A.M., Pfaffinger D., Lee J.C., Hinman J.;
Raingle point mutation (Trp72--Arg) in human apo(a) kringle 4-37 associated with a lysine binding defect in Lp(a).";
Biochim. Biophys. Acta 1227.445(1994).
-!- FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has sorine proteinase activity and is able of autoproteolysis. Inhibits tissue-type plasminogen activator 1.
Lp(a) may be a ligand for megalin/Gp 330.
-!- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
           SERINE PROTEASE ACTIVITY.
SERINE PROTEASE ACTIVITY.
MEDLINE=90076123; Pubmed=2531657;
Salonen E.-M., Jauhiainen M., Zardi L., Vaheri A., Ehnholm C.;
"Lipoprotein(a) binds to fibronectin and has serine proteinase activity capable of cleaving it.";
EMBO J. 8:4035-4040(1989).
                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=88039109; PubMed=3670400;
MCLean J.W., Tennison J.E., Kuang W.-J., Eaton D.L., Chen B Fless G.M., Scanu A.M., Lawn R.M.;
"CDNA sequence of human apolipoprotein(a) is homologous to
    PRT; 4548 AA
                                                                                                                                                                                                                                                                                                                                                                                                               REVIEW.
MEDLINE=90049223; PubMed=2530631;
Utermann G.;
The mysteries of lipoprotein(a).";
Science 246:904-910(1989).
                                                                                                                                                                                                                                                             plasminogen.";
Nature 330:132-137(1987),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  decorin.
APOA HUMAN
P08519;
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DISEASE: Elevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with atherosclerosis. Homology with plasminogem kringles IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin(ogen) binding.

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PEREL, X06520; CAA2518.1; -..

PEREL, X06520; CAA2518.1; -..

PEREL, X06521; S00657, S
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KRINGLE TYPE IV, 1.
KRINGLE TYPE IV, 2.
KRINGLE TYPE IV, 3.
KRINGLE TYPE IV, 4.
KRINGLE TYPE IV, 6.
KRINGLE TYPE IV, 6.
KRINGLE TYPE IV, 9.
KRINGLE TYPE IV, 9.
KRINGLE TYPE IV, 9.
KRINGLE TYPE IV, 110.
KRINGLE TYPE IV, 110.
KRINGLE TYPE IV, 112.
KRINGLE TYPE IV, 113.
KRINGLE TYPE IV, 12.
KRINGLE TYPE IV, 12.
KRINGLE TYPE IV, 15.
KRINGLE TYPE IV, 15.
KRINGLE TYPE IV, 16.
KRINGLE TYPE IV, 16.
KRINGLE TYPE IV, 19.
KRINGLE TYPE IV, 19.
KRINGLE TYPE IV, 19.
KRINGLE TYPE IV, 20.
KRINGLE TYPE IV, 20.
KRINGLE TYPE IV, 21.
KRINGLE TYPE IV, 21.
KRINGLE TYPE IV, 22.
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112 RQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTM-----NYCRNP 4176
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No. 121

No. 121

No. 124

No. 126.4 AND 525-550.

No. 127

No. 127

No. 128

No. 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
F12.
KRINGLE TYPE IV, 25.
KRINGLE TYPE IV, 26.
KRINGLE TYPE IV, 27.
KRINGLE TYPE IV, 29.
KRINGLE TYPE IV, 29.
KRINGLE TYPE IV, 30.
KRINGLE TYPE IV, 31.
KRINGLE TYPE IV, 31.
KRINGLE TYPE IV, 33.
KRINGLE TYPE IV, 33.
KRINGLE TYPE IV, 34.
KRINGLE TYPE IV, 34.
KRINGLE TYPE IV, 35.
KRINGLE TYPE IV, 36.
KRINGLE TYPE IV, 36.
KRINGLE TYPE IV, 36.
KRINGLE TYPE IV, 37.
KRINGLE TYPE IV, 36.
KRINGLE TYPE IV, 37.
KRINGLE TYPE IV, 36.
KRINGLE T
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4548 AA; 501313 MW; 96921BE96A465C5F CRC64;
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Best Local Similarity 37,88;
Conservative
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      RESULT 26
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AC P98140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 CYQGNGKSYRGTSSTINTGKKCQSW----VSWIPHSHSKIPANFDSGL-EMNYCRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQL---GLGKHNYCRNPD
                 immediately after dissociation from the clot.
-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Contains 5 kringle domains.
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R H58P; P00747; 1PWK.

R H58P; P00747; 1PWK.

R H58P; P00747; 1PWK.

R InterPro; 1PR001051; Kringle.

InterPro; 1PR001254; Peptidase S1.

R InterPro; 1PR00156; Peptidase S1.

R InterPro; 1PR00156; PR0THROMEN.

PRINTS; PR00018; KRINGLE.

R PRODON; PR00189; KRINGLE.

R PROSTIE; PS00130; KR; 1.

R PROSTIE; PS00130; KR; 1.

R PROSTIE; PS00131; RXPSIN_DOM; PARTIAL.

R PROSTIE; PS00134; TRYPSIN_DOM; PARTIAL.

R PROSTIE; PS0134; TRYPSIN_DOM; PARTIAL.

R PROSTIE; PS0134; TRYPSIN_SER; PARTIAL.

W TYSIUE remodeling; Blood coagulation; Kringle; Repeat.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovinae; Bovinae; Bos.
NCBL_TaxID=9913;
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Berglund L., Andersen M.D., Petersen T.E.;
"Cloning and characterization of the bovine plasminogen cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.3%; Score 149.5; DB 1; Length 169; 37.8%; Pred. No. 3.4e-10; ive 12; Mismatches 29; Indels 15;
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KRINGLE 4 (BY SIMILARITY).
KRINGLE 5 (BY SIMILARITY).
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34 112 KRINGLE 4 (BY SIMILARITY).
34 112 KRINGLE 5 (BY SIMILARITY).
55 95 BY SIMILARITY.
55 95 BY SIMILARITY.
169 AA, 18401 MW, 77A54214C49D010C CRC64;
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01-JAN-1988 (Rel. 06, Created)
NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Plasminogen precursor (EC 3.4.21.7).
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Best Local Similarity 37.8;
Matches 34; Conservative
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PLMN BOVIN
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=9125078; PubMed=1645711;

Ranalas J.G., Makker S.P.;

Ranalas J.G., Makker S.P.;

Ranalas J.G., Makker S.P.;

"Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor site for plasminogen.";

"Identification of the rat Heymann nephritis autoantigen (GP330) as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the unxinase-type plasminogen activator, collagenases and several complement zymogens, such as CI and CS.

It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

C.-: CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 SCYDDRDRGLSYRGMAGTTLSGAPCQSWAS----BATYWNVTAEQVLNWGLGDHAFCRNP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TCYE--GNGHFYRGKASTDIMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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BNZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with screptokinase.

MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
BY SIMILARITY.
BY SIM
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 DNRRRPWCYVQVGLKPLVQECMVHDC 84
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          RESULT 27
PLWN RAT
ID PLWN RAT
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                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88185329; PubMed=3356193;

Marti T., Schaller J., Rickli E.B., Schmid K., Kamerling J.P.,

Gerwig G-J., van Halbeek H., Vilegenthart J.F.;

"The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns.";

Lucosylation patterns.";

Eur. J. Biochem. 173:57:63(1988).

-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteclytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such activator, collagenases fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-xaa > Arg-|-xaa, hughers selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- BNZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptchinase.
-!- PTM: N-LINKED GLYCAN CONTAIN N-ACETYLLACTOSAMINE AND SIALIC ACID. D-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
-!- SIMILARITY: Belongs to opetidase family $1. Plasminogen subfamily.
-!- SIMILARITY: Contains 5 kringle domains.
                                                                                                                                                                                             SEQUENCE OF 706-812 FROM N.A.
MEDLINE-85023311; PubMed-6148961;
Malinowski D.P., Sadler J.E., Davie B.W.;
"Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.";
Biochemistry 23:4243-4250(1984).
                                 SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
MEDLINE-85203906; PubMed-3846522;
Schaller J., Moser P.W., Dannegger-Muller G.A.K., Rosselet S.J.,
Kampfer U., Rickli E.E.;
"Complete amino acid sequence of bovine plasminogen. Comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003609; Pan_app.
IPR001254; Peptidase_S1.
IPR001314; Peptidase_S1A.
IPR003966; Peptidase_S1A.pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR000001; Kringle.
                                                                                                                                                            Eur. J. Biochem. 149:267-278(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00722; CHYMOTRYPSIN.
PR00018; KRINGLE.
Int. Dairy J. 5:593-603 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X79402; CAA55939.1; -. EMBL; K02935; AAA30714.1; -.
                                                                                                                                                                                                                                                                                                                                     CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00051; kringle; Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlycoSuiteDB; P06868;
                                                                                                                                         plasminogen.
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384 CYHGNGQSYRGTSSTTITGRKCQSWSS-----MTPHRHLKTPENYPNAGL-TMNYCRNPD 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Ovarian carcinoma;
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
Suzuki Y., Nagai K., Sugano S., Ishli S., Kawai-Hio Y., Salto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBNOWN STANDARD; PRT; 462 AA.
OBNOUG; QBNOUG; QBNOWN; QBGGLB; QBBTP9;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
10-OCT-2005 (Rel. 42, Last amotation update)
10-OCT-2006 (Booker amotation update)
10-OCT-2007 (RAM2.)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                         SMART; SM00020; Tryg_SPc; 1.

PROSITE; PS00021; KRINGLE 1; 5.

PROSITE; PS50200; KRINGLE 2; 5.

PROSITE; PS00134; TRYPSIN Dow; 1.

PROSITE; PS00134; TRYPSIN JES; 1.

PROSITE; PS00135; TRYPSIN JES; 1.

Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
Tanaka S., Sudimachi K.,
"Human Kremanz and Wnt signaling.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N -> D (IN REF. 2).
Q -> H (IN REF. 2).
P -> L (IN REF. 2).
T -> R (IN REF. 3).
38A6AA691E220946 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=CAR 000015.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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/FTIG=CAR 000014.
O-LINKED (GALNAC.
                                                                                                                                                                                                                                                                                                                                                                   PLASMINOGEN.
PLASMIN HEAVY CHP
PLASMIN LIGHT CHP
KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
KRINGLE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2e-0
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 ADKSPWCYT---TDPRVRWEFCNLKKCSE 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 NRRRPWCYVQVGLKPLV--QECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.2%; Score 149; 39.3%; Pred. No. 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91216 MW;
Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 39.3
Matches 35, Conservative
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ProDom; PD000395; Kringle;

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REAL SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).

REAL SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).

REAL SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).

REAL SETABLES TO EXAMPLE TO THE SETATOR TO THE SECOND SETATOR TO THE SETATOR TO T
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human cDNA sequencing project.", Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-2; Synonyme=Kremen2a;
Isold=QBNCW0-2; Sequence=VSP_050509, VSP_050510;
Name=3; Synonyme=Kremen2b;
Isold=QBNCW0-3; Sequence=VSP_050511, VSP_050512;
Name=4; Synonyms=Kremen2c;
Isold=QBNCW0-4; Sequence=VSP_050513, VSP_050512;
-!- SIMILARITY: Contains 1 CUB domain.
-!- SIMILARITY: Contains 1 Kringle domain.
-!- SIMILARITY: Contains 1 Kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=1;
IsoId=Q8NCW0-1; Sequence=Displayed;
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PLMN ERIEU
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This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way conditied and this statement is not removed. Usage by and for commercial continuities a license agreement (See http://www.isb-sib.ch/announce/corsending and an email to license agreement (See http://www.isb-sib.ch/announce/corsending and an email to license@isb-sib.ch).

EMBL; AB086455; BAC00823.1; ...

EMBL; AB086355; BAC00824.1; ...

EMBL; AR08535; BAC00825.1; ...

EMBL; AR085333 AAH03333.1; ...

EMBL; AR09333; AAH03333.1; ...

EMBL; BC005933; AAH09383.1; ...

EMBL; BC005933; AAH09383.1; ...

EMBL; BC005933; AAH09383.1; ...

EMBL; BC00593; AAH09383.1; ...

EMBL; BC005933; AAH09383.1; ...

EMBL; BC005934; AAH09383.1; ...

EMBL; BC00505; EMBL; EMBRENZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew, HGNC:18797; KREMEN2.
InterPro: IPR000859; CUB.
InterPro: IPR000001; Kringle.
InterPro: IPR000899; WSC.
Fram: PP00431; CUB; 1.
Pfam: PP00051; Kringle; 1.
Pfam; PP01822; WSC: 1.
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Pfam; PF01822; WSC; 1. PRINTS; PR00018; KRINGLE.

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3 CYEGNGHFYRG---KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                               Missing (In isoform 2).
/FITG=VSP 050510.
ASYSTYTATASVALLILIGILRPRRRSCLLAPGKGPPALG ASRGPRRSWAWY -> GAVCWIREKGPRRWGLPGAPGEAG LCGTNSPEGWPCPAPPGTPRLNVLPRATGL (in
                                                                                                                                                                                                                                                                                     /FTId=VSP_050511.
Missing (In isoform 3).
FTId=VSP_050512.
ARVESTYTAVSVLLILLIGILREPLERRSCILAP -> GEAG
ARDGSESGSRPLAPILITAAVCPQPGSSRR (in isoform
                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
SCLLAPGKGPPALGASRGPRRSWAVWYQQPR -> CGALGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
NCBI TaxID=9365;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                     GLRADRWWGAGAPEGNRARKELLGS (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                         Score 148.5; DB 1; Length 462; Pred, No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                         /FIId=VSP 050513.

Missing (In isoform 4).
/FIId=VSP 050514.
202 Missing (In Ref. 2; BAC11365).
285 A -> D (in Ref. 2; BAC11365).
48849 MW; CE33015917A9AA68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Erinaceus europaeus (Western European hedgehog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Plasminogen precursor (EC 3.4.21.7).
                                                                                                                                                                                                                      FTIG=VSP_050509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810 AA
                                                                                                                                                                                                                                                                              soform 3
                                                                                                                                                                                                                                                                                                                                                                                                                               29; Conservative
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       SMART; SM00042; CUB; 1.
SMART; SM00130; KR; 1.
SMART; SM00321; WSC; 1.
                                                                                                                                                                                                                                                   420
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                                                                                                                                                                                                                                                                                                                                                                       164 2
285 2
462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
TISSUE=Liver;
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Q29485;
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                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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MEDLINE=96025778; PubMed=7592597;
Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
Byrne C.D., Fong K.J., Meer K., Patthy L.;
"The recurring evolution of lipoprotein(a). Insights from cloning hedgehog apolipoprotein(a).";
J. Biol. Chem. 270:24004-24009(1995).

EAVISIONS.
Lawn R.M.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a protecolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator; collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa, higher selectivity than trypsin. Converts fibrin into soluble

products.
-!- FUNTAR REGULATION: Converted into plasmin by plasminogen activators both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
-!- MISCELLANBOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Contains 5 kringle domains.

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EMBL: U3311; AAC48717.1; -..

REMEL: U3311; AAC48717.1; -..

REMEL: U46260; 146260.

RESP: POOT47: 1PWG.

RECPEC: IPRO09003; Cys_Ser_trypsin.

InterPro: IPR003001; Kringle.

RICEPPO: IPR003001; PRD14; PAN.

RICEPPO: IPR00314; PAN.

RECPPO: IPR00314; RAINGLE.

RECPPO: IPR00314; RAINGLE.

RECPPO: IPR00314; RAINGLE.

RECPPO: IPR00314; RAINGLE.

RECPPO: IPR00315; RAINGLE.

RECPPO: IPR00314; RAINGLE.

RECPPOSITE: PR00314; RAINGL

(BY (BY PLASMINOCEN.
PLASMIN HEAVY CHAIN A (I PLASMIN LIGHT CHAIN B (I SERINE PROTEASE.
KRINGLE 1.
KRINGLE 2. BY SIMILARITY. 19 810 810 810 181 Signal. SIGNAL CHAIN CHAIN DOMAIN DOMAIN DOMAIN

SIMILARITY) SIMILARITY)

3 CYBGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62 э Э .) (POTENTIAL) 29.1%; Score 148.5; DB 1; Length 810; 41.5%; Pred. No. 2.3e-09; rive 7; Mismatches 28; Indels 3; 352 KRINGLE 3.
456 KRINGLE 4.
561 KRINGLE 5.
622 CHARGE RELAY SYSTEM.
665 CHARGE RELAY SYSTEM.
760 CHARGE RELAY SYSTEM.
733 N-LINKED (GLCNAC. ...) (POTE 9.0902 NW; 8E75780946017A16 CRC64; 27; Conservative 352 456 561 622 665 760 339 Query Match Best Local Similarity 275 379 482 482 622 665 760 780 339 436 GPWCY 440 63 RPWCY 67 DOMAIN DOMAIN DOMAIN ACT SITE ACT SITE ACT SITE SEQUENCE Matches SCHEFFE ઠે ద ઠ 셤

RESULT 31 PLMN PIG ID PLMN PIG AC P06867;

01-JAN'-1988 (Rel. 06, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Plasminogen (EC 3.4.21.7). PLG.

Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus. Sus scrofa (Pig)

[1] SEQUENCE OF 1-560. SEQUENCE OF 1. Reempfer U., Rickli E.E., Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.E., Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the carbohydrate attachment sites with the human and bovine

SEQUENCE OF 450-790.
MEDLINE-85203907; PubMed=3846533;
Marti T., Schaller J., Rickli B.E.;
"Determination of the complete amino-acid sequence of miniplasminogen.";

porcine

Eur. J. Biochem. 149:279-285(1985).

MEDLINE=88185329; PubMed=3356193;
MEDLINE=88185329; PubMed=3356193;
MEDLINE=88185329; PubMed=3356193;
MEDLINE=88185329; PubMed=3356193;
MEDLINE=88185329; PubMed=3356193;
MET 1. Schaller J. Rickli E.E., Schmid K., Kamerling J.P.,
Merwig G.J., van Halbeek H., Vliegenthart J.F.;
Merwig G.J., van Halbeek H., Vliegenthart J. And C.J., and C.J.;
Millebrand factor:

ENZYME REGULATION: Converted into plasmin by plasminogen cativators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase. PTM: N-LINKED GLYCAN CONPAINS N-ACETYLLACTOSAMINE, SIALIC ACID AND

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358 CYRGNGESYRGTSSTTITGRKCQSW-----VSMTPHRHEKTPGNFPNAGL-TMNYCRNPD 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CYBGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHR---SDALQLGLGKHNYCRNPD 59
                                      (MICROHETEROGENEITY)

-!- MISCELLANDEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
-!- SIMILARITY: Belongs to peptidase family SI. Plasminogen subfamily.
-!- SIMILARITY: Contains 5 kringle domains.
PIR; PO0747; SHPG.
MEROPS; S01.233;
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                                                                                                                                                                                                      MIGETEC: JPR009003; Cys_Ser_trypsin.

MIGETEC: JPR009003; Cys_Ser_trypsin.

MIGETEC: JPR000001; Kringle.

MIGETEC: JPR000001; Kringle.

MIGETEC: JPR001014; PAN.

MIGHERETC: JPR001014; PAN.

MIGHERETC: JPR001014; PAN.

MINGLE: PAN.

MINGLE: PAN.

MINGLE: JAN.

MART; SM00130; KR.

MART; SM00130; KR.

MART; SM00130; KR.

MART; SM00130; KR.

MART; MINGLE: J.

MART; MINGLE: JAN.

MART; MINGLE: JA
IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
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Pred. No. 2.6e-09;
8; Mismatches 33; Indels 14;
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Q01974; Q9H8G1;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Tyrosine-protein kinase transmembrane receptor ROR2 precursor
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KRINGLE 2.
KRINGLE 4.
KRINGLE 4.
KRINGLE 5.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . .).
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O-LINKED (GALNAC. .).
/FIId=CAR 000020.
; F04EA06E74ECD58E CRC64;
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Local Similarity 38.2%;
hes 34; Conservative
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ROR2 HUMAN
ID ROR2 HT
AC Q01974
DT 16-OCT-
DT 15-MARR
DE TYIOSII
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RRATHUM.

RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,

Ra Brusel W., Skovby P., Karr B., Percin E.P., Akarsu N., Brunner H.G.,

RL Genet. 26:383-383 (2000).

1. FUNCTION: Tyrosine-protein kinase receptor which may be involved

1. In the early formation of the chondrocytes. It seems to be

1. required for cartilage and growth plate development.

1. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

1. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

1. SUBCELLULAR LOCATION: Type I membrane protein.

1. SUBCELLULAR LOCATION: Type I membrane protein.

1. SUBCELLULAR LOCATION: Type I membrane protein.

2. SUBCELLULAR LOCATION: Type I membrane protein.

3. SUBCELLULAR LOCATION: Type I membrane protein.

4. SUBCELLULAR LOCATION: Type I membrane protein.

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4. SUBCELLULAR LOCATION: Type I membrane protein.

5. SUBCELLULAR LOCATION: Type I membrane protein.

6. SUBCELLUL
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MEDLINE=20392394; PubMed=10932186;
Afzal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,
Ternes-Pereira E., Tueysuez B., Murday V.A., Patton M.A.,
Wilkie A.O.M., Jeffery S.;
"Recessive Robinow syndrome, allelic to dominant brachydactyly type I is caused by mutation of ROR2.";
Nat. Genet. 25:419-422(2000).
                                                                                                                                                              (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=9100347; PubMed=1334494;
Masiakowski P., Carroll R.D.;
"A novel family of cell surface receptors with tyrosine kinase-like domain.";
John 1. Chem. 267:26181-26190(1992).
J. Biol. Chem. 267:26181-26190 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 34-574 FROM N.A., AND VARIANT THR-245.
MEDLINE=20442029; PubMed=10986040;
Schwabe G.C., Tinschert S., Buschow C., Meinecke P., Wolff G.,
Gillessen-Kaesbach G., Oldridge M., Wilkie A.O.M., Koemec R.,
Mundlos S.,
"Distinct mutations in the receptor tyrosine kinase gene ROR2 cause
brachydactyly type B.",
Am. J. Hum. Genet. 67:822-831(2000).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 34-943 FROM N.A., AND VARIANT ILE-819.
MEDLINE-20164326; PubMed=10700182;
Oldridge M., Fortuna A.M., Maringa M., Propping P., Mansour S.,
Pollitt C., Dechiara T.M., Kimble R.B., Valenzuela D.M.,
Yancopoulos G.D., Wilkie A.O.M.;
Pominant mutations in RORZ, encoding an orphan receptor tyrosine
kinaee, cause brachydactyly type B.";
Nat. Genet. 24:275-278(2000).
                                                      Homo sapiens (Human).
Bukaryota, Methazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT RRS TYR-182. MEDALFR220392395; PubMed=10932187; MEDLLIRE_20392395; PubMed=10932187; MEDLLIRE_20392395; PubMed=10932187; Mer Bokhoven H., Calli J., Kayserlli H., van Beusekom E., Balci Brussel W., Skovby F., Kerr B., Percin E.P., Akarsu N., Brunner "Mutafion of the gene encoding the ROR2 tyrosine kinase causes autosomal recessive Robinow syndrome."; Mer Genet. 25:423-426(2000).
2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related OR NIRKR2.
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3 CYEGNGHFYRGKASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
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MEDLINE=99246426; PubMed=10231392;
Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T.; Liu Z.J.,
Platta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.;
"Spatio-temporally regulated expression of receptor tyrosine kinases,
mRorl, mRorl, mRors, during mouse development: implications in development
and function of the nervous system.";
Genes Cells 4:41-56(1999).
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                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
BY SIMILARITY.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinee, Mus
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annoration update)
17rosine-protein kinase transmembrane receptor ROR2 precursor (RC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2) (mROR2).
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             EXTRACELLULAR (POTENTIAL)
                                                          CYTOPLASMIC (POTENTIAL)
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
C -> Y (in RRS).
/FTId=VAR_010911.
R -> C (in RRS).
/FTId=VAR_010768.
R -> W (in RRS).
/FTId=VAR_010769.
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KRINGLE,
PROTEIN KINASE,
SER/THR-RICH,
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CHARACTERIZATION
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ID ROR2 MOUSE
AC Q92138;
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ROJ GO.0004114; F:transmembrane receptor protein tyrosine kin. ..;

ROJ GO.0004125; F:transmembrane receptor protein tyrosine kin. ..;

ROJ GO.000725; P:edevelopment; TAS.

ROJ GO.0007165; P:edevelopment; TAS.

RICEPTO: IPRO0024; Fz domain.

InterPro; IPRO00219; Fz domain.

InterPro; IPRO00119; IPRODE INTERPRODE INTERP
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TYROSINE-PROTEIN KINASE TRANSMEMBRANE
RECEPTOR ROR2.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR subfamily.
-!- SIMILARITY: Contains I frizzled (FZ) domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- SIMILARITY: Contains 1 kringle domain.
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HSSP; P00747; IKRN.
Genew, HGNC:10257; ROR2.
MIM; 602337; -.
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KRM2 MOUSE
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                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MEDLINE=20164325; PubMed=10700181;
DeChiara T.M., Kimble R.B., Poueymirou W.T., Rojas J., Masiakowski P., Valenzudła D.M., Yancopoulos (J.D.;
"Ror2, encoding a receptor-like tyrosine kinase, is required for cartilage and growth plate development.";
Nat. Genet. 24:271-274(2000).
-! FUNCTION: Tyrosine-protein kinase receptor which may be involved in the early formation of the chondrocytes. It seems to be required for cartilage and growth plate development.
-! CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-! SUBCELLULAR LOCATION: Type I membrane protein.
-! SUBCELLULAR LOCATION: Type I membrane protein kinases. ROR
                                                                                                                                                                                                                                                                                                                                                                                                                   ENEL; ABO10384; BAA75491.1; -

ENCL GO. GO. 001501; P: skeletal development; IMP.

InterPro; IPR0007018; Fz. domain.

EnterPro; IPR00145; Tyr_Dkinase.

EnterPro; IPR00145; Tyr_Dkinase.

EnterPro; IPR00145; Fz. domain.

EnterPro; 
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RECEPTOR ROR2.
                                                                                                                                                                                                                         subfamily.
-!- SIMILARITY: Contains 1 frizzled (FZ) domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- SIMILARITY: Contains 1 kringle domain.
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SER/THR-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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FZ,
KRINGLE.
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SER/THR-RICH.
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STRAIN=CSTBL/67, White Power of the Company of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 CYNGSGADYRGMASTTKSGHQCQPW----ALQHP-HSHRLSSTEFPELG-GGHAYCRNPG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHR---SDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Blckkopf receptor 2).
615 615 BY SIMILARITY.
646 646 PHOSPHORYLARITYON (AUTO-) (BY SIMILARITY).
83 135 BY SIMILARITY.
70 70 N-LINKED (GLCNAC. ...) (POTENTIAL).
188 188 N-LINKED (GLCNAC. ...) (POTENTIAL).
318 188 N-LINKED (GLCNAC. ...) (POTENTIAL).
944 AA; 105050 MW; CDZEBGC7103387A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   28.9%; Score 147.5; DB 1; Length 944;
41.4%; Pred. No. 3.5e-09;
ative 9; Mismatches 31; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 GQMEGPWCFTQ-NKNVRVBLCDVPPCS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 NRRR-PWCYVQVGLKPLVQECMVHDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCD; MGT:1920266; Kremen2.
InterPro: IPR000859; CUB.
InterPro: IPR000859; WSC.
InterPro: IPR00089; WSC.
Pfam; PP00051; Kringle.
Pfam; PP00051; Kringle; I.
Pfam; PP01051; Kringle; I.
PRINTS; PR0018; KRINGLE.
PRINTS; PR0018; KRINGLE.
SWART; SM00130; KR; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ457192; CAD29805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 41.4
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRM2 MOUSE
Q8K187;
ACT_SITE
MOD_RES
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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m

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DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
   CYEGNGHFYRGK---ASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                       Isold=Q01973-1; Sequence=Displayed;
Name=Short; Synonyms=T-ROR1;
Isold=Q01973-2; Sequence=VSP_005008;
TISSUE SPECIFICITY: Expressed Strongly in human heart, lung, and kidney, but weakly in the CNS. The short isoform is strongly
                                                                                                                                                                                                                                                                                                                          5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM SHORT).
MEDLINE=97030043; PubMed=8875995;
Reddy U.R., Phatek S., Pleasure D.;
"Human neural tissues express a truncated Rorl receptor tyrosine
kinase, lacking both extracellular and transmembrane domains.";
Oncogene 13:1555-1559(1996).
-!-FUNCTION: Tyrosine-protein kinase receptor whose role is not yet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A. (ISOFORM LONG).
MEDLINE=93100347; PubMd=1334494;
Masiakowski P., Carroll R.D.;
"A novel family of cell surface receptors with tyrosine kinase-like domain.";
J. Biol. Chem. 267:26181-26190(1992).
SMART; SM00321; WSC; 1.
PROSITE; PS01160; CUB; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
Wht signaling pathway; Glycoprocein; Kringle; Signal; Transmembrane.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOOR1 HUMAN STANDARD; PRT; 937 AA.

16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
17-MRA-2004 (Rel. 43, Last annotation update)
18-MRA-2004 (Neurotrophic tyrosine kinase, receptor-related 1).
18-MRA-2004 (Menan).
18-MRA-2004 (Menan).
18-MRA-2004 (Menan).
19-MRA-2004 (Menan).
19-MRA-
                                                                                                                                                                 WSC.
CUB.
N-LINED (GLCNAC. . .) (FOTENTIAL).
N-LINKED (GLCNAC. . .) (FOTENTIAL).
M; 6D58C4A2858E09DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                       28.7%; Score 146.5; DB 1; Length 461; 42.0%; Pred. No. 2.2e-09; iive 8; Mismatches 27; Indels 5;
                                                                                      KREMEN PROTEIN 2.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                             Ψ.
                                                                                                                                                                                                                                                             49170
                                                                                                                                                                                                                                                                                                      Local Similarity 42.0
les 29, Conservative
                                                                                         3863
3863
3864
321
321
322
350
350
350
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                                                                                                                                                                                                                                                                                                                                                                                                                60 NRRRPWCYV 68
                                                                                       255
364
364
387
134
120
2120
248
248
461
461
AA;
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                                                                                      CHAIN
DOWAIN
TRANSMEM
DOWAIN
DOWAIN
DOWAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 35
ROR1 HUMAN
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                                                                 EMBL, MN97673, AAA60275.1;

EMBL, MN97673, AAA60275.1;

EMBL, UN388494, AAA60275.1;

MIM, 602336;

CO, GO.0004714; Firtansmembrane receptor protein tyrosine kin...;

AC, GO.0004714; Firtansmembrane receptor protein tyrosine kin...;

BR InterPro; IPR00019; From kinase.

BR INTS; PR000109; From kinase.

BR INTS; PR000109; From kinase; I...

BR INTS; PR001019; From kinase; I...

BR INTS; PR001019; From kinase; I...

BR INTS; PR00101; From kinase; ATP-binding; Receptor;

Transferase; Tyrosine-Protein kinase; ATP-binding;

Transferase; Signal; Glancing, Allong, I...

BR INTS; PR00101; PROTEIN KINASE ATP; FALSE NEG;

Transferase; Tyrosine-Protein kinase;

Transferase; Tyrosine-Protein kinase;

Transferase; Signal; Allonging;

Transferase; Signal; Allonging;

Transferase; Signal; Allonging;

Transferase; Tyrosine-Protein kinase;

Transferase; Signal; Allonging;

Transferase;

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RECEPTOR ROR1.
EXTRACELLULAR (POTENTIAL).
expressed in fetal and adult CNS and in a variety of human cancers, including those originating from CNS or PNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
FZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH.
SER/THR-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRINGLE.
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Page 34

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OSGRETARO
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                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-99249426; PubMed=10231392; Magabukuro A., Ueda T., Liu Z.J., Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J., Hatta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.; Hatta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.; "Spatio-temporally regulated expression of receptor tyrosine kinases, mRori mRori, during mouse development: implications in development and function of the nervous system."; Genes Cells 4:41-56(1999).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Missing (In isoform Short).
/FITG-VSP 005008.
MM; OD0694DBF29F4773 CRC64;
                                                                                                                                                                                     3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLG--LGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                          RORI OR NTRKRI.

RURI Mus musculus (Mouse).

Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clear.
-! - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine prospate.
-! - SUBCELLULAR LOCATION: Type I membrane protein.
-! - SIMILARITY: Belongs to the Tyr family of protein kinases. ROR subfamily.
-! - SIMILARITY: Contains I frizzled (PZ) domain.
-! - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-! - SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase transmembrane receptor ROR1 precursor (BC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1) (MROR1).
                                                                                                                                                              .,
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                                                                                                                                   Query Match 28.6%; Score 146; DB 1; Length 937; Best Local Similarity 44.1%; Pred. No. 5.2e-09; Matches 30; Conservative 5; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                        937 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB010383; BAA75480.1; -. HSSP; P00747; 1CEA. MGD; MGI:1347520; Rorl. InterPro; IPR007024; Fz domain. InterPro; IPR007110; Ig-like. InterPro; IPR007110; Ig-c2.
                                                                                                              937 AA; 104312 MW;
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                                      47
66
184
315
549
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                                                                                                                                                                                                                                       61 RRR-PWCY
     615
645
749
1866
1544
154
                                                                                                                                                                                                                                                                                                                        RORI MOUSE
Q9Z139;
   ACT_SITE
MOD_RES
DISULPID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                            CARBOHYD
                                                                                                               SEQUENCE
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13 CYNSTGVDYRGTVSVTKSGRQCQPWNS----QYPHTHSFTALRFPELNGGHSYCRNPGN 367
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ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

M-LINKED (GLCNAC. . .) (POTENTIAL).

M-LINKED (GLCNAC. . .) (POTENTIAL).

MM; D728733267D1782C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLG--LGTGHYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%; Score 146; DB 1; Length 937;
44.1%; Pred. No. 5.2e-09;
tive 5; Mismatches 25; Indels 8; Gaps
InterPro; IPM00001; Kringle.

R InterPro; IPM0001245; Tyr_Ekinase.

R InterPro; IPM0001245; Tyr_Ekinase.

R InterPro; IPM0001245; Tyr_Ekinase.

R InterPro; IPM0001245; Tyr_Ekinase.

R InterPro; IPM001245; Tyr_Ekinase.

R InterPro; IPM001245; Tyr_Ekinase.

R InterPro; IPM00124; Ez; 1.

R Pfam; PF001061; Kringle; 1.

R PROMO15; Kringle; 1.

R ProDom; PD000001; Prot kinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R PROSITE; PS000021; KR; 1.

R PROSITE; PS000021; KRINGLE.; 1.

R ROSITE; PS000021; KRINGLE.; 1.

R ROSITE; PS00107; PROTEIN KINASE APP; FALSE_NEG.

R PROSITE; PS00107; PROTEIN KINASE APP; PALSE_NEG.

R PROSITE; PS00107; PROTEIN KINASE TYR; 1.

R PROSITE; PS00107; PROTEIN KINASE TRANSMEMBRANE

THANNOGLODULIN GOMAIN.

R TRANSMEMBRANE

THENDER TRANSMEMBRANE

THE STORY TYRESTORY TRANSMEMBRANE

THE STORY TYRESTORY TRANSMEMBRANE

THE STORY TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
TYROSINE-PROTEIN KINASE TRANSMEMBRANE
RECEPTOR ROR1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLG.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00747,
21-UL-1986 (Rel. 01, Created)
11-UAR-1999 (Rel. 10, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation update)
Plasminogen precursor (BC 3.4.21.7) [Contains: Angiostatin]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRINGLE.
PROTEIN KINASE.
SER/THR-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.6
Best Local Similarity 44.1
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 QKEAPWCF 375
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937 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
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MOD_RES
DISULFID
CARBOHYD
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CARBOHYD
CARBOHYD
SEQUENCE
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PLMN HUMAN
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OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES

Biol. Chem. 244:3590-3597(1969)

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Submitted (JUL-1977) to the PIR data bank.
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MEDLINE=69234739; PubMed=4240117;
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MEDLINE=77225245; Pubmed=142009;
                    NCBI_TaxID=9606;
  Mammalia;
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MEDLINES-97238710; PubMed=9102221;
Sim B.K., O'Reilly M.S., Lidang H., Fortier A.H., He W., Madsen J.W.,
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MEDLINE-92031503; PubMed-1657149;
Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
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MEDINES-2031502, Pubmeda-1657148,
Mulichak A.M., Tulinsky A., Ravichandran K.G.;
"Crystal and molecular structure of human plasminogen kringle
                                                                                                                                                                                                                                                                                                              FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
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Vali Z., Parthy L.;
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J. Biol. Chem. 259:13690-13694(1984).
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B., Yamano A., Whitlow M., Teeter M.M.;
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Biochemistry 30:10576-10588(1991).
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MEDINE-9334011; PubMed-8333443;

MEDINE-9334011; PubMed-8333443;

VOSDIMURE T., Yuhki, N., Wang M.H., Skeel A., Leonard B.J.;

VOSDIMURA T., Yuhki, N., Wang M.H., Skeel A., Leonard B.J.;

Cloning, Sequencing, and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of kringle proteins and locates the MSP gene on chromosome 3.";

J. Biol. Chem. 268:15461-15488(1993).

J. Biol. Chem. 268:15461-15488(1993).

J. FUNCTION: Probably has no proteolytic activity, since crucial AA characteristic of serine proteases catalytic sites are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I-PTM: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE HELD TOGETHER BY DISCULED BONDS. OR TWO SEPARATE POLYPEPTIDES.
-I-SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-I-SIMILARITY: Contains 4 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
HEPATOCYTE GROWTH PACTOR-LIKE PROTEIN.
PAP.
                                                                                                                  Han S., Stuart L.A., Friezner Degen S.J.; "Characterization of the DNT:582 locus on human chromosome 3: identification of a gene coding for four kringle domains with homology to hepatocyte growth factor."; Elochemistry 30:9768-9780(1991).
        SEQUENCE FROM N.A.
TISSUB-Liver;
MEDLINE=92002016; PubMed=1655021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M74178; AAA50165.1; --
EMBL; U37055; AAC50411.1; --
EMBL; L11224; AAA5972.1; --
PIR; A40331; A47136.
HSSP; P00747; 2PK4.
MEROPS; SO1.975; --
GENEW; HGNC:7380; MST1.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHR---SDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
MEDLINE-98198034; PubMed-9521645;
Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
Castellino F.J.;
Structure and ligand binding determinants of the recombinant kringle
5 domain of human plasminoden.";
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MEDLINE-94237157; PubMed=8181475;

Rejante M.R., Llinas M.;
"IH-NMR assignments and secondary structure of human plasminogen kringle 1.";
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MEDLINE-94237158; P
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28.2%; Score 144; DB 1; Length 810;
Best Local Similarity 37.5%; Pred. No. 7.7e-09;
Matches 33; Conservative 11; Mismatches 30; Indels 14; Gaps
                                                                                                 MEDLINE=96180681; PubMed=8611560; Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.; "Crystal structures of the recombinant kringle I domain of human plasminogen in complexes with the ligands epsilon-aminocaproic acid and trans-4-(aminomethyl)cyclohexane-1-carboxylic Acid."; Diochemistry 35:2567-2576(1996).
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Kringle (2 + 3) supermodule: spectroscopic/functional individuality
of plasminogen kringle domains.";
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Acta Crystallogr. D 53:169-178(1997).
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P26927; Q13350, Q14870;
P26927; Q13350, Q14870;
P26927; Q13350, Q14870;
O1-AUG-1992 (Rel. 23, Last sequence update)
O1-AUG-1992 (Rel. 23, Last sequence update)
28-F2B-2003 (Rel. 41, Last annotation update)
Stimulatory brotein) (MSP) (Macrophage stimulatory protein) (MSP) (Macrophage stimulatory protein)
MST1 OR HGFL.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
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MEDLINE-96194156; PubMed-8652577;

Sobhndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas
Rickli B.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 NRRRPWCYVQVGLKPLV--QECMVHDCA 85
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MEDLINE=90219023; PubMed=2157850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain of human plasminogen."; iochemistry 37:3258-3271(1998).
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RESULT 38 HGFL HUMAN

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4 CMFGNGKGYRGKKATTVMGIPCQEWAA-----QEPHRHSIFTPETNPQAGLEK-NYCRNP
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PLASMIN LIGHT CHAIN B.

KRINGLE 5.

SERINE PROTEASE.
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
STREPTOKINASE-BINDING SITE (PROBABLE).
STREPTOKINASE-BINDING SITE (PROBABLE).
SITE OF SUBSTRATE SPECIFICITY
BY SIMILARITY.
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Best Local Similarity 41.4%; Pred. No. 6.7e-09;
Matches 36; Conservative 5; Mismatches 34; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 AA; 36678 MW; C8C0271B6C6AC8D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 40
PLMN MACMU
ID PLMN MACMU
AC P12545;
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TISSUE=10175123; PubMed=2626424;

MEDLINE=90175123; PubMed=2626424;

Schaller J., Straub C., Kaempfer U., Rickli B.E.;

Schaller J., Straub C., Kaempfer U., Rickli B.E.;

"Complete amino acid sequence of canine miniplasminogen.";

In "Complete amino acid sequence of canine miniplasminogen.";

In "Complete amino acid sequence of canine miniplasminogen.";

Protein Seq. Data Anal. 2:445-450(1989).

In protein Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embroyonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenase and several complement zymogens, such as Cl and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von willebrand factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLG--KHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.9%; Score 142.5; DB 1; Length 711;
Best Local Similarity 33.3%; Pred. No. 9.9e-09;
Matches 30; Conservative 13; Mismatches 34; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL). (POTENTIAL). (POTENTIAL).
     BY SIMILARITY.
BY SIM
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E -> K (in dbSNP:7798). | FIId=VAR 014569.

L -> F (IN REF. 2). | L -> F (SPED21F180290E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y -> C.
/FTId=VAR_006631.
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1D PLMN CANFA STANDARD; PRT; 333 AA.

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DF 16-OCT-2001 (Rel. 40, Last annotation update)

DF 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 GSEAPWCFT---LRPGWRAAFCYQIRRCTD 363
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          623 6
711 AA;
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CARBOHYD
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377 CYHGDGQSYRGISSTITIGKKCQSWSS----MIPHWHEKIPENPENAGL-TMNYCRNPD 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.6%; Score 141; DB 1; Length 810;
Best Local Similarity 37.5%; Pred. No. 1.7e-08;
Matches 33; Conservative 10; Mismatches 31; Indels 14; Gaps
 PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
                                                                                                                                                                           REINGLE 1.
RRINGLE 2.
RRINGLE 3.
RRINGLE 4.
RRINGLE 4.
RRINGLE 5.
RRINGLE 5.
RRINGLE 5.
RRINGLE 5.
RRINGLE 5.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
OMEGA-AMINOCARBOXYLIC ACIDS.
OMEGA-AMINOCARBOXYLIC ACIDS.
OMEGA-AMINOCARBOXYLIC ACIDS.
OMEGA-AMINOCARBOXYLIC ACIDS.
OMEGA-AMINOCARBOXYLIC ACIDS.
OMEGA-AMINOCARBOXYLIC ACIDS.
                                                                                       PLASMINOGEN.
PLASMIN HEAVY CHAIN A.
ACTIVATION PEPTIDE.
PLASMIN SHORT FORM OF CHAIN.
PLASMIN LIGHT CHAIN B.
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90255 MW;
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28-FEB-2003 (
10-OCT-2003 (
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CARBOHYD
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RORI DROME
     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             -!- ENZYME REGULATION: Converted into plasmin by plasminogen activators. both plasminogen and its activator being bound to fibrin. Activated with catalytic amounts of streptokinase.
-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after discociation from the clot.
-!- MISCELLANEOUS: In the presence of the inhibitor, the activation involves only cleavage after Ags-580, resulting in 2 chains held together by 2 disulfide bonds Without the inhibitor, the activation involves also removal of the activation peptide.
-!- SIMILARITY: Belongs to peptidase family SI. Plasminogen subfamily.
                                                                                     Macaca mulatta (Rhesus macaque).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca
                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89174660, PubMed=2925643;
Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-EEB-2003 (Rel. 41, Last annotation update)
Plasminogen precursor (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04697; AAA36901.1; --
PIR; B3286; B30848
HSSP, B00147; IPWK.
MEROPS; S01.233; --
InterPro; IPR003001; Kringle.
InterPro; IPR003001; Kringle.
InterPro; IPR003004; FAN.
InterPro; IPR00306; FAN.
InterPro; IPR00124; Peptidase_SIA.
InterPro; IPR001254; Peptidase_SIA.
InterPro; IPR001254; Peptidase_SIA.
InterPro; IPR001254; Peptidase_SIA.
Pfam; PF00051; Kringle; 5.
Pfam; PF00051; Kringle; 5.
Pfam; PF00089; Kringle; 5.
PRINTS; PR00130; KRINGLE.
PRINTS; PR0130; KRINGLE.
PRODOM; PD000395; Kringle; 5.
SWART; SM00130; KR; 4.
SWART; SM00130; KR; 4.
SWART; SM000130; KRINGLE.
PROSTIE; PS00021; KRINGLE.
                                                                                                                                                             NCBI_TaxID=9544;
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(BY SIMILARITY)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DDW; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00239; RECREPTOR, TYR, 11; 1.
Transferase; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor; Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation; Signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. # TYROSINE-PROTEIN KINASE TRANSMEMBRANE
                                        SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       REMBL; L20297; AAA58860.1; -..
REMBL; AZ002996; CAA05743.1; -..
REMBL; AZ002996; CAA05743.1; -..
REMBL; AA48289; AA452885.1; -..
REMBL; AA48289; AA452895.1; -..
REMBL; AA48289; AA452895.1; -..
REMBL; AA48289; AA45289; CAA05743.1; -..
REMBL; AA82289; AA45289; Ror.
ROJ; GO:0004713; F:protein-tyrosine kinase activity; NAS.
ROJ; GO:0007417; P:central nervous system development; IEP.
ROJ; GO:0007417; P:central nervous system development; IEP.
ROJ; GO:0000418; P:protein amino acid phosphorylation; NAS.
RICEPPO; IPRO0001; Kringle.
RILEPPO; IPRO0001; RecepttyrkinsI.
RILEPPO; IPRO0011; RecepttyrkinsI.
RILEPPO; IPRO0051; Ryr_pkinase.
RILEPPO; PRO0826; Tyr_pkinase.
REMBL; PF00069; pkinase.
REMBL; PF00069; pkinase.
REMBL; PF00069; pkinase.
REMBL; PF00069; pkinase.
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(GLCNAC. . .)
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                                                                                -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD000395; Kringle; 1.
Probom; PD000001; Prot_Kinase; 1.
SMART; SM00130; KR; 1.
SMART; SM00219; TYrKc; 1.
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78142 MW;
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PRINTS; PROCIOS; TYRKINASE
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PROSITE; PS00021: KRINGI
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                                        SUCENCE FROM N.A.

SUCENCE FROM N.A.

SUCENCE FROM N.A.

Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Brandon R.C., Rogers Y.H.C., Plazel R.C., Change M., Pefeiffer B.D.,

Bandon R.C., Rogers Y.H.C., Blazel R.C., Change M., Pefeiffer B.D.,

Man K.H., Doyle C., Baxer E.G., Helt G., Walson C.R., Miklos G.L.G.,

An Enndon R.C., Rogers Y.H.C., Blazel R.C., Change M., Pefeiffer B.D.,

Man K.H., Doyle C., Baxer B. H.H.J., Andrews-Pfannkoch C. Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayersktaroglu L., Beasley E.M.,

Ballew R.M., Cawley B. Berman B.P., Berman B.P., Benchies P., Brottier P.,

Butris K.C., Busam D.A., Bauler H., Cadieu E., Center A., Chandre B.D.,

Butris K.C., Busam D.A., Bauler H., Cadieu E., Center A., Chandre B.D.,

Butris K.C., Busam D.A., Berman B.P., Bhandari D., Boslshavo S.,

Butris K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Cherry J.M., Cawley S., Delicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Cherry J.M., Cawley S., Delicher M., Deng Z., Mays A.D., Dew I., Dietz S.M.,

B. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

B. Dodson K., Doup L.E., Gorrell J.H., Gu Z., Ganbart W.M., Glasser K.,

Andrin M., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

Anterio M., Harvey D.A., Heiman T.J., Mernandez J.R., Houck J.,

Anterio M., Harvey D.A., Heiman T.J., Mernandez J.R., Houck J.,

Anterio M., Matchi B., McTicosh T.C., Modeod M.D., McTong W., Lank Y.,

Mount S.M., Moy M., Murphy B., Murphy L., Murzhy D.M., Natori B.,

Reibert K., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Spier B., Spradling A.C., Turner R., Wenter E., Weng S., Yao, X.,

Mang Z.-Y., Wassarman D.A., Weinsteck G.M., Weissenbach J., Wang C.,

Reibert K., Spradling A.C., Branger R., Weissenbach J., Wang C.,

Sheng X.H., Zhong F.M., Stapleton M., Shug S., Zhu X., Smith H. G.,

Shish R. C., Stach R. R., Rubin G.M., Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SÚBCELLULÂR LÔCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
"Sampling the genomic pool of protein tyrosine kinase genes using the
polymerase chain reaction with genomic DNA.";
Biochem. Biophys. Res. Commun. 249:660-667(1998).
-!- FUNCTION: Tyrosine-protein kinase receptor that functions during
early stages of neuronal development.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Conton-S; TISSUE=Larval brain;
MEDLINE=93348222; PubMed=8394009;
Milson C., Goberdhan D.C.I., Steller H.;
"Dror, a potential neurotrophic receptor gene, encodes a Drosophila homolog of the vertebrate Ror family of Trk-related receptor tyrosine
                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Pshydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
.y.osine-protein kinase transmembrane receptor Ror precursor (EC 2.7.1.112) (dRor).
                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 545-597 FROM N.A. MEDLINE=98401146; PubMed=9731193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Length 685;

DB 1;

Score 139;

27.3%;

Query Match

BAA01064.1;

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DOMAIN
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                                                                                                   1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUES ARMANY fibrorms LONG AND SHORT), AND SEQUENCE OF 496-504. TISSUES Mammary fibrorblast;
Sassis Mammary fibrorblast;
Sassis M. Nishio M., Sassis T., Enami J.;
"Identification of mouse mammary fibroblast-derived mammary growth factor as hepatocyte growth factor.";
Biochem. Biophys. Res. Commun. 199:772-779(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUENCE FROM N.A.

TISSUE-Liver;

MEDINE-94060105; PubMed=8241272;

MEDINE-94060105; PubMed=8241272;

Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth factor.";

Biochim. Biophys. Acta 1216:299-303(1993).

-i. FUNCTION: HGF is a potent mitogen for mature parenchymal hepatocyte cells, seems to be an hepatotrophic factor, and acts a growth factor for a broad spectrum of tissues and cell types. It has no detectable protease activity.

-i. SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=54363381, PubMed=8081873,
Lee C.C., Kozak C.A., Yamada K.M.;
"Structure, genetic mapping, and expression of the mouse Hgf/scatter
factor gene.";
                         28; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                 HGF MOUSE STANDARD; PRT; 728 AA. Q080648 i Q61662; Q64607; Q64007; Q1-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Hepatocyte growth factor precursor (Scatter factor) (SF) (Hepatopoeitin A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
34.5%; Pred. No. 2.4e-08; ative 19; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q08048-1; Sequence=Displayed;
                                                                                                                                                                                                  286 VENSPWCFVDSSRERIIELCDIPKCAD 312
                                                                                                                                                                   61 -RRRPWCYVQVGLKPLVQECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell Adhes. Commun. 1:101-111(1993)
Best Local Similarity 34.5
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                      RESULT 42
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| EMBL; | D10213; BAA01064.1; -...
| REMBL; | M10213; BAA01065.1; -...
| REMBL; | S71816; AAB31055.1; -...
| REMBL; | S71816; AAB3105.1; -...
| REMBL; | S71816; ABA0185.1; -...
| REMBL; | S71816; ABA0185.1; -...
| REMBL; | S71816; ABA0185.1; -...
| REMOPOS; | S71816; ABA0185.1; -...
| REMINE | PRO0031; | REMOPOS; | REMINER; | SMOON; | REMOPOS; | REMINER; | REMOPOS; | REMINER; | REMEMEN; | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 CIQGQGGGYRGTSNTIWNGIPCQRWDS-----QYPHKHDITPENFKCKDLRENYCRNP 358
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SERINE PROTEAGE-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTEN N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 DNRRRPWCY-----VQVGLKPLVQECMV----HDCADG 87
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(Rel. 16, Last sequence update)
(Rel. 41, Last annotation update)
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KRINGLE 2.
KRINGLE 3.
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82944 MW;
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728 AA;
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P17945;
01-NOV-1990 (
01-NOV-1990 (
28-FEB-2003 (
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Best Local Simi]
Matches 31; (
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Gaps

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306 CIKGQGEGYRGTINIIWNGIPCQRWDS-----QYPHKHDITPENFKCKDLRENYCRNP 358
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MEDINE-Placenta;
Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
Golda E., Daikuhara Y., Kitamura N.;
Molecular cloning and sequence analysis of cDNA for human hepatocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CYECNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLG----KHNYCRNP
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MEDLINE=91025062; PubMed=2145836;
Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T.,
Asami O., Hagiya M., Nakamura T., Shimizu S.;
"Isolation and expression of cDNA for different forms of hepatocyte
growth factor from human leukocyte.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                              (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.6%; Score 135.5; DB 1; Length 728; 32.0%; Pred. No. 6.5e-08; ive 11; Mismatches 36; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91340155; PubMed-1831432; Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.; "Organization of the human hepatocyte growth factor-encoding Gene 102:213-219(1991).
    289 KRINGLE 2.
384 KRINGLE 3.
470 KRINGLE 4.
728 SERINE PROTEASE-LIKE.
97 BY SIMILARITY.
607 INTERCHAIN (BY SIMILARITY.
295 N-LINKED (GLCNAC. . .) (POTEN N-LINKED M-LINKED M-LIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGF HUMAN STANDARD; PRT; 728 AA.
P14210; Q99VL9; Q9UDG;
01-74N-1990 (Rel. 13, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Hepatopote growth factor precursor (Scatter factor) (SF)
(Hepatopoeitin A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 DGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDCYRG 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 DNRRRPWCY----VQVGLKPLVQECMV---HDCADG 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 32.09
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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InterPro; IPR000001; Kringle.

InterPro; IPR000001; Kringle.

InterPro; IPR000001; Kringle.

InterPro; IPR0013609; Pan app.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Pan, propose program, Program, Propose program, Propose program, Program, Propose program, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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HEPATOCYTE GROWTH FACTOR BETA CHAIN.
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Deduced primary structure of rat hepatocyte growth factor and expression of the mRNA in rat tissues.";
Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-Wistar: TISSUB-Liver:
MEDLINE-9022197; PubMed=2119229;
TOSHIRO K., Hadjya M., Nishizawa T., Seki T., Shimonishi M., Shimizu S., Nakamura T.;
Hepatocyte growth factor precursor (Scatter factor) (SF) (Hepatopoeitin A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
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EMBL, X54400; CAA38266.1; --
PIK, A35644, A35644.
MHSSP, P14210; 1BHT.
MEROPS, S01.978; ---
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STRAIN=Wistar; TISSUE=Liver;
                                                                                                                                  Rattus norvegicus (Rat).
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The way co:co:ct cz yam ent

S1. Plasminogen subfamily

disulfide bond.
-!- SIMILARITY: Belongs to peptidase family
-!- SIMILARITY: Contains 4 kringle domains.

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N [5]
REQUENCE FROM N.A.
TSGUE=Embryonic fibroblast;
XX MEDLINE=9134939; PubMed=1831266;
RA MEDLINE=9134939; PubMed=1831266;
RA Rieder H., Fonatsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
RA Rieder W.;
RA Birchmeier W.;
RT "Evidence for the identity of human scatter factor and human
RT "Evidence for Us. S.A. 88:7001-7005(1991).
RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91207365; PubMed=1826837; Yoshiyama Y., Arakakai N., Naka D., Takahashi K., Hirono S., Kondo J., Voshiyama Y., Arakakai N., Naka D., Tsubouchi H., Ishii T., Hishida T., Daikuhara Y.; Hishida T., Daikuhara Hishida T., Daikuhara Hishida T., Daikuhara Hishida T., Daikuhara Hishida T., Takahara Hishida T., Daikuhara Hishida T., Takahara Hishida T., Tak
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SEQUENCE OF 249-695 FROM N.A.
MEDLINE-1369928; PubMed-1832556;
Miyazawa K., Kitamura A., Kitamura N.;
"Structural organization and the transcription initiation site of the human hepatocyte growth factor gene.";
Biochemistry 30:9170-9176(1991).
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MEDILNE-99129192; PubMed=1482348;

Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,

Nakamura T., Shimizu S.;

"Hepatcoyee growth factor is linked by O-glycosylated oligosaccharide
on the alpha chain.";

Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92331602; PubMed=1321034;
Lokker N.A., Mark M.R., Luis B.A., Bennett G.L., Robbins K.A.,
Lokker J.B., Godowski P.J.;
Baker J.B., Godowski P.J.;
Structure-function analysis of hepatocyte growth factor:
identification of variants that lack mitogenic activity yet retain
high affinity receptor binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson
Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.,
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Courtney L., Elliot G., Angell S.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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MUTAGENESIS
              REAL TRANSPORTED TO THE SERVICE SERVIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, D90334; BAA14348.11

EMBL, D90318; BAA14348.11

EMBL, D90329; BAA14348.11

EMBL, D90322; BAA14348.11

EMBL, D90322; BAA14348.11

EMBL, D90322; BAA14348.11

EMBL, D90323; BAA14348.11

EMBL, D90325; BAA14348.11

EMBL, D90325; BAA14348.11

EMBL, D90326; BAA14348.11

EMBL, D90326; BAA14348.11

EMBL, D90332; BAA14348.11

EMBL, M75329; BAA14348.11

EMBL, M75329; BAA14348.11

EMBL, M75329; BAA14348.11

EMBL, M75329; AAA52650.11

EMBL, M75329; AAA5346.11

EMBL, M75331; AAG53460.11

EMBL, M75974; AAG53460.11

EMBL, M75974; AAG53460.11

EMBL, M75974; AAG53460.11

EMBL, M75974; AAG53460.11

EMBL, M75976; AAG53460.11

EMBL, M75976; AAG53460.11

EMBL, M75978; AAG53460.11

EMBL, M75980; AAG53460.11

EMBL, M75978; AAG53460
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STRUCTURE BY NNR OF 31-127.

MEDINE=9815423; Pubmed=9491272;

Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,

Rubin J.S., Bottaro D.P., Byrd R.A.;

"The solution structure of the N-terminal domain of hepatocyte growth factor reveals a potential heparin-binding site.";

MEDLINE=99036859; PubMed=9817840; OF 35-210.
MEDLINE=99036859; PubMed=9817840; OF 35-210.
MEDLINE=99036859; PubMed=9817840; OILSCH M. J. Cokker N.A., GodGwaki P.J., de Vos A.M.;
Ultsch M., Lokker N.A., GodGwaki P.J., de Vos A.M.;
factor at 2.0-A resolution.";
Structure of fil38.319381998;
-1- FUNCTION: HGF is a potent mitogen for mature parenchymal hepatocyte cells, seems to be an hepatotrophic factor, and acts as growth factor for a broad spectrum of tissues and cell types. It has no detectable protease activity.
-1- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a

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                                                                                                                                                                                                                                                                                                                                                                                                                                           305 CIQGQGEGYRGTVNTIWNGIPCQRWDS-----QYPHEHDWTPENFKCKDLRENYCRNPDG 359
                                                                                                                                                                                                                                                                                                                                                                                            CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAH--RSDALQLGLGKHNYCRNPDN 60
PROSITE; PS50070; KRINGLE 2; 4.

PROSITE; PS50240; TRYPSIN_DOM; 1.

Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal; 3D-structure; Polymorphism; Pyrrolidone carboxylic acid.

SIGNAL 32 494 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALBAC; TISSUE-Liver;
STRAIN-BALBAC; TISSUE-Liver;
MEDLINE-92002017; Pubmed=1832957;
MEDLINE-92002017; Pubmed=1832957;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
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Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
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Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
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Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner L.A., Han S., Jamison C.S.;
Friezner Degen S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner L.A., Han S.J. Stuart L.A., Han S., Jamison C.S.;
Friezner L.A., Han S., Han 
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-!- BUVELOPMENTAL STAGE: Is expressed at low levels during gestation.

Just before birth the level increases dramatically and remains stable afterwards.

-!- PTW: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
                                                                                                                                                                                                                                                                                  Score 133.5; DB 1; Length 728;
Pred. No. 1.1e-07;
10; Mismatches 37; Indels 15; Gaps
                                                                                                                                          HEPATOCYTE GROWTH FACTOR ALPHA CHAIN. HEPATOCYTE GROWTH FACTOR BETA CHAIN. PYRROLIDONE CARBOXYLIC ACID. PAPP.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hepatocyte growth factor like protein precursor (Macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 SESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRG 394
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HSSP; P00747; 1KRN.
MEROPS; S01.975; -.
MGD; MGI:96080; MSE1.
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MST1 OR HGFL.
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> Q (IN GENOMIC SEQUENCE). BBCE02EF85213ACC CRC64;
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KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
SERINE PROTEASE-LIKE.
BY SIMILARITY.

GO; GO:0007566; P:embryo implantation; IC.
InterPro; IPR009001; Kringle.
InterPro; IPR003001; Kringle.
InterPro; IPR003001; PAN
InterPro; IPR003009; PAN app.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001254; Peptidase_SIA.
InterPro; IPR00134; Peptidase_SIA.
InterPro; IPR00314; Peptidase_SIA.
InterPro; IPR00316; Peptidase_SIA.
InterPro; IPR00316; PAN; I.
Pfam; PR00021; Kringle; 4.
Pfam; PR00021; Kringle; 4.
PRINTS; PR00125; CRNHGLE.
PRINTS; PR00139; KRINGLE.
PROSTIR; PR000305; KRINGLE; 4.
SWART; SW00013; FR; 4.
SWART; SW00020; Tryp_SPC; I.
PROSTIR; PS00021; KRINGLE 1; 4.
PROSTIR; PS00021; KRINGLE 2; 4.
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80588 MW;
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RY TISSUELLIVER.

RA STAURS-12388257; PubMed=12477932;

RA Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Ratschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Rapleton M., Scares M.B., Earner A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Tohinyuki S., Carninci P., Prange C., Stapleton M.J., Usdin T.B., Tohinyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibs R.A., Shey Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rhey Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzzywinski M.I., Skaleka U., Smailus D.E., Butterfield Y.S.N., Krzzywinski M.I., Skaleka U., Smailus D.E., Gheneration and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.!

RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). PLG.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090; SEQUENCE OF 1-16 FROM N.A.
STRAIN-129/SvJ; TISSUE-Liver;
PubMed-12149246; TISSUE-Liver;
PubMed-12149246; Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
Pannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
"Localization of regulatory elements mediating constitutive and
cytokine-stimulated plasminogen gene expression.";
[5] SEQUENCE FROM N.A.

MEDLINE=91184812; PubMed=2081600;

Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;

"Characterization of the cDNA coding for mouse plasminogen and localization of the gene to mouse chromosome 17.";

Genomics 8:49-61(1990). [2]
SEQUENCE FROM N.A.
SERBIN-129/Sv;
Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger
Nagaraja R.;
"Genomic sequence analysis in the mouse t-complex region.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. P20918; Q8CIS2; Q91WJ5; 01-FEB-1991 (Rel. 17, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 43, Last annoration update) Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].

100 May 20 10.00:00 2004

CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.

MEDLINE=95042728; PubMed=7525077;
O'Rellly M.S., Holmgren L., Shingy Y., Chen C., Rosenthal R.A.,
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
Moses M. R. (1994).

Cell 79:315-328 (1994).

Cell 79:315-328 (1994).

Cell 79:315-328 (1994).

Cell 79:315-328 (1994).

Cell 79:316-328 (1994).

Cell 79:3

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SIMILARITY: Contains at least 2 kringle domains.
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                                                                                                                                                                                                                                                                                                                                                                                            63 RPWCYVQVGLKPLVQECMVHDCADG 87
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Best Local Similarity 32.5.
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28; Conservative
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315
325
325 AA;
        PIR; S33879; S33879
HSSP; P00747; 5HPG.
MEROPS; S01.233; -.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         products.
SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Affolter M., Schaller J., Rickli E.E.;
Isolation, Characterization and partial amino acid sequence of
lamprey plasminogen.";
Protein Seq. Data Anal. 5:207-211(1993).
-! FWOUTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation.
-! CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa, higher selectivity than trypsin. Converts fibrin into soluble
                                                                                                                                                                                                                                                                                                                         Gaps
                 SIMILARITY).
SIMILARITY).
SIMILARITY).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.
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;; Pred. No. 1.9e-07;
13; Mismatches 36; Indels
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C -> H (IN REF. 1).
C -> D (IN REF. 1).
C -> D (IN REF. 1).
W, 24173260E6A2FFDZ CRC64;
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        SERINE PROTEASE.
CHARGE RELAY SYSTEM (1
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CHARGE RELAY SYSTEM (1
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fregments).
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                                            90781 MW;
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Best Local Similarity 33.7%;
Matches 29; Conservative 1:
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                                                                                                                                                                                                                                                                                     812 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels 16; Gaps
R InterPro; IPR009003; Cys_Ser_trypsin.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1.
R PRINTS; PR00139; KRINGle.
R PRINTS; PR00130; KRINGle.
R SMART; SM00130; KRY 2.
R SMART; SM00020; TryP_SPC; 1.
R PROSITE; PS00021; KRINGLE_1; 2.
R PROSITE; PS00134; TRYPSIN IP 2.
R PROSITE; PS00135; TRYPSIN IP 2.
R PROSITE; PS00135; TRYPSIN IP 18; PARTIAL.
R PROSITE; PS00135; TRYPSIN IP 18; PARTIAL.
R PROSITE; PS00135; TRYPSIN SER; PARTIAL.
W Hydrolase; Serine procease; Plasma; Glycoprotein; Fibrinolysis;
W Tissue remodeling; Blood coagulation; Kringle; Zymogen.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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SETRAIN=CS7BL/6; TISSUE=Liver;
MEDLINE=9102551; PubMed=222810;
Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
Fitzgibbon J.J., Pai J.-A., Chapman V.M., Bliott R.W.;
"Characterization of the cDNA coding for mouse prothrombin and
localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35194 MW; 1B5F0B539AC6ED3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 131; DB 1;
Pred. No. 9.3e-08;
5; Mismatches 36;
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
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CARBOHYD
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NO. 131

NO. 131

NEDLINE-SOLUTION:

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                 MEDIATORS N. 1120E-117932,

MEDIATORS N. 1120E-117932,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Mactow K.H., Schaefer C.F., Bhat N. K.,

Altschul S.F., Zeeberg B., Mactow K.H., Schaefer C.F., Bhat N. K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullaby S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muxiny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Reneration and initial analysis of more than 15,000 full-length

RT Human and mouse cDNA sequences.,

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of thrombin.

MISCELLANEOUS: Thrombin can itself cleave the amino terminal
MISCELLANEOUS: Thrombin can itself cleave the amino terminal
fragment (fragment 1) of the prothrombin, prior to its activation
by factor xa.
SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X52308, CAA36548.1, -..
EMBL, BC013662, AAH3662.1; -
EMBL, M81394, AAA40435.1, -..
PIR, A38827, A38827.
HSSP, P00734, 1B7X.
STRAIN=FVB/N; TISSUE=Liver;
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InterPro, IPR009003; Cys Ser trypsin. InterPro, IPR002383; GLA blood. InterPro, IPR000001; Kringle.

HSSP; P00734; 1B7X. WEROPS; S01.217; -. WGD; MGI:88380; F2.

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3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD-NR
                                                                                                                                                                                                                                                                                                                              J; Glycoprotein; Repeat;
acid; Acute phase; Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 125.5; DB 1; Length 618; Pred. No. 7.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
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B89F719AAFD601E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
KRINGLE 1.
KRINGLE 2.
SERINE PROTEASE.
CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A_Dr.

InterPro; IPR00296; Peptidase_S1A_Dr.

InterPro; IPR00296; Peptidase_S1A_Dr.

Pfam; PP00059; VitK_dep_GLA.

Pfam; PP00089; trypsln; 1.

PRINTS; PR00018; trypsln; 1.

PRINTS; PR001018; KRINGLE.

PRINTS; PR001018; KRINGLE.

PROMITS; PR001018; KRINGLE.

PROMITS; PR001019; KR; 2.

SWART; SM00100; KR; 2.

SWART; SM00100; KR; 2.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS001014; TRYPSIN_DOM; 1.

PROSITE; PS001035; TRYPSIN_DOM; 1.

PROSITE; PS001035; TRYPSIN_DOM; 1.

PROSITE; PS001035; TRYPSIN_DOM; 1.

PROSITE; PS001036; TRYPSIN_DOM; 1.

PROSITE; PS001
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31.8%;
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Best Local Similarity 31.8%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                553 :
618 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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CLTERGRIX/QGNLAVITIGSPCLPWNSLPAKTLSKYQDFDPEVKL---VENFCRNPDWDE 271
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MEDLINE-83231469; PubMed-6305407;
Degen S.J.F., McGillivray R.T.A., Davie E.W.;
"Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin.";
Biochemistry 22:2087-2097(1983).
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MEDLINE=90327074; PubMed=2374926;
Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
Rydel T.C., Fenton J.W. II;
"The structure of a complex of recombinant hirudin and human alpha-thrombin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=90059942; PubMed=2583108;
Bode W., Mayr I., Baumann U., Hubber R., Stone S.R., Hofsteenge J.;
"The refined 1.9 A crysteal structure of human alpha-thrombin:
interaction with D-Phe-Pro-Arg chloromethylketone and significance
                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabiet M.J., Blashill A., Furie B., Furie B.C.; "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin activation in human plasma,", J. Biol. Chem. 261:12210-13215(1986).
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MEDLINE=77207112; PubMed=873923;
Butkowski R.J., Elion J., Downing M.R., Mann K.G.,
"Primary structure of human prethrombin 2 and alpha-thrombin.";
J. Biol. Chem. 252:4942-4957(1977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=77193964; PubMed=266717; Malz D.A., Hewett-Emmett D., Seegers W.H.; Malz D.A., Hewett-Emmett D., Seegers W.H.; Manino acid sequence of human prothrombin fragments 1 and 2."; Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
1-JUL-1980 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88077877; PubMed-2825773; Degen S.J.F., Davie E.W.; Nucleotide sequence of the gene for human prothrombin."; Biochemistry 26:6165-6177(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANT MET-165.
Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., L.
Cozuna M., Poel C.L., Toth B.J., Yi Q., Nickerson D.A.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Tyr-Pro-Pro-Trp insertion segment."; EMBO J. 8:3467-3475(1989).
                                                                                                             295
                                                                 86
                                                                                             272 EGAWCYV-AGOPGDFEYCNLNYCEE
                                                                                                                                                                                                                   PRT;
                                                               RRPWCYVQVGLKPLVQECMVHDCAD
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                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      sapiens (Human)
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VARIANT DYSPROTHROMBINEMIA VAL-601.
MEDLINE=89247398; PubMed=2719946;
Henriksen R.A., Mann K.G.;
"Substitution of valine for glycine-558 in the congenital dysthrombin thrombin Quick II alters primary substrate specificity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cysteine
                                                                              Cardin A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT DYSPROTHROMBINEMIA CYS-425.
MEDLINE-89207504; PubMed=3242619;
Henriksen R.A., Mann K.G.;
"Identification of the primary structural defect in the dysthrombin thrombin Quick I: substitution of cysteine for arginine-382.";
Biochemistry 27:9160-9165(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iwanaga S., "Prothrombin Salakta: substitution of glutamic acid-466 by alanine reduces the fibringen clotting activity and the esterase activity.
                                                                                                                                                                                                                                                                                       MEDLINE=97357286; PubMed=9214615; van de Locht A., Bode W., Huber R., 1e Bonniec B.F., Stone S.R., bsmon C.T., Stubbs M.T.; The thrombin E1920-BFTI complex reveals gross structural rearrangements: implications for the interaction with antithrombin and thrombomodulin..; EMBO J. 16:2977-2984(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Prothrombin Himi: a compound heterozygote for two dysfunctional prothrombin molecules (Met-337-->Thr and Arg-388-->His)."; Blood 80:2275-2280(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [11]
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
MEDLINE=99162521; PubMed=10051558;
Guinto E.R., Caccia S., Fose T., Fuetterer K., Waksman G., di C"Unexpected crucial role of residue 225 in serine proteases.";
Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
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MEDLINE=92378975; PubMed=1354985;
Miyata T., Aruga R., Umeyama H., Bezeaud A., Guillin M.-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT DYSPROTHROMBINEMIA CYS-314.
WARDINES-87033739, PUDMEd=371562;
Rabbiet M.-J., Furie B.C., Furie B.;
"Molecular defect of prothrombin Barcelona. Substitution of
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=94350942; PubMed=8071320;
Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T.,
Correa P.E., Fenton J.W. II, Tulinsky A.;
"Crystallographic structure of human gamma-thrombin.";
J. Biol. Chem. 269:22000-22006 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT DYSPROTHROMBINEMIA HIS-314.
MEDLINE=95169898; PubMed=7865694;
James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
Prothrombin Padua I: incomplete activation due to subscitution at a factor Xa cleavage site.",
Blood Coagul. Fibrinolysis 5:841-844(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS DYSPROTHROMBINEMIA THR-380 AND HIS-431.
                                                                                                                                                                                                                    [10]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for arginine at residue 273.";
J. Biol. Chem. 261:15045-15048(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hromb. Haemost. 73:203-209(1995)
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PB1266.

PB1266.

PB1266.

15-DEC-1998 (Rel. 37, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

28-FB2-2003 (Rel. 41, Last annotation update)

Plasminogen (EC 3.4.21.7) (Fragment).

Putaminogen (EC 3.4.21.7) (Fragment).

Ovis aries (Sheep).

Ovis aries (Sheep).

Mammalia; Dutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprine; Ovis.

343 AA

STANDARD;

RESULT 50 PLMN SHEEP ID PLMN_SHEEP

270 EGVWCYV 276 62 RRPWCYV

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us-09-880-503-1.rsp

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VARIANT DYSPROTHERMIA LYS-200.

WARIANT DYSPROTHERMIA LYS-200.

WEDLINE-83204687; PubMed=6405779;

Board P.G., Shaw D.C.;

Board P.G., Shaw D.C.;

Board P.G., Shaw D.C.;

Control leads to Lys) and the localization of a third type 3 (157 dlu leads to Lys) and the localization of a third type 3 (157 dlu leads to Lys) and the localization of a third type 3 (157 dlu leads to Lys) and the localization of a third type 3 (157 dlu leads to Lys) and the localization of a third last type 3 (157 dlu leads to Lys) and the localization of single-nucleotide polymorphisms in coding regions of the last to Lysia and Lysia and
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Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
Lander B.S.;
Nat. Genet. 23:373-373 (1999).
L. FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
converts fibrinogen to fibrin and activates factors V, VII, VIII,
XIII, and, in complex with thrombomodulin, protein C.
CATLIVITY: Perferential cleavage: Arg-|-Gly; activates fibrinogen to fibrin and releases fibrinopeptide A and B.
C. -- CATLIVITY: Expressed by the liver and secreted in plasma.
C. -- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
C. -- PTW: THE GAMMA-CARBOXVENTINMY EXSIDUES, WHICH BIND CALCIUM IONS,
RESULT FROM THE CARBOXVIATION OF GLUTAMYL RESIDUES
C. -- PTW: THE GAMMA-CARBOXVIATION WITH A NEGATIVELY
CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92256895; PubMed=1349838;
Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,
Itakura M.;
"Detection of a single base substitution of the gene for prothrombin Tokushima. The application of PCR-SSCP for the genetic and molecular analysis of dysprothrombinemia.";
Int. J. Hematol. 55:93-100(1992).
                                                                                 MEDIANT DYSPROTHROMBINEMIA TRP-461.
MEDIJINE=87185407; PubMed=3567158;
Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
Miyata T., Morita T., Inomoto T., Kawauchi S.,
Ilwanaga S.;
"Prothrombin Tokushima, a replacement of arginine-418 by tryptophan that impairs the fibrinogen clotting activity of derived thrombin Piochemistry 26:1117-1122(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT DYSPROTHROMBINEMIA TRP-461.
WARIANT DYSPROTHROMBINEMIA TRP-461.
MINDLINE=87101511, PLDMed-3801671,
Inomoro T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,
Miyoshi K., Morita T., Iwanaga S.,
Miyoshi K., Morita T., Iwanaga S.,
Miyoshi K., Morita T., Iwanaga S.,
Miyoshi K., Morita T., Wanaga S.,
Miyoshi K., Wanaga S.,
Miy
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REAL MACHINE-93149995; PubMed=1492092;

RA MEDINE-93149995; PubMed=1492092;

RA SCHAINE-93149995; PubMed=1492092;

RA SCHAINE-93149995; PubMed=1492092;

R. Proceding Seq. Date Anal. S:21-25(1992).

-- PUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including compressed and experience of ovolution it weakens the will and and inflammation; in ovolution it weakens the wills cited Graafian inflammation; in ovolution it weakens the wills of the Graafian or ollagenses and several complement zymogens, such as 13 and 13 octored inflammation; in ovolution it weakens the will and on willebrand factor.

-- CAPLIVITION activity in the complement zymogens, such as 2 and 2 and 2 octored factor selectivity than trypsin. Converts fibrin into soluble produce selectivity than trypsin. Converts fibrin into soluble produce selectivity than trypsin. Converts fibrin into soluble activators, both plasminogen and its activator being bound to infini. Gamon be activated by alpha 2-antiplasmin and than activators, both plasminogen and its activator being bound to infini. Cannot be activated by alpha 2-antiplasmin and therefore the contains at least 2 kringle domains.

-- SMILARIY: Belists, SHESS SHOWN; SHOONS SHESS SHESS SHESS SHESS SHOWN; SHOONS SHOONS SHESS SHESS SHOWN; SHOONS SHOONS SHESS SHESS SHOONS SHOONS SHESS SHESS SHOONS SHESS SHOONS SHESS SHOONS SHESS SHESS SHOONS SHESS SHESS SHOONS SHESS SHESS SHOONS SHESS SHESS SHESS SHOONS SHESS SHESS SHESS SHESS SHOONS SHESS S
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LIGHT CHAIN A.
KRINGLE 4.
KRINGLE 5.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
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DOMAIN
213 CVPDRGQQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQL---VENFCRNPDGDE 269
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Query Match 24.3%; Score 124; DB 1; Length 622; Best Local Similarity 38.8%; Pred. No. 1.2e-06; Matches 26; Conservative 8; Mismatches 29; Indels

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May 25, 2004, 14:44:05 ; Search time 14.5767 Seconds (without alignments) 1904.795 Million cell updates/sec
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510
1 KTCYEGNGHFYRGKASTDTM.....QVGLKPLVQECMVHDCADGK 88
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	Q96se8 homo sapien	Q8mil0 oryctolagus	Q8mhy7 oryctolagus	Q9tva8 bos taurus	Q8c612 mus musculu	Q9xt70 oryctolagus	O8mkbl oryctolagus	Q7z7n2 homo sapien	Q9bu99 homo sapien	Q86yk8 homo sapien	ОШОС	Q9bzw1 homo sapien	Q8sq23 sus scrofa	Q8k0d2 mus musculu	Q800y7 meleagris g	Q14520 homo sapien
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                       SEQUENCE FROM N.A.

Fu J., Bai X., Ruan C.;

"Cloning and expression of the amino-terminal fragment of human urokinase-type plasminogen activator.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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- Similaria Acad. Sci. US.A. 99:10665-10670 (2002).

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1...

- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

GO, GO:0004263; Rechymotrypsin activity; IEA.
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Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann R.,
Dichek D.A.;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Urokinase-type plasminogen activator.
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70 KTCYHGDGHSYRGKANTDIMDRPCLAMNSANVLIKTYHAHRPDALQLGLGKGHYCRNPDH 129
GO; GO:0016301; F:kinase activity; IEA.

RGO; GO:0008233; F:peptidase activity; IEA.

RGO; GO:0004295; F:trypeldase activity; IEA.

RGO; GO:0004295; F:trypelia and peptidolysis; IEA.

RGO; GO:0006509; P:trypelia and peptidolysis; IEA.

RICEPPO: IPRO00603; CRS Ser trypsin.

RICEPPO: IPRO00601; Kringle.

RICEPPO: IPRO01314; Peptidase S1.

REART; SRO0132; KRINGLE.

REART; SRO0133; KR. II.

REART; SRO0130; KR. II.

REART; SRO0130; KR. II.

REART; SRO0130; KR. II.

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SEQUENCE FROM N.A.

Yano W., Watanabe M.;

Yano W., Watanabe M.;

Yano W., Watanabe M.;

Yano W., Watanabe M.;

Complete Gds.";

Complete Gds.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

L. SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.

-1- SIMILARITY: COUPAINS I RRINGLE DOMAIN.

EMBL; AR029517; AAK40239.1; -.

EMBL; AR029517; AAK40239.1; -.

RD; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chypsin activity; IEA.

GO; GO:0004263; F:chypsin activity; IEA.

GO; GO:0004265; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:000508; P:proceolysis and peptidolysis; IEA.

InterPro; IPR009003; Cys_Ser_trypsin.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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C STRAIN=CSTBL/61, TISSUB-Ovary;

X MEDLINE=22354683; PubMed=12466851;

A The FANTON Consortium,

A the FANTON Consortium,

A the RIKEN denome Exploration Research Group Phase I & II Team;

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                                                                                                                                                                                                                                                                           1 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                           1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).

Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.9%; Score 387; DB 11; Length 231; Best Local Similarity 72.7%; Pred. No. 3.7e-37; Matches 64; Conservative 10; Mismatches 14; Indels
                                                        77.6%; Score 396; DB 6; Length 157; 76.1%; Pred. No. 2.2e-38; ive 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF 1; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00001; KRINGLE 2; 1.
NON TER 211 231 AA; 25510 MW; 25E8980A682737F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel, 23, Created)
01-WAR-2003 (TrEMBLrel, 23, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9XT70;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|||||||:||:
129 QKRPWCYVQIGLRQFVQECMVHDCSLSK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                         SE ORRPWCYVOIGLKOFVOFCMVODCSVGK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                    61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasminogen activator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRODDIS; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
                                                                                                                                            67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                        Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9XT70
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ID 09
AC 09
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
R InterPro; IPR006209; EGP_like.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001214; Peptidase_S1.

R InterPro; IPR001314; Peptidase_S1.

R InterPro; IPR001314; Peptidase_S1.

R PRONO51; Kringle; 1.

R PRINTS; PR00018; Kringle; 1.

R PRINTS; PR00018; Kringle; 1.

R PRINTS; PR00018; Kringle; 1.

R PRONO130; KR; ISP_SC; 1.

R PROSITE; PS00021; KRINGLE_1; 1.

R PROSITE; PS00021; KRINGLE_1; 1.

R PROSITE; PS00134; TRYPSIN_DH; 1.

R PROSITE; PS00134; TRYPSIN_HS; 1.

R PROSITE; PS00135; TRYPSIN_HS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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TISSUE-Skeletal muscle;

MEDLINB=21071388; PubMed=11204721;

MEDLINB=221071388; PubMed=11204721;

A Balcerzak D., Querenguesser L., Dixon W.T., Baracos V.E.;

T. Coordinate expression of matrix-degrading proteinases and their activators and inhibitors in bovine skeletal muscle.";

T. J. Anim. Sci. 79:94-107(2001).

C -! SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

R EMBL, AFR4761; AAD30301.1; -..

H HSSP; P00749; 1UK.

GO; GO:0016301; F:Kinase activity; IEA.

R InterPro; IPR006209; EGF like.

InterPro; IPR000019; Kringle.

R PRINTS; PR000018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY.2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAY-2003 (TYEMBLrel. 14, Last sequence update)
01-JUN-2003 (TYEMBLrel. 24, Last annotation update)
Urokinase plasminogen activator (Fragment).
Bos taurus (Bovine).
Bos taurus (Bovine).
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidee; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.4%; Score 415; DB 6;
79.5%; Pred. No. 3.9e-40;
tive 7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 ORRPWCYVQVGLKQLIQECKVHDCSSGK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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PROSITE; PS00013; KRINGLE 1; 1.
PROSITE; PS0070; KRINGLE 2; 1.
Glycoprotein; Kinase; Kringle.
NON TER 1 157
SEQUENCE 157 AA; 17858 MW; 1
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SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 79.59
....hes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Q7Z7N2
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Q7Z7N2
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R GO; GO:0004263; F:chymotrypsin activity; IEA.

R GO; GO:0006301; F:kinase activity; IEA.

R GO; GO:000823; F:cppfidase activity; IEA.

R GO; GO:0006508; F:ppfidase activity; IEA.

R GO; GO:0006508; F:pproteolysis and peptidolysis; IEA.

INTERPRO: IPR000001; Kringle.

R InterPro: IPR001254; Peptidase_S1.

INTERPRO: IPR001314; Peptidase_S1.

R Pfam; PR00051; Kringle; 1.

R PROMING; RR000395; Kringle; 1.

R PRART; SM00130; KR; II.

R PROSITE; PS00017; KRINGLE 2; 1.

R RROSITE; PS00017; KRINGLE 2; 1.

R RROSITE; PS00134; TRYPSIN_HS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDRPCLAWNSANVLTKTYHAHRPDALQLGLGKHNYCRNPDHQRRPWCYVQVGLKQLIQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 MGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBMXB1;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tissue-type plasminogen activator.
Tissue-type plasminogen activator.
Dyctologus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Lepoxidae; Oryctolagus.
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Urokinase-type plasminogen activator (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.4%; Score 313; DB 6; Length 214; 78.3%; Pred. No. 1.5e-28; ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
Sugiki M., Yoshida E., Anai K., Maruyama M.;
Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submirted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-! SIMILARITY: CONTAINS 2 KRINGLE DOWAINS.
EMBL; AY029518; AAK40240.1; -.
GO; GO:0005576; C:extracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 214 AA; 24314 MW; 69975C41C32B0D7E CRC64;
                                                                                                               Local Similarity 78.3 tes 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 MVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KVHDSSGKK 69
                                                                                          SEQUENCE FROM N.A.
                                                                  NCBI TaxID=9986;
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Matches
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CONTRIBUTION OF THE CONTRI
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186 SKPWCYVPKAGKYSSEFCSTPACSEG 211
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                                                                                                                                                                                                                                                              Tissue plasminogen activator.
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                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                      Q86YK8
Q86YK8;
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   RESULT 10
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                                           TCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strauberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Strauberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

-: SIMILARITY: CONTAINS 2 KRINGLE DOWAINS.
REMBL; BC002795; AAH02795.1; --
ROO'S GO:0004295; P: Trypsin activity; IEA.
GO; GO:0004293; F: Peptidase activity; IEA.
ROO; GO:0006209; F: Peptidase activity; IEA.
RITHERPO: IPR00001; Kringle.
RITHERPO: IPR0001124; Peptidase S1.
RITHERPO: IPR000114; Feptidase S1.
RITHERPO: ROOOS1; Kringle.
REMINES; RR00181; KRINGLE.
REMART; SM00191; RR; 2.
RART; SM00191; RR; 2.
RART; SM00191; RR; 2.
RART; SM00191; RR; 2.
RART; SM00191; RR; 2.
RRART; SM00191; RR; 2.
RRART; SM00191; RR; 2.
RRART; SM00191; RR; 2.
RRART; RR0011E, RSINGLE.
RROSITE; RS00194; TRYPEIN LOM; 1.
RROSITE; RS00194; TRYPEIN LOM; 1.
RROSITE; RS00194; TRYPEIN HIS; 1.
RROSITE; RS00194; TRYPEIN HIS; 1.
RROSITE; RS00195; TRYPEIN HIS; 1.
RROSITE; RS00194; TRYPEIN HIS; 1.
RROSITE; RS00194; TRYPEIN HIS; 1.
RROSITE; RS00195; TRYPEIN HIS; 1.
RROSITE; RS00194; TRYPEIN HIS; 1.
RROFFLERE RS00194; TRYPEIN HIS; 1.
RROSITE; RS00194; TRYPEIN HIS; 1.
RROSITE; RS00194; TRYPEIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 44.3%; Score 226; DB 4; Length 516; Similarity 47.7%; Pred. No. 5.8e-18; 41; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 AA; 57370 MW; BAB31901FDC96800 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to plasminogen activator, tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKPWCYVFKAGKYSSEFCSTPACSEG 165
                                                                                                                                                                                                               186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
                                                                                                                                            62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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SEQUENCE 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=skin
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                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                Q9BU99
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126 TCYEDQGISYRGTWSTABSGABCTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TCYBGNGHFYRGKASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36, Indels 0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 44.3%; Score 226; DB 4; Length 562;
Local Similarity 47.7%; Pred. No. 6.3e-18;
Hes 41; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                 Liu Y.. Xu L., Zeng Y., He X.;

Liu Y. Xu L., Zeng Y., He X.;

"cDNA of tissue plasminogen activator.";

Bubli AV221101; AA034406.1; -

EMBL; AV221101; AA034406.1; -

R Q0; G0:0004263; F:chymotrypsin activity; IEA.

G0; G0:0004263; F:chymotrypsin activity; IEA.

G0; G0:0004263; F:chymotrypsin activity; IEA.

G0; G0:0004295; F:trypsin activity; IEA.

G0; G0:0004295; F:trypsin activity; IEA.

R D0; G0:0004295; F:trypsin activity; IEA.

R InterPro; IPR000093; Rib_mcin.

InterPro; IPR000093; Rib_mcin.

InterPro; IPR001314; Peptidase_S1.

InterPro; IPR00134; Peptidase_S1.

InterPro; IPR00134; Peptidase_S1.

InterPro; IPR00134; Peptidase_S1.

InterPro; IPR00139; Ini. 1.

P Fam; PF00008; EGF; 1.

IR PRINTS; PR00018; KRINGLE.

PROMO; PD000395; KRINGLE.

SMART; SM00020; TRYPESIN.

PROSITE; PS01025; FEIRCNECTIN 1; 1.

PROSITE; PS01025; FEIRCNECTIN 1; 1.

PROSITE; PS01025; FRINJELE 1; 2.

PROSITE; PS01026; EGF_2; 1.

PROSITE; PS01026; EGF_2; 1.

PROSITE; PS01026; ERPSIN DCM; 1.

PROSITE; PS01034; TRYPESIN DCM; 1.

PROSITE; PS00134; TRYPESIN DCM; 1.

PROSITE; PS00134; TRYPESIN SER; 1.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen/activator kringle.
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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48 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA 107
                                                                                                                                                                                                                                                    3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
T-plasminogen activate.
T-plasminogen activate.
Sus screfa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
[11]
    PROSITE, PS50240; TRYPSIN DOM, 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER, 1.
Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
NON TER 395
SEQÜENCE 395 AA; 44323 MW; 3FBD4A2P0B7C11C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00134; TRYPSIN-HIS; 1.
PS00135; TRYPSIN-SER; 1.
domain; Glycoprotein; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.2%; Score 215; DB 4; Length 395; Best Local Similarity 47.0%; Pred. No. 8.4e-17; Matches 39; Conservative 8; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                 108 KPWCHVLKNRRLTWEYCDVPSCS 130
                                                                                                                                                                                                                                                                                                                                         63 RPWCYVQVGLKPLVQECMVHDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
Q8SQ23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCEI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.8%; Score 218.5; DB 4; Length 90; Best Local Similarity 49.4%; Pred. No. 6.7e-18; Matches 41; Conservative 5; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The brain-type plasminogen activator ";

A brain-type plasminogen activator ";

"A brain-type plasminogen activator ";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.

R BABL; APZ60825; AAK11956.1; -.

R HSSP; PRO750; APS.

R GO: GO:0005576; C:extracellular; IEA.

GO: GO:0008235; F:peptidase activity; IEA.

GO: GO:0008235; F:peptidase activity; IEA.

GO: GO:0008235; F:peptidase activity; IEA.

R InterPro; IPR000031; R:peptidase.

R InterPro; IPR000031; R:peptidase.

R InterPro; IPR000134; Peptidase.

R InterPro; IPR000134; Peptidase.

R PETAM; PR000089; KX:ngle: 1.

R PETAM; PR000089; KX:ngle: 1.

R PETAM; PR000189; KX:ngle: 1.

R PRNNTS; PR000189; KX:ngle: 1.

R SMART; SM00108; KX:NglE: 1.

R SMART; SM00108; KX:NglE: 1.

R PROSITE; PS000121; KX:NGLE: 1.
                                             Dou D.;

"Production of kringle fragment.";

"Production of kringle fragment.";

Submitted (JUN 2000) to the EMBL/GenBank/DDBJ databases.

--- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

REMBL, AF28882; AAM52248.1;

InterPro; IPRO00001; Kringle.

PRIMTS; PRO0018; KRINGLE.

PRODUM; PD000395; KRINGLE.

R PROSITE; PS00021; KRI, 1.

R PROSITE; PS00021; KRINGLE.

R PROSITE; PS00021; KRINGLE.

R PROSITE; PS00021; KRINGLE.
                                                                                                                                                                                                                                                                                                          Glycoprotein, Kringle.
SEQUENCE 90 AA, 9804 MW; A33887F9FDF4C7B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JOCT-2003 (TrEMBLrel. 25, Last annotation update)
Neonatal thrombolytic agent alpha-form (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 KPWCYT-TNPRKLYDYCDVPQCA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 RPWCYVQVGLKPLVQECMVHDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
[1]
SEQUENCE FROM N.A.
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Q9BZW1;
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Q9BZW1
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CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR RESULT 15 **2800Y7** g ò à 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61 0; Gaps 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, 41.1%; Score 209.5; DB 11; Length 517; 45.8%; Pred. No. 4.9e-16; ive 13; Mismatches 31; Indels 1; Query Match
41.2%; Score 210; DB 6; Length 562;
Best Local Similarity 43.7%; Pred. No. 4.7e-16;
Matches 38; Conservative 9; Mismatches 40; Indels Serine protease. SEQUENCE 562 AA; 63668 MW; F9E6B4C77CB101E8 CRC64; 186 SKPWCYIFKAEKYSPDFCSTPACTKEK 212 62 RRPWCYVQVGLKPLVQECMVHDCADGK 88 Query Match
Best Local Similarity 45.8
Matches 38; Conservative PRELIMINARY; NCBI_TaxID=10090; Q8K0D2; Q8K0D2 RESULT 14 Q8K0D2 S 28 d à δ

Gaps

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MEDLINE=22122796; PubMed=12128063; MEDLINE=22122796; PubMed=12128063; Holbbarger D.R., Becker A.E., Thurston R.J., Rice C.D.; Hosbarger D.R., Becker A.E., Thurston R.J., Rice C.D.; Mexpession of a hepatcoyte growth-factor activator protein in turkey (Meleagris gallopavo) deferent duct epithelial cells."; Comp. Biochem. Physiol. 132:769-777 (2002). Q800Y7;
Q800Y7;
Q800Y7;
Q1-UNA-2003 (TrEMBLrel. 24, Created)
Q1-UNA-2003 (TrEMBLrel. 25, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocyte growth factor activator (Fragment).
Melaegris gallopavo (Common turkey).
Bukaryota; Metazoa; Chordata; Crantata; Verrebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris. Nouserger D.R., Becker A.E., Thurston R.J., Rice C.D.;

Holsberger D.R., Becker A.E., Thurston R.J., Rice C.D.;

Submitted (JAN-2003) to the EmBL/GenBank/DDBJ databases.

R GO; GO:0004256; C:extracellular; IEA.

GO; GO:0004256; F:typsin activity; IEA.

R InterPro; IPR000620; EGF_like.

InterPro; IPR000620; EGF_like.

InterPro; IPR000621; Fibritale.

InterPro; IPR000621; Fibritale.

R InterPro; IPR000621; Fibritale.

InterPro; IPR000639; Fibritale.

InterPro; IPR000639; Fibritale.

InterPro; IPR000639; Fibritale.

InterPro; IPR00639; Fibritale.

InterPro; IP Indela Length 39.6%; Score 202; DB 13; 43.4%; Pred. No. 3.9e-15; tive 10; Mismatches 37; 540 AA 11 KPWCFVKVNSEKVKWEYCDVTVC 233 63 RPWCYVQVGLKPLVQE-CMVHDC 84 Conservative PRELIMINARY; 1 Similarity
36; Conservat Query Match Best Local S Matches 36 us-09-880-503-1.rspt

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                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TOTALE M.,

"PUTITIONAL CHARAL STATE OF LINE ENDINGUISHING DATA OF THE SEGRET STATE SEGRET STATE SEGRET SEGRET STATE SEGRET SEG
   CYBGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                            014520; 0000663.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
HGF activator like protein (Hyaluronan binding protein 2).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
Kitamura N.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5C1907230784ACD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                    560 AA
                                                                                                                        63 RPWCYVQVGLKPLVQECMVHDCA 85
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SEQUENCE 560
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=White Leghorn;

RA MISLINE=97199025; PubMed=9047000;

RA MEDINES-97199025; PubMed=9047000;

RA JOHNSON A.L., Bridgham J.T., Anthony R.V.;

RT messenger tribonucleic acid during follicle development and atresia.";

RT messenger tribonucleic acid during follicle development and atresia.";

RL SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

BAC1. Reprod. 56.581-581.

CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

BREOPS; S01.232; -.

DR GO, GO:00008233; F::peptidase activity; IEA.

BROOPS; S01.032; -.

BROOPS; S01.032; -.

BROOPS; S01.032; -.

BROOPS; RINGLE ASE LITYPSIN.

BROOPS; RINGLE SET LITYPSIN.

BROOPS; RINGLE 1.

BROOPS; Kringle; 2.

BR PROSITE; PSS00021; KRINGLE 1; 1.

BR PROSITE; PSS00021; KRINGLE 2; 2.

BROOSTE; PSS0007; KRINGLE 2; 2.

BR PROSITE; PSS00034; TRYPSIN HIS; 1.

BROOSTE; PSS00034; TRYPSIN HIS; 1.

BROOSTE; PSS00034; TRYPSIN HIS; 1.

BROOSTE; PSS00034; TRYPSIN HIS; 1.

BROSITE; PSS00134; TRYPSIN HIS; 1.

BROOSTE; PSS00134; TRYPSIN HIS; 1.

BROOSTE; PSS00134; TRYPSIN HIS; 1.

BROOSTE; PSS00240; TRYPSIN HIS; 1.

BROOPTE; PSS002
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                                                                                                                                                                                                                                    3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
                                                                                                                                                                                   3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPA.

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Gallus.

NCBI_TaxID=9031;
                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
Query Match 37.9%; Score 193.5; DB 4; Length 560; Best Local Similarity 41.7%; Pred. No. 4e-14; Matches 35; Conservative 15; Mismatches 33; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.5%; Score 191; DB 13; Length 2 Best Local Similarity 43.9%; Pred. No. 2.6e-14; Matches 36; Conservative 7; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Tissue-type plasminogen activator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             63 RPWCYVQVGLKPLVQE-CMVHDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPWCHVWKDROLTWEYCDVPQC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 RPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 17
290675
AC 090675;
DT 01-NOV-
DT 01-NOV-
DT 01-OCT-
DB TISSUE-
CS GAILUS;
OC ACADINSON
CC ACADINSON
```

RESULT 18

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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 44.0%; Pred. No. 2.8e-13;
Matches 37; Conservative 8; Mismatches 34; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PRO1020; TYP_EPC; 1.

PROSITE; PRO1020; EGF 1; 2.

PROSITE; PS01023; FIBENECTIN 1; 1.

PROSITE; PS01023; FIBENECTIN 2; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS00021; KRINGLE 2; 1.

PROSITE; PS0004; TRYPSIN DON; 1.

PROSITE; PS00134; TRYPSIN DON; 1.

PROSITE; PS0135; TRYPSIN DON; 1.

PROSITE; PS0135; TRYPSIN SER; 1.

PROSITE; PS0135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                              Schloesser M., Schwager S., Engel W.;
Submitted (JUL-1996) to the EMEL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; X99571; CAA67891.1; -.
HSSP; F00760; 1AQ7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI. MGI. 1891012; F12.

MGI. MGI. 1891012; F12.

GO; GO:0004263; F: chymotrypsin activity; IEA.

GO; GO:0004295; F: chymotrypsin activity; IEA.

GO; GO:0006303; F: pryceolysis and peptidolysis; IEA.

GO; GO:0006508; F: pryceolysis and peptidolysis; IEA.

InterPro; IRR009003; Gys Sex trypsin.

InterPro; IRR000093; FidPinctnl.

InterPro; IRR000083; FidPinctnl.

InterPro; IRR000562; FN Type_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease.
SEQUENCE 597 AA, 65638 MW; F3AC07C37D0C0FBA CRC64;
                                                                                             Created)
Last sequence update)
Last annotation update)
                                                 597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO00083; Fibracian:
InterPro; IPR000562; FN Type_II.
InterPro; IPR00510; IEGF.
InterPro; IPR001010; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; fn; 1.
Pfam; PF00051; Kringle; 1.
Pfam; PF00051; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO072; CTPADALINE, PRINTS; PRO013; FNTYPEII.
PRINTS; PRO013; FNTYPEII.
PRODOM; PRO018; FNTNGLE.
PRODOM; PRO00395; FNTNGLE.
SWART; SW00181; EGF; 2.
SWART; SW00181; EGF; 2.
SWART; SW00181; EGF; 2.
SWART; SW00180; FNZ; 1.
                                                                                   01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25, Factor XII.
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                              035727
  RESULT 19
035727
                                                                           SOLUTION SOLUTION SERVICE SERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 CFLGNGTEYRGVASTAASGLSCLAWNSDLLYQELHVDSVAAAVLLGLGPHAYCRNPDKDE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus (Mouse).

Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00021; KRINGLE 2; 1.
PROSITE; PS50170; KRINGLE 2; 1.
PROSITE; PS00134; TRYPSIN TS; 1.
PROSITE; PS00135; TRYPSIN TS; 1.
PROSITE; PS00135; TRYPSIN TS; 1.
Kringle; Protesse; Psorine Spr 1ik domain; Glycoprotein; Hydrolase; SEQUENCE 653 AA; 70553 MM; FE18D90174ED6FDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                TISSUBELLY. TABLES ALVELY, STRUBLES ALVELY, STRUBBERGR. TISSUBLE ALVELY, STRUBBERGR. TO SUBMITTED BY THE STRUBBERGR. TO SUBMITTED BY THE STRUBBERGR. TO STRUBBERTY: BELONGS TO PEPTIDASE PAMILY SI. - I- SIMILARITY: CONTAINS I KRINGLE DOMAIN.

REAL, SCO19376; AAH19376. 1, r.

REAL, SCO19376; FICHYMOTETYPSIN ACTIVITY; IEA.

ROS, GO:0004263; FICHYMOTETYPSIN ACTIVITY; IEA.

BR GO; GO:0004295; FICHYPSIN ACTIVITY; IEA.

BR HICEPPO; IPROGO33; FIGF C.

BR INTERPRO; IPROGO39; EGF LIKE.

BR INTERPRO; IPROGO39; EGF LIKE.

BR INTERPRO; IPROGO39; FIFTENTALII.

BR INTERPRO; IPROGO31; FIFTENTALII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pem; PF00009; EGF; 2.
Pfam; PF00039; fn1; 1.
Pfam; PF00040; fn2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00072; CHYMOTRYPSIN;
PRINTS; PR00013; ENTYPEII.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0000995; FN Type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 53.0
35; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 RPWCYV 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 RPWCYV 68
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
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TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDN

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228 TCYEGRGLSYRGQAGTTQSGAPCQRW----TVEATYRNMTEKQALSWGLGHHAFCRNPDN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R PRIMTS; PROUGES; CHYPELL;

R PRIMTS; PROUGES; CHYPELL;

R PRIMTS; PROUGES; CHYPELL;

R PRODOM; PD000955; KIINGLE;

R SMART; SM00181; EGF; 2.

R SMART; SM00181; EGF; 1.

R PROSITE; PS01823; FIERONECTIN 1; 1.

R PROSITE; PS01823; FIERONECTIN 2; 1.

R PROSITE; PS01823; FIERONECTIN 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616 AA; 68012 MW; 4C5FE3D71EBBD1A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.8%; Score 177.5;
                                                                                                                              284 DTRPWCFVWSGDRLSWDYCGLEQC 307
                                                                     61 RRRPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2003 (TrEMBLrel. 25, FXII.
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease
SEQUENCE 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                       097507
                                                                                                                                                                                                                              RESULT 21
                                                                                                                                                                                                                                                            097507
                                                                                                                       용
         셤
                                                                     ò
216 TCYEGRGLSYRGQAGTTQSGAPCQRW----TVEATYRNMTEKQALSWGLGHHAFCRNPDN 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                          080VC5 PRELIMINARY; PRT; 609 AA.
080VC5;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to coagulation factor XII (Hageman factor) (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

36.6%; Score 186.5; DB 11; Length 609;
Best Local Similarity 44.0%; Pred. No. 2.8e-13;
Matches 37; Conservative 8; Mismatches 34; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROW N.A.
SIGNAIN-FVB/N; TISSUE-Liver;
STRAIN-FVB/N; TISSUE-Liver;
Strausberg R.,
Submitted (YAR.-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BC049867; AAH49867.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0004263; F:calcium ion binding; IEA.
GO; GO:0004263; F:calcium ion binding; IEA.
GO; GO:0004263; F:calcium ion binding; IEA.
GO; GO:0004263; F:crypsin activity; IEA.
GO; GO:0004263; F:crypsin activity; IEA.
GO; GO:0004263; F:crypsin activity; IEA.
InterPro; IPR00181; BGF_Ca.
InterPro; IPR00181; Firingle.
InterPro; IPR001814; Peptidase S1.
InterPro; IPR001814; IPR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       609 AA; 66783 MW; DF97D4DB2369B6D2 CRC64;
                                                                                                          272 DTRPWCFVWSGDRLSWDYCGLEQC 295
                                                               61 RRRPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00018; KRINGLE.
PD000995; FN Type II; 1.
PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART, SM00181, E
SMART, SM00181, E
SMART, SM0059, F
SMART, SM0059, F
SMART, SM00020, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00722;
PRINTS; PR00013;
PRINTS; PR00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
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Q80YCS
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 24
Q8AXY6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                 SO THE SECOND PRINTED BY A RESTRICT OF THE SECOND PRINTED BY A RES
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                                                    5
                                                                                                                                                                              217 CYSDRĞLSYRGMAQTTLSGAPCQPWAS----EATYWNMTAEQALNWGLGDHAFCRNPDND 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22308973; PubMed=12421700;
AD Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;
AD Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;
AD Evelopment 129:5587-5596(2002).
CNS patterning..;
CNS patterning..;
ANS DAVISORIS; ANG4661.1; -..
EMBL; AY150813; AAN64661.1; -..
EMBL; AY150813; AAN64661.1; -..
EMBL; AY150813; ANG661.1; -..
EMBL; AY150813; ANG61.1; -..
EMBL; ANG018; Kringle; 1.
EMBL; ANG018; KRINGIE.
EMBL; ANG018; KRINGIE.
ENGRITE; PS00011; KRINGIE.
ENGRITE; PS00011;
                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CYEGNGHFYRGKAS-TDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 CFTVNGRDYRGTVSQAGPEGTPCLYWNQTT--QHLYNAQSDPDGELGLGNHNYCRNPDAD 86
                                                                                                                          3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIY-HAHRSDALQLGLGKHNYCRNPDNR
                                                    5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q81ZZS PRELIMINARY; PRT; 615 AA.
Q81ZZS; Q12ZS; Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
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Best Local Similarity 44.6%; Pred. No. 3.2e-12;
Matches 37; Conservative 6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 AA
                                                                                                                                                                                                                                                                                                                                                273 TRPWCFVWRGDQLSWQYCRLARC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                       62 RRPWCYVQVGLKPLVQECMVHDC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 VQPWCYV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kremen2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8AXX3
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Matches
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Q81ZZS
1D Q81ZZ
1D Q81ZZ
DT 01-MA
DT 01-MA
DT 01-OC
DE COGO
OS HOMO
OS EUKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8AXX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SON THE THE PRINCE OF THE PRIN
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2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDN 60
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Muscle-specific receptor tyrosine kinase MuSK.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                             A Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;

Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;

I wolecular chracterization of coaggulation factor XII-Mie.";

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL, Ab095845; BAC23095.1; -.

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0004263; F:chymotrypsin activity; IEA.

R GO; GO:0004263; F:chymotrypsin activity; IEA.

R GO; GO:0004508; P:procelysis and peptidolysis; IEA.

R InterPro; IPR001881; EGFCa.

R InterPro; IPR001881; EGFCa.

R InterPro; IPR000503; Fibrnotn.

R InterPro; IPR000504; Fibrnotn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.4%; Score 170.5; DB 4; Length 615; 48.5%; Pred. No. 2.1e-11; ive 6; Mismatches 24; Indels 5;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00021; KRINGLE 1; 1. PROSITE; PS00021; KRINGLE 2; 1. PROSITE; PS5040; TRYPEIN DOM; 1. PROSITE; PS00134; TRYPEIN DOM; 1. PROSITE; PS00135; TRYPEIN SER; 1. SEQUENCE 615 AA; 67735 MW; 030508870A0C7EDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               947 AA.
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33; Conservative
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454 AA

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PRELIMINARY;
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    SEQUENCE FROM N.A.
MEDLINE-20538710; PubMed=11083926;
ID F.C., Glass D.G., Gles D.R., Cheung J., Lai K.O., Fu A.K.,
Yancopoulos G.D., IP N.Y.;
"Cloning and characterization of muscle-specific kinase in chicken.";
Mol. Cell. Neurosci. 16:661-673 (2000).
                                                                                                                                         A Gies D., Glass D.J., Yancopoulos G.D.;
A Gies D., Glass D.J., Yancopoulos G.D.;
A SEQUENCE FROW N.A.
B Gies D., Glass D.J., Yancopoulos G.D.;
E Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
R GO; GO:00015272; Edwichter Communication of Communicatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                947 AA; 105588 MW; E6C3FCC5796CC8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor; Kinase
SEQUENCE 947 A
 Gallus.
NCBI_TaxID=9031;
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Q9UIRS
Q9UIRS;
                                                              RESULT 26
                                                                                                                  SCOSSEDER
                                                                                                              463 RICYSGNGQFYQGWANVTASGIPCQKWS-----DQAPHLHRRTPQVFPELSDA----- 510
                                                                          1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHR-----SDALQLGLGK
                                        27;
Query Match
32.1%; Score 163.5; DB 13; Length 947;
Best Local Similarity 38.8%; Pred. No. 2.2e-10;
Matches 38; Conservative 6; Mismatches 27; Indels 27;
                                                                                                                                                                                        511 ENYCRNPGGENERPWCYTK---DPSVTWEYCSVSPCGD 545
                                                                                                                                                    52 HNYCRNP-DNRRRPWCYVQVGLKPLV--QECMVHDCAD 86
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25

RESULT 046506

9 δ

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3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

COX L.A., Jett C., Hixson J.E.;

Wollecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
Site Mutation is Associated with Deletion of a Single Exon in a Null
Allele.";
                                                                                                                       Papio hamadryas (Hamadryas baboon).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apolipoprotein(a) (Fragment).
APOA.
APOA.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00122; CHINCTRYPSIN.

PRINTS; PR00122; CHINCTRYPSIN.

PRINTS; PR001019; KRINGLE.

PRODON; PD000309; KRINGLE.

RAMAT; SM00130; KR; Z.

SMART; SM00130; KR; Z.

PROSITE; PS50070; KRINGLE 1; Z.

PROSITE; PS50040; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

Glycoprotein, Hydrolase; Kringle; Lipoprotein; Protease; 3.

Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.0%; Score 158; DB 6; Length.454; 39.8%; Pred. No. 4.4e-10; ive 10; Mismatches 31; Indels 1
                                                                                                                                                                                                                                                                                                                                                                NON TER 1 1 SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BABAPOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 DIGPWCFT---MDPSVRWEYCNLTRCSD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RRRPWCYVQVGLKPLV--QECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Best Local Similarity 39.8'
Matches 35; Conservative
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Probon, PD000395, Kringle; 5.
SMART; SM00130, KR; 4.
SMART; SM00473; PAN AF; 1.
PROSTIE; PS00021; Tryp_SPC; 1.
PROSTIE; PS00001; KRINGLE 1; 5.
PROSTIE; PS50070; KRINGLE 2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasminogen.
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                  RESULT 28
018783
       SWEERS
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAINAB: TISSUE=Body,

A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T. Max S.I., Wang J., Haieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haieh F.,

A Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Roask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Willalon D.K., Wuzny D.M., Sodesyren B.J., Lu X., Gibbs R.A.,

R Raha S., Modan A., Young A.C., Shevchenko Y., Boulfard G.G.,

R Radisquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radisquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radisquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radisquez A.C., Shevchenko Y., Boulfard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radisquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radisquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radisquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Radisquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Rodriguez S.J., Marra M.A.,

"Green E.D., Schnetch A., Scheln J.E.,

"Green E.D., Order E.D., Schnetch A., Scheln J.E.,

"Green E.D., Merley W. Schlet E.D., Schnetch A., Scheln J.E.,

"Green E.D., Merley R.M., R., Touchen B.D., Dicken E.D., Schnetch A., Scheln J.E.,

"Green E.D., Mother E.J., Mother E.J., Schnetch A., Scheln J.E.,

"Green E.D., Mother E.J., Schnetch A., Scheln J.E.,

"Green E.D., Schnetch A., Scheln J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATV--LQQTYHAHRSDALQLGLGKHNYCRNP 58
                      PROCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTM-----NYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   075XB3;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Brachydanio rezio (Zebrafish) (Danio rezio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinoperygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                            30.6%; Score 156; DB 4; Length 113; 37.8%; Pred. No. 1.7e-10; ive 12; Mismatches 32; Indels ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 DNRRRPWCYVQVGLKPLV--QECMVHDCAD
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 37.8 tes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                          Best_Loc
Matches
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Q7SXB3
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RESUBENCE FROM N.A.

RESUBENCE FROM N.A.

RESUBENCE FROM N.A.

RESUBENCE FROM N.A.

LAWN R.M., Schwartz K., Patthy L.;

Lawn R.M., Schwartz K., Patthy L.;

RESUBENCE FROM N.A.

RESUBENCE ON SCHOOL OF A SCHOOL O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 KDCITNNGEDYRGTQQKTSSGSICLSWRSLNL-----KFKDSQTGVGDHNFCRNPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macropus eugenii (Tammar wallaby).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 30.5%; Score 155.5; DB 13; Length 263; Local Similarity 35.6%; Pred. No. 4.8e-10; les 31; Conservative 8; Mismatches 39; Indels 9;
                                                                                                                                     SEQUENCE FROM N.A.
STRAINEAB: TISSUB=Body;
Straubberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BC055675; AAH55675.1; -.
Hypothetical protein:
SEQUENCE 263 AA; 28777 MM; 8BEBC117EC7C8A58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQE-CMVHDCAD 86
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S K R R R

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282 CYHGNGQSYRGTSSTTITGRKCQSWSSMT-----PHRHEKTPEHFPEAGL-TMNYCRN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL----QLGLGKHNYCRN
                                                                                                                                                                                       Pirie-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O., Polkman J., Waters D.J.; "Angiostatin is Detectable in the Urine of Dogs with Spontaneous Bone Cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
    01-MAR-2002 (TrEMBLrel. 20, Created)
U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Plasminogen (Fragment).
Plasminiliaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kanalas J.J., Makker S.P.;
"Identification of the rat Heymann nephritis autoantigen (GP330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 151.5; DB 6; Length 359;
Pred. No. 2e-09;
5; Mismatches 21; Indels 13
                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.

EMBL; AXC69885; AAL58819.1; -.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:thrombin activity; IEA.

InterPro; IPR00196; P:torteolysis and peptidolysis; IEA.

InterPro; IPR00196; F:thrombin.

PRINTS; PR00191; KRINGLE.

PRINTS; PR0019095; Kringle; 4.

PROSITE; PS00021; KRINGLE 1; 4.

PROSITE; PS50071; KRINGLE 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: cDNA and gene structure.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 359
359 AA; 41172 MW; 776D35F4AB0BDD9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MXY-2000 (TYEMBLrel. 13, Created)
01-MXY-2000 (TYEMBLrel. 13, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
Plasminogen protein precursor (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=91250378; PubMed=1645711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 PDADKSPWCY 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 PDNRRRPWCY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                        NCBI_TaxID=9615;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
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                                                                                                                                                        Gaps
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SEQUENCE FROM N.A.

MEDLINE-21181705; PubMed=11285247;

Ogorelkova M., Kraft H.G., Ehnholm C., Utermann G.;

"Single nuclectide polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";

Hun. Mol. Genet. 10:815-824 (2001).

-- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

EMBL; AF158659; AAF03678.1; "JOINED.

HSSP, PO0747; 2PR4.

ILTER-PRO; IRTURALE PROMOTO, Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                 Query Match
30.2%; Score 154; DB 6; Length 806;
Best Local Similarity 35.5%; Pred. No. 2.4e-09;
Matches 33; Conservative 11; Mismatches 25; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8,
PROSITE; PSS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESFR; 1.
GlyCoprotein; Hydrolase; Kringle; Protease; Serine protease.
SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.0%; Score 153; DB 4; Length 113; 39.3%; Pred. No. 3.8e-10; Live 8; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 AA; 12815 MW; 4F80ADF8708548CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Apolipoprotein(a) (Fragment).
                                                                                                                                                                                                                                                                                                       420 CRNPDGDKSPWCYT---MDPTVRWEFCNLEKCS 449
                                                                                                                                                                                                                                                                      55 CRNPDNRRRPWCYVQVGLKPLV--QECMVHDCA 85
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                                                                                                                                                                                                                                                                                                                                                                                                              113 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 RPWCYVQVGLKPLV--QECMVHDC 84
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ycoprotein; Kringle; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 RPWCYT---MDPSVRWEYCNLTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00051; Kringle; 1.
PRINTS; PR00018; KRINGLE.
PRODOM; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Human)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Q8WMR1;
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Q8WMR1
ID Q8WMR:
AC Q8WMR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strauberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG30848; AAHD848.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004889; F:transferase activity; IEA.
GO; GO:0004889; F:transmembrane receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
                                                                         Histy, Mould of the Colon of th
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29.2%; Score 149; DB 13; Length 716;
Best Local Similarity 33.0%; Pred. No. 8.2e-09;
Matches 33; Conservative 10; Mismatches 35; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 TCFKERGEGYRGKANTTISGIPCQRWDSQTPQSHRFLPEKXPCKGLD
(MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 NPDGSEAPWCFTTLPGMRMAYCFQIKRCKDDVLEPDCYHG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 NPDNRRRPWCYVQV-----GLKPLVQBCMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-07T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                      LARITY: CONTAINS 4 KRINGLE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8K0Q8;
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O
                                                                                           3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQL---GLGKHNYCRNPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.3%; Score 149.5; DB 11; Length 812; 37.8%; Pred. No. 8.2e-09; ive 12; Mismatches 29; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             812 PLASMINOGEN.
90535 MW; 8C703C51410EBC9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Growth factor Livertine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 N-RRRPWCYVQVGLKPLV--QECMVHDCAD 86
  receptor site for plasminogen.";
J. Biol. Chem. 266:10825-10829(1991).
-!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
EMBL; AJ242649; CAB46014.1;
-HSSP; PO0747; 1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Ruiz i Altaba A., Thery C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN 20
SEQUENCE 812 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Q8BSP6
Q8BSP6;
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Q8BSP6
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STRAIN=C27BL/6J; TISSUE=Heart;

MEDININE=2334663; PubMed=12466851;

A The FANYOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research droup phase I & II Team;

A the RIKEN Genome Exploration Research droup phase I & II Team;

A the RIKEN Genome Exploration Research droup phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration of Analysis of The Color Colo
GO, GO: 0006468; P:protein amino acid phosphorylation; IEA.

InterPro: IPR0002024; Pz domain.

R InterPro: IPR0002024; Pz domain.

R InterPro: IPR0002029; Ser thz pkinase.

R InterPro: IPR00129; Proc. kinase.

R InterPro: IPR00129; Pz pkinase.

R InterPro: IPR00129; Pz pkinase.

R InterPro: IPR00132; Fz; 1.

Pg mi PP001312; Fz; 1.

Pg mi PP001312; Fz; 1.

Pg mi PP001312; Fz; 1.

Pg pfam; PP00101; KRINGLE.

Pg pfam; PP00101; Proc. kinase; 1.

PR00131; Proc. kinase; 1.

Probom; PP00001; Proc. kinase; 1.

Probom; PP00019; Proc. kinase; 1.

Probom; PP00019; Proc. kinase; 1.

PR0SITE; PS00021; KRINGLE 1; 1.

PR0SITE; PS00021; KRINGLE 2; 1.

PR0SITE; PS00011; PROTEIN KINASE DOM; 1.

PR0SITE; PS00011; PROTEIN KINASE DOM; 1.

PR0SITE; PS0011; PROTEIN KINASE TYR; 1.

PROSITE; PS0011; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 CYNGSGADYRGMASTTKSGHQCQPW----ALQHP-HSHRLSSTEPPELG-GGHAYCRNPG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CYEGNGHPYRGKASTDIMGRPCLPWNSAIVLQQIYHAHR---SDALQLGLGKHNYCRNPD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.1%; Score 148.5; DB 11; Length 801;
41.8%; Pred. No. 1.1e-08;
ative 9; Mismatches 31; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metaza, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 801 AA; 89201 MW; 3A5928326C8B885D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor tyrosine kinase-like orphan receptor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 GOMEGPWCFTQ-NKNVRVELCDVPPCSPRDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NRRR-PWCYVOVGLKPLVQECMVHDCA--DG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 944 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 41.8 1es 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8C3W2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CYHGDGRSYRGISSTTVTGRICQSWSS--MIPHWHQRIPENYPNAGL-TENYCRNPDSGK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
DJ1182A14.3 (Similar to MST1 (Macrophage stimulating 1 (Hepatocyte DJ1182A14.3)).
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.8%; Score 147; DB 4; Length 113; 36.0%; Pred. No. 1.9e-09; 1ve 14; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA; 12697 MW; 51D4461D9C66312E CRC64;
                                                                                                                                                                                                                           01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAX-2003 (TrEMBLrel. 23, Last annotation update)
Apolipoprotein(a) (Fragment).
                                                                                                                                                                                  Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 OPWCYT---TDPCVRWEYCNLTQCSE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 RPWCYVQVGLKPLV--QECMVHDCAD 86
            84
                                         68 SPWCYT---MDPNVRWEYCNLTOC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Kringle; Lipoprotein.
            63 RPWCYVQVGLKPLV--QECMVHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00051; kringle; 1.
PRINTS; PR00018; KRINGLE.
ProDom; PD000399; Kringle; 1.
SMART; SM00130; KR; 1.
PROSITE; PS00011; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 36.0%
les 31; Conservative
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Bird C.;
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                Q9UIR6
                                                                                                                                 RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOLUTION SOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 CYNGSGADYRGWASTTKSGHQCQPW----ALQHP-HSHRLSSTEFPELG-GGHAYCRNPG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CYBGNGHFYRGKASIDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHR---SDALQLGLGKHNYCRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                       29.1%; Score 148.5; DB 11; Length 944; 41.8%; Pred. No. 1.3e-08; ive 9; Mismatches 31; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.0%; Score 148; DB 4; Length 105; larity 38.1%; Pred. No. 1.4e-09; Conservative 8; Mismatches 36; Indels
                                            SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM00109; IG; 1.

SMART; SM00109; IG; 1.

SMART; SM00119; Tvx; 1.

SMART; SM00119; Tvx; 1.

SMART; SM00119; Tvx; 1.

PROSITE; PSS0038; IG ILKE; 1.

PROSITE; PSS0001; KRINGLE 1; 1.

PROSITE; PSS0001; KRINGLE 2; 1.

PROSITE; PSS0010; PROTEIN KINASE DOM; 1.

PROSITE; PS0010; PROTEIN KINASE DOM; 1.

PROSITE; PS0010; PROTEIN KINASE TXR; 1.

SEQUENCE 944 AA; 105053 MW; IBBD416BE3170401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AA; 11882 MW; GECBGC02CD30EFA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 GOMEGPWCFTQ-NKNVRVELCDVPPCSPRDG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 NRRR-PWCYVQVGLKPLVQECMVHDCA--DG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Kringle; Lipoprotein.
PD0000395; Kringle; 1.
PD0000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apolipoprotein(a) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                        38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UIR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 36
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313 CYNSTGVDYRGTVSVTKSGRQCQPWNS-----QYPHTHTFTALRFPEINGGHSYCRNPGN 367
                                                                                                                                                  3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLG--LGKHNYCRNPDN
                                                                                                                                Gaps
                                                                                                                                                                                                                                         013208 PRELIMINARY; PRT; 567 AA.
013208;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocyte growth factor-like protein homolog.
Homo sapiens (Human).
Bamanalia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                 .,
8
            Prints; PRO0018; KRINGLE.
Prodom; PB00018; KRINGLE.
SWART; SM00408; IGC2; 1.
SWART; SM00130; KR; 1.
SROSITE; PSC0018; FZ; 1.
PROSITE; PSC0021; KRINGLE.; 1.
PROSITE; PSC0021; KRINGLE.; 1.
Glycoprotein; Immunoglobulin domain; Kinase; Kringle; Receptor.
SEQUENCE 393 AA; 43825 MW; IF93DCBBBF53855 CRC64;
                                                                                                               Length 393;
                                                                                                              Query Match
28.6%; Score 146; DB 4; Length 393;
Best Local Similarity 44.1%; Pred. No. 9.6e-09;
Matches 30; Conservative 5; Mismatches 25; Indels
                                                                                                                                                                                               368 QKEAPWCF 375
                                                                                                                                                                                    61 RRR-PWCY 67
                                                                                                                                                                                                                                 RESULT 40
Q13208
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                                                                                                                                                                                                                                                                                                                          2 TCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLG--KHNYCRNPD 59
                                                                                                                                                                                                                                                                           Query Match
28.8; Score 147; DB 4; Length 648;
Best Local Similarity 33.0%; Pred. No. 1.3e-08;
Matches 32; Conservative 13; Mismatches 36; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       OBERBO, CIETEMBLE, 17, Created)
O1-UJN-2001 (TERMELE, 17, Last sequence update)
O1-UJN-2001 (TERMELE, 17, Last sequence update)
O1-OCT-2003 (TERMELE, 25, Last annotation update)
Similar to receptor tyrosine kinase-like orphan receptor 1.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia, Butheria; Primates; Catarrhini; Hominidae; Homo.
PSOURNCE FROM N.A.

TISSUE-Muscle;
A Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
C -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
REBL; BCO06374, AAH06374.1;
RHSSP; PROO747; 1CEA.
RGO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016020; E:Minase activity; IEA.
DR GO; GO:0002488; F:Kransmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR001024; F2 domain.
DR InterPro; IPR00109; IG2-like.
DR InterPro; IPR00109; IG2-like.
DR InterPro; IPR00109; Kringle.
DR InterPro; IPR00109; Kringle.
DR Ffam; PF00147; ig; 1.
                                                                                                                                                                                                                                                                                                                                                             292 GSEAPWCFTLRPGMRVGFCYQIRRCTDDVRPQDCYHG 328
                                                                                                                                                                                                                                                                                                                                                  60 NRRRPWCY----VQVGLKPLVQEC----MVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BRB6
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RESIDENCE FROM N.A.

REQUIREDESTSTANDAY STENDER-Adipose tissue;

RETAINACSTREE-23354683; PubMed=12466851;

REDININE=23354683; PubMed=12466851;

REDININE=23354683; PubMed=12466851;

THE FANTON CONSORTIUM.

THE RAITON CONSOR
                                                                                                                                                                                                                                                          313 CYNSTGVDYRGTVSVTKSGRQCQPWNS----QYPHTHSFTALRFPELNGGHSYCRNPGN 367
                                                                                                                                                                                                                3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLG--LGKHNYCRNPDN
                                                                                        Query Match 28.6%; Score 146; DB 11; Length 937;
Best Local Similarity 44.1%; Pred. No. 2.4e-08;
Matches 30; Conservative 5; Mismatches 25; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
         PROSITE; PS00109; PROTEIN KINASE TYR; 1.
SEQUENCE 937 AA; 104118 MM; CB440323CA66EC28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor tyrosine kinase-like orphan receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  937 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            368 QKEAPWCF 375
                                                                                                                                                                                                                                                                                                                           61 RRR-PWCY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8BG10
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RE SEQUENCE FROM N.A.

RESULTED 225246683; PubMed=1246681;

A. The PANTOM COMSORTING.

B. MALLO ACOUSTON COMPANION.

B. MALLO ACOUSTON COMPANION.

A. THE PANTOM COMSORTING.

B. MALLO ACOUSTON COMPANION.

B.
                                                                                                                                                                  2 TCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLG--KHNYCRNPD 59
                                                                                                                                                                                                      Query Match 28.6%; Score 146; DB 4; Length 567;
Best Local Similarity 33.0%; Pred. No. 1.4e-08;
Matches 32; Conservative 12; Mismatches 37; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
567 AA; 64117 MW; 3FC38B07F1645810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
(1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
(1-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor tyrosine kinase-like orphan receptor 1.
                                                                                                                                                                                                                                                                                                                              312 GSEAPWCFTLRPGTRVGFCYQIRRCTDDVRPQDCYHG 348
                                                                                                                                                                                                                                                                                60 NRRRPWCY----VQVGLKPLVQEC----MVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             937 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
SQ SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBBNP9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8BNP9
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 41
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90555 MW; B05C7D4B0D020B3C CRC64;
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Best Local Similarity 38.03
Matches 35; Conservative
                   810 AA;
                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT O
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ACTISSTED-Liver;

AD HILDER CONTROL OF TECOMbinant C.G., Dodd I., Carey J.E., Lawrence G.M.P.,

AD HILDER CONTROL OF TECOMbinant human plasminogen and aglycoplasminogen in the character of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                       313 CYNSTGVDYRGTVSVTKSGRQCQPWNS----QYPHTHSFTALRFPELNGGHSYCRNPGN 367
                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                               3 CYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLG--LGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                               ..
60
                                                                                                                                                                                                   Length 937;
                                                                                                                                                                                           Ouery Match
28.6%; Score 146; DB 11; Length 93
Best Local Similarity 44.1%; Pred. No. 2.4e-08;
Matches 30; Conservative 5; Mismatches 25; Indels
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
SEQUENCE 937 AA; 104088 WW; D6F2D84267D03C69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Plasminogen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 QKEAPWCF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RRR-PWCY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q15146
Q15146;
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377 CYHGDGQSYRGTSSTTTTGKKCQSWSS-----MTPHRHQKTPENYPNAGL-TMNYCRNPD 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHR-----SDALQLGLGKHNYC 55
                                                                                                                                                                                                                                                                                                                   3 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHR----SDALQLGLGKHNYCRNPD
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LA BESSET D.I., Wilson S.W.;

Bassett D.I., Wilson S.W.;

Bassett D.I., Wilson S.W.;

Bassett D.I., Wilson S.W.;

Bassett D.I., Wilson S.W.;

Barly expression of zebrafish Hepatocyte Growth Factor-Like I underted to the state of the state 
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| Pfam; PF00051; kringle; 4. |
| Pfam; PF00054; PAN; 1. |
| R Pfam; PF00089; krypsin; 1. |
| R Pfam; PR00189; krypsin; 1. |
| R PRINTS; PR00189; KRINGLE. |
| R PRINTS; PR00189; KRINGLE. |
| R PROMOT; SM00473; PAN AP; 1. |
| R SMART; SM00473; PAN AP; 1. |
| R ROSITE; PS00021; KRINGLE 1; 4. |
| R ROSITE; PS00021; KRINGLE 2; 4. |
| R ROSITE; PS00021; KRINGLE 2; 4. |
| R ROSITE; PS00040; RRINGLE 2; 4. |
| R ROSITE; PS0040; RRINGLE 2; 4. |
| R ROSITE; PS004040; RRINGLE 2; 4. |
| R ROSITE; PR004040; RRINGLE 2; 4. |
| R ROSITE; PR004040; RRINGLE 2; 4. |
| R ROSITE; PR004040; RRINGLE 2; 4. |
| R ROSITE; PR0
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Query Match

28.2%; Score 144; DB 4; Length 810;
Best Local Similarity 37.5%; Pred. No. 3.6e-08;
Matches 33; Conservative 11; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q90ZN6 PRELIMINARY; PRT; 709 AA. Q90ZN6, CPGAZONG; (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hepatocyte growth factor-like 1.
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Local Similarity 36.5%
es 31; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9BLY1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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Q9BLY1
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KOTATOL Of DAF-7 TGF expression and neuronal process development by a receptor tyrosine kinase Kinase Kin.8 in C. elegans.";

Lobusited (FEB-1999) to the EMBL/GenBank/DDBJ databases.

L. SIMILARITY: CONTAINS 1 KRINGLE DOWAIN.

EMBL, 235595; CAA84639-2; ---

EMBL, 235955; CAA84639-2; ---

EMBL, 247808; CAB61003.1; ---

EMBL, AJ132947; CAC29085.1; ---

EMBL, AJ182940; TEXENDED TEXE
                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TYENBLREI. 01, Created)
01-NOY-2000 (TYENBLREI. 13, Last sequence update)
01-OCT-2003 (TYENBLREI. 25, Last annotation update)
01-OCT-2003 (TYENBLREI. 25, Last annotation update)
COIGG. 8 OR KIN-8
Caenorhabditis elegans.
Caenorhabditis elegans.
Elwaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
NABABDITIS (Caenorhabditis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mortimore B.J.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berks M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                            |||| :| ||||
RNPDGDRIGFWCYT-TDPERRYESCNIPQCKD 189
   RNPD-NRRRPWCYVQVGLKPLVQECMVHDCAD 86
                                                                                                                                                                                                                                                     902 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEÇUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase; 1
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PRINTS; PR000109; TYRKINASE.
ProDom; PD00001095; Kringle; 1.
ProDom; P0000001; Prot kinase
SMART; SM00408; IGC2; 1.
SMART; SM00130; KR; 1.
SMART; SM00119; TYRK; 1.
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=N2;
26
                                                                   159
                                                                                                                                                                                                     Q17576
ID Q17576
AC Q17576;
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3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TREMBLrel. 25, Last annotation update)
8eceptor tyrosine kinase (C. elegans CaM-1 protein) (corresponding sequence C01G6.8a).
C01G6.8 OR KIN-8 OR CAM-1.
Caenorhabditis elegans.
Enkaryota, Metazoa, Nematoda, Chromadorea, Rhabditidae, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koga M., Take-uchi M., Tameishi T., Ohshima Y.; "Control of DAF-7 TGF expression and neuronal process development by receptor tyrosine kinase KIN-8 in C. elegans."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
PROSITE; PSC003; IG_LIKE; 1.
PROSITE; PSC0021; KRINGLE 1; FALSE_NEG.
PROSITE; PSC0070; KRINGLE 1; FALSE_NEG.
PROSITE; PSC0010; PROTEIN KINASE ATP; 1.
PROSITE; PSC0101; PROTEIN KINASE ATP; 1.
PROSITE; PSC0109; PROTEIN KINASE TYR; 1.
ATP-binding; Immunoglobulin domain; Kinase; Kringle; Transferase; Tyrosine-protein kinase
SEQUENCE 902 AA; 101038 MW; 2A03D76D07C552BS CRC64;
                                                                                                                                                                                                                                                                                                                                                          28.0%; Score 143; DB 5; Length 902; 36.5%; Pred. No. 5.3e-08; Live 12; Mismatches 30; Indels 12;
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Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: CONTAINS I KRINGLE DOMAIN.

R. EMBL; AJ122946; CAC29084.1; -.

R. EMBL; Z3595; CAD36478.1; -.

R. EMBL; Z3595; CAD3647.1; JOINED.

R. EMBL; Z3595; CAD36487.1; JOINED.

R. EMBL; Z3595; CAD36487.1; -.

R. MormPep; CO16020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:00164888; F:transmembrane receptor activity; IEA.
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Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berks M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 SRPWCY---SKPMGQEEYCDVPQC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 -RPWCYVQVGLKPLVQE--CMVHDC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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WEDLINE=95266939; PubMed=7749817;
WEDLINE=95266939; PubMed=7749817;
WEDLINE=95266939; PubMed=7749817;
WEDLINE=95266939; PubMed=7749817;
WEDLINE=95266939; PubMed=7749817;
WEDLINE=95266939; PubMed=1749817;
WEDLINE=95266939; PubMed=1749817;
WEDLINE=95266939; WEDLINE=9536931;
WEDLINE=10091818; AAA85693.1;
WEDLINE=10091818; AAA85693.1;
WEDLINE=10091818; PROOFF; WEINGLE=184899;
WESPP: POOFF; WEINGLE=184899;
WESPP: POOFF; WEINGLE=184899;
WESPP: POOFF; WEINGLE=18499;
WENTE; PROOFF; WEINGLE=18499;
WENTE: PROOFF; WEINGLE=184999;
WENTE: PROOFF; WEINGLE=18499;
WENTE: PROOFF;
WENTE: PROOFF;
WENTE: PROOFF;
WENTE: PROOFF;
WENTE: PROOFF;
WENTE:
              439 VYYMSLWETFLIHTHNQKYSVPQLKESSGLENNYCRNPDNDQRGPWCFT---TDPSVFWE 495
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                                                                                                                      53 -----NYCRNPDN-RRRPWCYVQVGLKPLV--Q 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAX-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor tyrosine kinase Xror2.
XROR2.
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.5%; Score 140; DB 4; Length 132; Best Local Similarity 38.6%; Pred. No. 1.5e-08; Matches 34; Conservative 7; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Kringle.
SEQUENCE 132 AA; 14886 MW; 3794AD30A586DBBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       930 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRRPWCYVQVGLKPLV--QECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               496 YCNLKRCSE 504
                                                                                                                                                                                                                                                                78 ECMVHDCAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APOARGC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8AV69
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Q8AV69
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 48
Q16609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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GO; GO: 0005975; P:carbohydrate metabolism; IEA.

GO; GO: 0007275; P:development; IEA.

GO; GO: 0007275; P:development; IEA.

InterPro; IPR000024; FZ domain.

InterPro; IPR001019; FZ domain.

INTERPRO; FZ domain.

INTERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Xu C.S., Li W.O., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma H.

Yang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,

Yang K.J., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;

"Liver regeneration after PH";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY325159; AAP925560.1;

EMBL, AY325159; AAP925560.1;

SEQUENCE 759 AA, 86056 MW; 1422EFAC05C6DFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 28.0%; Score 143; DB 5; Length 928; Local Similarity 36.5%; Pred. No. 5.4e-08; es 31; Conservative 12; Mismatches 30; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
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27.5%; Score 140.5; DB 11; Length 759;
Best Local Similarity 28.7%; Pred. No. 8.6e-08;
Matches 37; Conservative 12; Mismatches 27; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103864 MW; F13B8C9BCAB30D20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 -RPWCYVQVGLKPLVQE--CMVHDC 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tyrosine-protein kinase
SEQUENCE 928 AA; 103
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Best Loca Matches

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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                  NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                        3 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAH---RSDALQLGLGKHNYCRNPD 59
                                                            SEQUENCE FROM N.A.
MEDLINE=22286220; PubMed=12399314;
Hikasa H., Shibata M., Hiratani I., Taira M.;
"The Xenopus receptor tyrosine kinase Xror2 modulates morphogenetic movements of the axial mesoderm and neuroectoderm via Wnt signalling.";
                                                                                                                                                                                                                                                                                                                                           8; Mismatches 25; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                  090865;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocyte growth factor-like/macrophage stimulating protein.
HGF1/MSP.
Gallus gallus (Chicken).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                               Length 930;
                                                                                                                                                                                                                                                                                                                 SEQUENCE 930 AA; 104081 MW; C68454572411A8B6 CRC64;
                                                                                                                                                                                                                                                                                                                              27.5%; Score 140; DB 13; 39.4%; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                             PROSITE; PS50011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                           28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             366 GOMEGPWCFTQ 376
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 60 NRRR-PWCYVQ 69
      Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                            Kinase
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Q90865
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                                                                                                                              Thery C., Sharpen, "Expression of HGF/SF, HGFL/MSP and c-met suggests new functions "Expression of HGF/SF, HGFL/MSP and c-met suggests new functions during early chick development.";

Dev. Genet. 17:90-101(1995)

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.

EMBL; X84043; CAA58862.1;

HSSP; P00747; ICEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; SOL.977; LEA.

RESPIPATOR SOL.977; LEA.

RO; GO:0004263; F:chymotrypsin activity; IEA.

RO; GO:0004263; F:chymotrypsin activity; IEA.

RO; GO:0004263; F:chymotrypsin activity; IEA.

RO; GO:0004269; F:trypsin activity; IEA.

RO; GO:0004508; F:trypsin activity; IEA.

RO; GO:0004508; F:trypsin activity; IEA.

RO; RICEPPO: IPRO00301; Kringle.

RICEPPO: IPRO03009; Pan. app.

RICEPPO: IPRO03009; Pan. app.

INTERPO: IPRO0314; Peptidase_S1.

RICEPPO: IPRO0314; Peptidase_S1.

RICEPPO: IPRO0314; Peptidase_S1.

REPPO: IPRO0314; Peptidase_S1.

RR PENNTS; PRO0015; Kringle; 4.

RR PRINTS; PRO0019; KRINGLE.

RR PRINTS; PRO0019; KRINGLE.

RR PROSTITE; PRO0021; KRINGLE.

RR ROSTITE; PRO00221; KRING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 -NRRRPWCYVQVGLKPLV--QECMVHDCAD 86
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                                                                                                    MEDLINE=96029010; PubMed=7554499;
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Best Local Similarity 38.9'
SEQUENCE FROM N.A.
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0; Gaps
APPLICANT: NIWA, MINEO
APPLICANT: SALTO, YOSHIMASA
APPLICANT: BASAKI, HIOSHI
APPLICANT: HAVASHI, MASAKO
APPLICANT: HAVASHI, MASAKO
APPLICANT: HAVASHI, MASAKOU
TITLE OF: INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI,
APPLICANT: KOBANASHI MASAKOZU
TITLE OF: INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI,
APPRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI,
ATTER OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI,
ATTER OBLON, SPIVAK, MCCLELLAND, MAIER & OCOMPATER: LEMP COMPATION
MEDIUM TYPE: Floppy disk
COMPUTER: READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEMP COMPATION
OCHUTER: LEMP COMPATION
OCHUTER: LEMP COMPATION
APPLICATION NUMBER: US/08/811,949
FILLING DATE: OS-MAR-1997
CLASSIFICATION NUMBER: 18-96-0
TELECOMMUNICATION NUMBER: 18-96-0
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42.2%; Score 215; DB 2; Length 354;
est Local Similarity 47.0%; Pred, No. 9e-18;
stches 39; Conservative 8; Mismatches 36; Indels
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3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62

63 RPWCYVQVGLKPLVQECMVHDCA 85

cch completed: May 25, 2004, 15:00:00 time : 8.0929 secs

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7 CYFGNGSAYRGTHSLIESGASCLPWNSMILIGKVYTAQNPSAQALGLGKGNYCRNPDGDA 66
       3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                25 CYFGNGSAYRGTHSLTESGASCLFWNSMILIGKVYTÄONPSÄOALGLGKHNYCRNPDGDA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRR
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: NINA, MINEO
APPLICANT: SASKI, HITOSHI
APPLICANT: SASKI, HITOSHI
APPLICANT: RASKI, HITOSHI
APPLICANT: RASKI, HITOSHI
APPLICANT: ROBAYASHI, MASAKO
APPLICANT: ROBAYASHI, MASAKO
APPLICANT: ROBAYASHI, MASAKAZU
TITLE OF INVENTION: 1 IISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ATRINGTON
ADDRESSEE: P.C.
ATRINGTON
STRET: VA
COUNTRY: USA
ZIATE: VA
COUNTRY: USA
ZIATE: 2222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUW TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: OBLOW, NORMAN F: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 18-966-0
TELEPRONE: 703-413-220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acide
TYPE: amino acide
TYPE: maino acide
TYPE: maino acide
TYPE: maino acide
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Best Local Similarity 47.0%; Pred. No. 8.7e-18;
Matches 39; Conservative 8; Mismatches 36
                                                                                                                                                                                   85 KPWCHVLKNRRLTWEYCDVPSCS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 KPWCHVLKNRRLTWEYCDVPSCS 89
                                                                                                                                        63 REWCYVQVGLKPLVQECMVHDCA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-811-949-61; Sequence 61, Application US/08811949; Patent No. 5840533; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08811949
Patent No. 5840533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 RSCYEDQGISYRGTWTTAESGAECTNWNSSALAQKPYSGRRPDPIRLGLGNHNYCRNPDR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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WPELICANT: Monor, Steven M.
WPELICANT: Ruben, Steven M.
WPELICANT: Ruben, Steven M.
WPELICANT: Ebner, Reinhard
WILLS BEFERENCE: PR378P1
WRENT PELLINGN: Tissue Plasminogen Activator-Like Protease
TILE REFERENCE: PF378P1
WRENT FILING DATE: 1999-10-04
WALLER FILING DATE: 1999-10-04
WALLER FILING DATE: 1999-05-28
WARLER FILING DATE: 1997-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
CORRESPONDENCE ADDRESS:
ADDRESSEB: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEB: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Indels
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER IBM FC compatible
COMPUTER: IBM FC compatible
COMPATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSITCATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSITCATION NUMBER: 18-966-0
TELECOMMUNICATION NUMBER: 18-966-0
TELECOMMUNICATION NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEFREX: 703-413-3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.2%; Score 215; DB 4;
47.0%; Pred. No. 8.1e-18;
iive 8; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ery Match 42.4%; Score 216; DB 2; st Local Similarity 43.7%; Pred. No. 9.6e-18; tches 38; Conservative 12; Mismatches 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 DSKPWCYVFKAGKYSSEFCSTPACSEG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 3, Application US/09411977
tent No. 6372473
NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
8-811-949-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ery Match
st Local Similarity
tches 39; Conserva
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ORGANISM: Homo 8
9-411-977-3
                                                                                                                                     CITY: ARI
STATE: VA
COUNTRY:
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US-09-618-669-10

; Sequence 10, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
    APPLICANT: Radrosius, Dorthee
    APPLICANT: Schwaffler, Joerg
    TITLE OF INVENTION: RACRESE PROTEINS BY CO-SECRETION OF MOLECULAR
    TITLE OF INVENTION: CHAPERONES
    FILE REFERENCE: 2008-07-19
    CURRENT FILING DATE: 1999-07-19
    PRIOR PILING DATE: 1999-07-29
    NUMBER OF SEQ ID NOS: 10
    SOFTWARE: Patentin Ver. 2.1
    SSEQ ID NO 10
    LENGTH: 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 378;
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42.5%; Score 217; DB 4; Length 37.
Best Local Similarity 47.0%; Pred. No. 5.6e-18;
Matches 39; Conservative 8; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 63, Application US/08811949
Fatent No. 5440533
GENERAL INFORMATION:
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYAGHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: RESPASSAKE
APPLICANT: KOBAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKO
NUMBER OF SEQUENCES: 67
91 KPWCHVLTNRRLTWEYCDVPSCS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 RPWCYVQVGLKPLVQECMVHDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 RPWCYVQVGLKPLVQECMVHDCA 85
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US-09-618-869-10
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.0
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 47
US-08-811-949-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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5 1676-5
7-01 NO. 5244676
1-01 NO. 524676
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1-01 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     very Match
42.7%; Score 218; DB 6; Length 562;
sst Local Similarity 45.9%; Pred. No. 6.8e-18;
stches 39; Conservative 10; Mismatches 36; Indels
                  Diskette, 3.50 inch, 1.0 Mb storage
                                                                                                                                          :||:|
187 KPWCHVLKNRRLTWEYCDVPSCSEG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 RPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 RRPWCYVQVGLKPLVQECMVHDCA 85
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         MEDIUM TYPE: Diskette, 3.50
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein 38-427-640-8
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sst Local Similarity
ttches 39; Conservi
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US-08-811-949-57
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US-08-427-640-8
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                                                                                   3 CYEGNGHFYRGKASTDTMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62
                                                                                                           2 CYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGUGNHNYCRNPDRDS 61
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                                                    0; Gaps
             Score 221, DB 2; Length 437;
Pred. No. 2.2e-18;
9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 221; DB 2; Length 437;
Pred. No. 2.2e-18;
9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                        APPLICANT: NITAM, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYSHI, MASAKO
APPLICANT: HAYSHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOBAYNSHI, MASAKAZU
APPLICANT: NOBANINO: 115SUB PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: P.C. P.C. TI 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 18-966-0
TELEPHONE: 703-413-3000
                                                                                                                                                                                   62 KPWCYVFKAGKYSSEFCSTPACSEG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 RPWCYVQVGLKPLVQECMVHDCADG 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       quence 55, Application US/08811949
tent No. 5840533
ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.3%;
             th 43.3%;
| Similarity 47.1%;
40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ery Match
st Local Similarity 47.1
tches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
8-811-949-55
                                                                                                                                                                                                                                                                       8-811-949-55
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CITY: AR
STATE: V
             ery Match
st Local S
tches 40
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Sequence 8, Application US/08427640
Patent No. 5658788
GENERAL INFORMATION:
APPLICANT: Berg et al.
TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN.
COUNTRY: U.S.A.
ZIP: 46285
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDS
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                                                              APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAXSHI, MASAKO
APPLICANT: HAXSHI, MASAKO
APPLICANT: NOTANI, JOUJI
ITILEO INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
43.3%; Score 221; DB 2; Length 43'
Best Local Similarity 47.1%; Pred. No. 2.2e-18;
Matches 40; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                 STREET: 1755 S. JEPPERSON DAVIS HIGHWAY, SUITE 400 STATE: WELLINGTON COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REPERBENGING NUMBER: 24,618
REPERBENGING NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 RPWCYVQVGLKPLVQECMVHDCADG 87
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Application US/08811949
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TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 amino acids
amino acid
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MOLECULE TYPE: protein

US-08-811-949-57
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USA
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Gaps ó

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2 CYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDS 61
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                                                                                                                                                                                                                                                                                                                                                                                  Length 437;
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                                                                                                                                                                                                                                                                                                                                                                               Score 221; DB 2; Length 43
Pred. No. 2.2e-18;
9; Mismatches 36; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
TIING DATE: 05/08/811,949
FILING DATE: 05/08/811,949
FIRESTENCE/DOCKET NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHINASA
APPLICANT: SASATI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 RPWCYVQVGLKPLVQECMVHDCADG 87
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62 KPWCYVFKAGKYSSEFCSTPACSEG 86
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
  CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFRENCE/DOCKET NUMBER: 18-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
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1 Similarity 47.1%;
40; Conservative 9
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TOPOLOGY: 1'---
'OLECHIE
                                                                                                                                                                                                                                       LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-49
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Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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ADDRESSEE:
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CITY: A
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                                                                          2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                Gaps
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1773-2

1 CONTY, JANUAR: HE, CHA-MER, HSIUNG, NANCY, REDDY, VBERWURI B.;

1 CONTY, JEFFREY F.; DACKOWSKI, WILLIAM, DOUGLAS, RICHARD;

2 DEPAREY F.; DACKOWSKI, WILLIAM, DOUGLAS, RICHARD;

3 TITLE OF INVENTION: HUMAN UTBRINE TISSUE PLASMINGEN

1 TITLE OF INVENTION: HUMAN UTBRINE TISSUE PLASMINGEN

1 VATOR PRODUCED BY RECOMBIANT DNA

1 NAMBER OF SEQUENCES: 6

CURRENT APPLICATION DATA:

RILING DATE: 01-0CT-1985

PRIOR APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tery Match 44.3%; Score 226; DB 6; Length 562; st Local Similarity 47.7%; Pred. No. 7.4e-19; tches 41; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                             36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
PTI-ING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: P.C..., GELVAK, MCCLELLAND, MAIER & NBUS
T: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Guence 49, Application US/08811949
"Guence 49, Application US/08811949
"Lenn No. 5846533
"EXERAL INPORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SASAZI, HIOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HAYASHI, MASAKO
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS
ADDRESSEE: P.C.
STORDEN
    ilarity 47.7%; Pred. No. 7.4e-19;
Conservative 9; Mismatches 36
                                                                                                                                                                                                    186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
                                                                                                                                                                   62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 RRPWCYVQVGLKPLVQECMVHDCADG 87
st Local Similarity tches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ID NO:2:
LENGTH: 562
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2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5185259
HAPLICANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA, DIANE;
                                                                                                                                                           Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEHAR, GORDON A.

TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINGEN

ACTIVATOR
NUMBER OF SEQUENCES: 15

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/489,855

FILING DATE: 02-MAR-1990

FILING DATE: 09-FEB-1987

APPLICATION NUMBER: 12,694

FILING DATE: 09-FEB-1987

APPLICATION NUMBER: 38,052

FILING DATE: 07-APR-1983

APPLICATION NUMBER: 398,003

FILING DATE: 14-UUL-1982

APPLICATION NUMBER: 374,860

FILING DATE: 05-MAY-1982
                                                                                                                                                      Query Match

44.3%; Score 226; DB 4;
Best Local Similarity 47.7%; Pred. No. 7.4e-19;
Matches 41; Conservative 9; Mismatches 36,
                                                                                                                                                                                                                                                                                                                                                                     186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
                                                                                                                                                                                                                                                                                                                                     62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 RRPWCYVQVGLKPLVQECMVHDCADG 87
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
NUMBER OF SEQ ID NOS: 4
                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5200340-2
;Patent No. 5200340
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                                                                                                              US-09-703-695A-4
                       SEQ ID NO 4
LENGTH: 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TILE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS
TILE REFERENCE: P178R1
URRENT APPLICATION NUMBER: US/09/703, 695A
URRENT FILING DATE: 2000-11-01
RIOR APPLICATION NUMBER: US 60/163,607
RIOR PILING DATE: 1999-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TCYEGNGHFYRGKASTDIMGRPCLPWNSATVLOOTYHAHRSDALQLGLGKHNYCRNPDNR
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APPLICANT: Delcuve, Genevieve
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.3%; Score 226; DB 2; Length 562;
47.7%; Pred. No. 7.4e-19;
tive 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/883,795A
FILIAG DATE: 27-JUN 1997
CLASSIFICATION: 435
                                                         186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
              62 RRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 SKPWCYVFKAGKYSSEFCSTPACSEG 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Gravelle, Micheline
RECISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                     quence 38, Application US/08883795A
tent No. 5985607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quence 4, Application US/09703695A
tent No. 6593097
NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERAX: (416) 364-7311
TELERAX: (416) 361-1398
NPORMATION FOR SEQ ID NO: 38.
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein (tPA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Toronto
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                                                                                                                          ILT 34
8-883-795A-38
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9-703-695A-4
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2 TCYBGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                           Gaps
44.3%; Score 226; DB 6; Length 562;
47.7%; Pred. No. 7.4e-19;
iive 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA, PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.3%; Score 226;
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2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
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MEDIUM TYPE: FOLORY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT MARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT MAPPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
ATTORNEY/ACENT INFORMATION:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/ACENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 148/42448
FILING DATE: 1020, 528-8840
TELEPPAX: (202) 628-8844
INFORMATION POR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TTPE: amino acid
TTPE: amino acid
TTPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
44.3%; Score 226; DB 2; Length 562;
Best Local Similarity 47.7%; Pred. No. 7.4e-19;
Matches 41; Conservative 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                  Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WNENDT, Stephan
APPLICANT: WNENDT, Stephan
APPLICANT: WNENDT, Stephan
APPLICANT: BINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Prenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                          Query Match
44.3%; Score 226; DB 2; Length 56
Best Local Similarity 47.7%; Pred. No. 7.4e-19;
Matches 41; Conservative 9; Mismatches 36; Indels
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               43:
                                                                                  : 562 amino acids
amino acid
3X: linear
           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                             ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-811-949-43
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US-08-560-098A-50
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                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TCYEGNGHPYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR
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                                                                                                                                                                                                                                                                                              JLT 31
340-6
-ent No. 5200340
-ent No. 5200340
APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
APPLICANT: FOSTER, SCHT, YOSHITAKE, SHINJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ARLINGTON
STATE: UA
COUTRY: UA
CONTRY: UBA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: UBM PC compatible
COURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSITCATION: 435
ATTCRNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE SECTION OF SECTION
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|:|| SKPWCYVPKAGKYSBEFCSTPACSEG 176
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                                                                                                                 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIVATORS
NUMBER OF SEQUENCES:
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ast Local Similarity
atches 41; Conserval
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LENGTH: 546
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2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOOTYHAHRSDALOLGLGKHNYCRNPDNR 61
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NUMBER OF SECUENCES: 15
CURRENT APPLICATION DATA:
FILING DATE: 0.2 MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12,694
FILING DATE: 09-FEB-1997
APPLICATION NUMBER: 12,694
FILING DATE: 09-FEB-1987
APPLICATION NUMBER: 389,003
FILING DATE: 14-JUL-1982
APPLICATION NUMBER: 371,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 SKPWCYVFKAGKYSSEFCSTPACSEG 176
                                                                                                                                   151 SKPWCYVFKAGKYSSEFCSTPACSEG 176
                                                                                          62 RRPWCYVQVGLKPLVQECMVHDCADG 87
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Best Local Similarity 47.7%;
Matches 41; Conservative 9
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Best Local Similarity 47.77
Matches 41; Conservative
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;Patent No.
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FILLE OF INVENTION:
TITLE OF INVENTION: Tiesue Plasminogen Activator Having Fibrin
TITLE OF INVENTION: Tiesue Plasminogen Activator Having Fibrin
TITLE OF INVENTION: Tiesue Plasminogen Activator Having Fibrin
TITLE OF INVENTION: Specific Properties
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
STREBT: 460 Point San Bruno Blvd
CITY: South San Francisco
STREBT: ADDRESSEE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READALE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COUNTRY: USA
ZIP: 94080
COMPUTER: Datin (Genetech)
COMPUTER: Datin (Genetech)
CONSTRAIN APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01025A
FILING DATE: 19910214
CLASSIFICATION NUMBER: 07/486,657
FILING DATE: March 1990
ATTORIEY APPLICATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 454F2
TELECOMMUNICATION INFORMATION:
TELEPRAN: 415/265-1981
TELEPRAN: 415/265-1981
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47.7%; Pred. No. 6.9e-19;
tive 9; Mismatches 36; Indels
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| ::|
| SKPWCYVFKAGKYSSEFCSTPACSEG 176
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24 618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-2000
NFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTER STICS:
LENGTH: 527 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 RRPWCYVQVGLKPLVQECMVHDCADG 87
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(NFORWATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 527 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
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st Local Similarity
stches 41; Conserva
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91 TCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRD 150
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; Patent No. 5520913
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR HAVING
; TITLE OF ROPERTIES
; NUMBER OF SEQUENCES: 35
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 05/08/88,451
; PRIOR APPLICATION NUMBER: 384,608
; FILING DATE: 03-07-1991
; PRIOR APPLICATION NUMBER: 24-00-1991
; PRIOR APPLICATION NUMBER: 24-00-1991
; PLING DATE: 24-00-1989
; FILING DATE: 22-00-1988
; FILING DATE: 02-SEP-1988
                                                                                                                                                                                                                                                                                    ant No. 5185259
APPLICANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA, DIANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.3%; Score 226; DB 6; Length 527; 47.7%; Pred. No. 6.9e-19; Live 9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 226; DB 6; Length 52
Pred. No. 6.9e-19;
9; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                             RR, GORDON A.
TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
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44.3%; Score 226; DB 1;
47.7%; Pred. No. 6.9e-19;
iive 9; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 SKPWCYVPKAGKYSSEFCSTPACSEG 176
TITLE OF INVENTION: Method for Alt NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: IN.
COUNTRY: U.S.A.
ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RRPWCYVQVGLKPLVQECMVHDCADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/08811949 Patent No. 5840533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 47.7
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-609-510B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 61
                                                            1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                   Gape
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47.3%; Score 241; DB 2; Length 477;
sst Local Similarity 50.0%; Pred. No. 9.8e-21;
tches 42; Conservative 12; Mismatches 30; Indels
                                                                                                                                                                                                                                                                  duence 51, Application US/08560098A

TENERAL INFORMATION:
BENERAL INFORMATION:
APPLICANT: WINDEL WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TILLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDITOR TYPE: Plopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRICK APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGRAY INFORMATION:
NAME: EVANS, UGSEPh D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELENCOMMUNICATION INFORMATION:
TELENCOMMUNICATION INFORMATION:
TELENCOMMUNICATION INFORMATION:
                4; Indels
              0; Mismatches
                                                                                                                                                                                            108 KRRPWCYYQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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)7-609-510B-16
Aquence 16, Application US/07609510B
.tent No. 5326700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: (202) 628-8844 (NFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 477 amino acids amino acids
              84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
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              tches
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Method for Altering Post-Translational Processing of Tissue Pi
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CORRESPONDENCE ADDRESS: 67
CORRESPONDENCE ADDRESS: 67
ADDRESSES: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, APPLICANT: APPLICANT: APPLICANT: NOTANI, MAGNESS: APPLICANT: NOTANI, MAGNESS: APPRESSES: NOTANI, MAGNESS: APPLICANT: NOTANI, MAGNESS: APPRESSES: APPLICANT: NOTANI, MAGNESS: APPLICANT: NOTANI, MAGNESS: APPRESSES: APPLICANT: NOTANI, MAGNESS: APPRESSES: APPRESSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
FILLING DATE: 19901106
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CRARACTERISTICS:
LEBNGTH: SZ7 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALURESSEE: P.C. SPIVAK, MCCLELLAND, MAIER & NEUS STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON PATER STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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6 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08142590B
Patent No. 6120765
GENERAL INFORMATION:
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCESS: ADDRESSE: LAHYTE & COCKPIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 486; DB 3; Length 157; Pred. No. 1.1e-50;
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
NAMB/KEY: misc_feature
OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
US-09-101-272G-62
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.9%; Score 489; DB 4; Length 89; Best Local Similarity 100.0%; Pred. No. 2.5e-51; Matches 84; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                            CURRENT FILING DATE: 1998-07-08
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: 19 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MOBIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,590B
FILING DATE: 25-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,318
FILING DATE: 02-APR-1993
ATPOINGY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-009CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 RRRPWCYVQVGLKPLVQECMVHDC 89
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TOPOLOGY: 1:-
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKGNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                 tent No. 597644

tent No. 597644

ENERAL INFORMATION:
APPLICANT: WNENDT. Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: GYBEFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCES ADDRESS:
ADDRESSEE: Broenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.8%; Score 499; DB 2; Length 411; 98.9%; Pred. No. 9.6e-52; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Felease #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
FILING DATE: 17-NOV-1995
ATTORNEY APELICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY AGENT INFORMATION:
NAME: EVANS, OSSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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9-101-272G-62
quence 62, Application US/09101272G
cent No. 6509445
bent No. 6509445
PPLICANT: NISSII NOSG
PPLICANT: NISSII NOSG
ITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 RRRPWCYVQVGLKLLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 628-8844
NFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
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GOETINCK,

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49 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 108
                                                                                                                                         49 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDN 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                    1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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| Sequence | Application US/09181816 |
| Patent No. 6277810 |
| GENERAL INFORMATION |
| APPLICANT: MAZAR, Andrew P. |
| APPLICANT: UNEXTION |
| TITLE OF INVENTION | PLASMINOGEN ACTIVATOR RECEPTOR |
| TITLE OF INVENTION | PLASMINOGEN ACTIVATOR RECEPTOR |
| CURRENT APPLICATION UNDER: US/09/181, 816 |
| CURRENT FILING DATE: 1998-10-29
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Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.0%; Score 505; DB 4; Length 20
100.0%; Pred. No. 7.9e-53;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 5.2, Application US/09101272G
; Patent No. 6509445
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT NISSIN FOOD PRODUCE CO., Ltd.
; TILLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFREENCE: 165097
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR PLILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO S: 107
; SEQ ID NO S: 201
Query Match
99.0%; Score 505; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 7.5e-53;
Matches 87; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.0%; Score 500; DB 3; 98.9%; Pred. No. 7.3e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: ATPHI-CL chimeric protein US-09-101-272G-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 RRRPWCYVQVGLKPLVQECMVHDCADG 135
                                                                                                                                                                                                                                                109 RRRPWCYVQVGLKPLVQECMVHDCADG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
                                                                                                                                                                                                   61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.01
...hag 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.95
Matches 87; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                       RESULT 20
US-09-101-272G-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 411
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                                                                                                                                                                                                                                                ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26.269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                          Proteins having Fibrinolytic and
Coagulation-inhibiting Properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quence 80, Application US/09101272G
ntenn No. 6509445
EMERAL INFORMATION:
PPLICANT NISSIN FOOD PRODUCTS CO., Ltd.
TILE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
TILE REPERENCE 1650970
TURRENT PELLON NUMBER: US/09/101,272G
TURRENT PELLON DATE: 1998-07-08
PRIOR APPLICATION NUMBER: UP 1059/1996
PRIOR FILING DATE: 1996-01-08
VUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
                       TITLE OF INVENTION: Coagulation-inhibiting Proper NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: 60 CORRESPONDENCE ADDRESS: 60 CORRESPONDENCE EVENSON, MCKEOWN, Edwards & Lenahan STREET: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 RRRPWCYVQVGLKPLVQECMVHDCADGK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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          Gerd Josef
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: (202) 628-8844 (NPORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 432 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lery Match 100.
St Local Similarity 100.
Atches 88; Conservative
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       STEFFENS,
                                                                                                                                                                              CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
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68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIBBB29-1,
SIBBB29-1,
Patent No. SIBBB29
; Patent No. SIBBB29
; TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
; TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
; UNWBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/340,007
; FILING DATE: 18-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAWE/KEY: misc_feature

| LOCATION: (20)...()

| OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)

US-09-101-272G-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                   Sequence 1, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICAMT: Nissin Food Products Co., Ltd.
TITLE OP INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1996-07-08
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 510; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.9e-53;
Matches 88; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 RERPWCYVOVGLKPLVOECMVHDCADGK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 RRRPWCYVQVGLKPLVQECMVHDCADGK 155
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Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WRENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
1es 88; Conservative
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: mat peptide
LOCATION: (21)..()
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
US-08-560-098A-47
                          US-09-101-272G-1
                                                                                                                                                                                                                                                                                                                                         LENGTH: 431
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Best Local Si
Matches 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 198..203
OTHER INFORMATION: /label= modified
OTHER INFORMATION: /note= "six amino acids deleted in mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ery Match 100.0%; Score 510; DB 6; Length 430; st Local Similarity 100.0%; Pred. No. 4.9e-53; tches 88; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UT 15
1569-2
ent No. 5219569
APPLICANT: BLABER, MICHAEL;HEYNEKER, HERBERT L.;VEHAR,
DON A.
TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631673
FILING DATE: 20-DEC-1990
ATTORNEY, AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCES/DOCKET NUMBER: TSI108Cont.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= peptide
/note= "WAP signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 RRRPWCYVQVGLKPLVQECMVHDCADGK 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,858
FILING DATE: 16-AUG-1985
PRIOR APPLICATION NUMBER: 725,468
FILING DATE: 22-APR-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IOCATION: 1.19
OTHER INFORMATION: /labe
OTHER INFORMATION: /note
FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                         : 430 amino acids
AMINO ACID
                                                                                                                                                                                                                       TELEPAX: (404) B15-6555
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ery Match
st Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 430
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LOCATION:
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Gaps

108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135

1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60

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APPLICANT: DESCRIAND, 1986

APPLICANT: BABLLAT, Christelle
APPLICANT: PERRICAUDET,
APPLICANT: PERRICAUDET,
Michel
APPLICANTON: Por The Treatment of Tumors
FILE OF INVENTION: Por The Treatment of Tumors
FILE REPRENCE: A2778A-US
CURRENT PLING DATE: 1999-10-05
FRIOR APPLICATION NUMBER: PCT/EP98/02491
FRIOR APPLICANTON NUMBER: 60/044,980
FRIOR PLING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
ILENGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
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Patent No. 5648553
GENERAL INFORMATION:
APPLICAMT Wei, Cha-Mer
TITLE OF INVENTION: Inhibitor-Resistant Urokinase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Kilpatrick & Cody
STREET: 1100 Peachtree Street Suite 2800
CITY: Atlanta
CTIY: Atlanta
CTIY: Atlanta
COUNTRY: USA
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPUTER
COM
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APPLICATION NUMBER: US/07/942,157A FILING DATE: 19920908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 510; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-53;
Matches 88; Conservative 0; Mismatches 0;
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                                                                                                                                                            Sequence 2, Application US/09403736
Patent No. 6638502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRISCELLI, Frank
OPOLON, Paule
SORIA, Claudine
RAGOT, Thierry
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; ORGANISM: humanurokinase
US-09-403-736-2
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aventis S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEGRAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-942-157A-3
                                           RESULT 13
US-09-403-736-2
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48 KICYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHYCRNPDN 107
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SOCTIVARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE: OS/08/153,799
FILING APPLICATION NUMBER: US 07/847975
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/87975
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING A
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350-153-799
                                                                                                                                                                                                                                                                108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                  61 RRRPWCYVQVGLKPLVQBCMVHDCADGK 88
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lery Match 100.
st Local Similarity 100.
ttches 88; Conservative
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18-153-799-18
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48 KTCYEGNGHFYRGKASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Patent No. 5759542

GENERAL INCRANION: COMPOSITIONS AND METHODS FOR THE DELIVERY TITLE OF INVENTION: COMPOSITIONS BY PLATELETS FOR THE TREATMENT OF TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF TITLE OF INVENTION: SEQUENCES: 18

CONRESPONDENCE ADDRESS: 18

COUNTRY: 10.5 A.

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.48 MB

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DISKETTE, 1.994

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DISKETTE, 1.994

CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/286,748B

FILING DATE: ANGURE FORMATION:
MAME: 1. Peter FORMATION:
MAME: 1. Peter FORMATION:
MEDIUM TOWNER: (617) 542-5070

TELEPHONE: (617) 542-5070

TELEPHONE: (617) 542-5070
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                                                                                                                                                                                                                                                                                                                         Length 411
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                 100.0%; Score 510; DB 1;
100.0%; Pred. No. 4.6e-53;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                  TELECOMMUNICATION INFORMATION:
TELEPRAX: (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.09
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 88; Conserva
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STRANDEDNESS: sir
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US-08-286-748B-18
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
FILLING DATE:
CLASCTOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 10
9-087-163-1
quence 1, Application US/08087163
tent No. 5472692
ENRRAL INFORMATION:
APPLICANT: Lit, Jian-Ning
APPLICANT: Gurewich, Victor
TITLE OF INVENTION: PRO-URCKINASE MUTANTS
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READALLE FORM:
WEDIUM TYPE: 13.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFTATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: PRIORWATION:
APPLICATION NUMBER:
FILING DATE: PRIORWATION:
APPLICATION NUMBER:
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04353/003001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BYANS. JOSEPH D.
REGISTRATION NUMBER: 26,269
REFRENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELECHONIS: (202) 628-8844
NFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TTPE: amino acids
TTPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICANT: WNENDY Stephan
APPLICANT: WNENDY Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOCHA, Blke
APPLICANT: JANOCHA, Blke
APPLICANT: JANOCHA, Blke
APPLICANT: JANOCHA, Blke
APPLICANT: HEINZEL-WHELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
CORRESPONDENCE ADDRESS: 25
CORRESPONDENCE ADDRESS: Eveneon, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISW PC Compatible
COMPUTER: ISW PC Compatible
COMPUTER: ISW PC Compatible
COMPUTER: ISW PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECHONE: (202) 628-8840
TELECHONE: (202) 628-8840
     Application US/08967024C
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPCLOSY: linear
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US-08-967-024C-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                       1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                     2 KTCYBGNGHFYRGKASTDTMGRPCLFWNSATVLQQTYHAHRSDALQLGLGKHNYCRNFDN 61
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lery Match 100.0%; Score 510; DB 1; Length 365; st Local Similarity 100.0%; Pred. No. 4e-53; tches 88; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TREADABLE FORM:
DOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P4 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH 26,269
REFERENCE/DOCKET NUMBER: 148/42446
TELEPHONE: (202) 628-8844
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 maino acids

LENGTH: 393 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WNENDT, Stephan, Regina
APPLICANT: HEINZEL, WIELAND, Regina
APPLICANT: STEFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
CORRESPONDENCE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 510; DB 2; 100.0%; Pred. No. 4.4e-53;
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                                                                                                                                                                                                     61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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                                                                                                                                                                                                                                                                                                                                               8-560-098A-44
quence 44, Application US/08560098A
Lent No. 5976841
ENBRAL INFORMATION:
APPLICANT: WNENDT, Stephan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          est Local Similarity 100.
toches 88; Conservative
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ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
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62
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                                                            Gaps
Query Match
100.0%; Score 510; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 4.4e-53;
Matches 88; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/08967024C
| Patent No. 6133011
| GENERAL INFORMATION:
| APPLICANT: WINNOT, Stephan
| APPLICANT: STEFFENS, Gerd Josef
| APPLICANT: JANOCHA, Elke
| APPLICANT: JANOCHA, Elke
| APPLICANT: HEINZEL-WIELAND, Regina
| TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic CORRESPONDENCES: 25
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                        63 RRRPWCYVQVGLKPLVQECMVHDCADGK 90
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ZIP: 20005
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LT 8 18-967-024C-24

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GENERAL INFORMATION:
APPLICANT: STEFENS, GERD J.
APPLICANT: STEFENS, GERD J.
APPLICANT: STEFENS, GERD J.
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: SAUNDERS, JOHERS, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
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100.0%; Score 510; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 4e-53;
Matches 88; Conservative 0; Mismatches 0; Indels (
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MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUGNERNY APPLICATION DATA:
APPLICATION NUMBER: US/08/720,012
FILING DATE: 27-SEP-1996
FILING DATE: 05-UJU-1993
APPLICATION NUMBER: US 08/093,741
FILING DATE: 15-UJU-1993
ATTORNEY/AGENT INPOMMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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               REGISTRATION NUMBER: 26,269
REPERENCE/DOCKET NUMBER: 148/.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8840
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEFHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TOPOLOGY:
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APPLICANT: STEPENS, GERD J.
APPLICANT: STEPENS, GERD J.
APPLICANT: STEPENS, GERD J.
APPLICANT: STEPENS, GERD J.
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: SANNDERS, DEREK J.
TITLE OF INVENTION: IMPROVED FIRENDIATIC CHARACTERISTICS AND THROWBIN
TITLE OF INVENTION: INHIBITING EFFECT
NUMBER OF SEQUENCES, 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N. W. Suite 700
CITY: Washington, D.C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 KICYBGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KTCYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ery Match 100.0%; Score 510; DB 4; Length 208; st Local Similarity 100.0%; Pred. No. 2.1e-53; tches 88; Conservative 0; Mismatches 0; Indels
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CUNTRAY: U.S.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,741
FILING DATE: 20-JUL-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
                                                                                                                                          LT 4

19. 101-272G-98

Guence 98, Application US/09101272G

tent No. 6509445

WERAL INFORMATION:
PPLICANT: Nissin Food Froducts Co., Ltd.
TILE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
ILE REPERENCE: 650979

URRENT PLIING DATE: 1998-07-08

RICR APPLICATION NUMBER: UF 1059/1996

RICR APPLICATION NUMBER: UF 1059/1996

RICR APPLICATION NUMBER: UF 1059/1996

OURRENT PLIING DATE: 1996-01-08

OURRENT PLING DATE: 1996-01-08

OURRENT PLING DATE: 1996-01-08

OURRENT PLING DATE: 1996-01-08

OFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: ATFHI-ML chimeric protein
9-101-272G-98
128 RRRPWCYVQVGLKPLVQECMVHDCADGK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 RRRPWCYVQVGLKPLVQECMVHDCADGK 136
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8-093-741-83
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68 KTCYEGNGHPYRGKASTDIWGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDN 127
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Best Local Similarity 100.0%; Score 510; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 2e-53;
Matches 88; Conservative 0; Mismatches 0; Indels
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US-09-101-272G-73
Sequence 73, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissain Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 050979
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1996-07-08
PRIOR APPLICATION NUMBER: US/09/1096
NUMBER OF SEQ ID NOS: 107
SOCTUMENT PLING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOCTUMENT: 200
TYPE: PRIOR
TYPE: PRI
CREMETH: 200
TYPE: PRIOR
                                                                  PRIOR CAPACITICATION DATA:

APPLICATION NUMBER: US 08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
APPLICATION NUMBER: US 08/256,927
FILING DATE: 38-UJU-1994
APPLICATION NUMBER: FF 92/01064
APPLICATION NUMBER: FF 92/01064
FILING DATE: 31-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMICH Ph. D., JUL1e K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: P-38,619
TELEPHONE: (610) 454-3839
APPLICATION NUMBER: US/09/984,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 RRRPWCYVQVGLKPLVQECMVHDCADGK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
) MOLECULE TYPE: protein
) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-984-186-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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; NAME/KEY: misc feature
; OTHEN INFORMATION: AIF domain of uPA
US-09-101-2726-73
                             FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 88; Conservative
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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: ER 92/01064
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1993
ATTORNEY/AGENT IRFORMATION:
NAME: Smith Ph.D. Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERONE: (610) 454-3809
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TTYPE: amino acids
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MEDIUM TYEE: Floppy disk
COMPUTER: Macintosh
COPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
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09-984-186-12
squence 12, Application US/09984186
squence 12, Application US/09984186
squence 12, Application US/09984186
squence 12, Application Fournier, Alain
Fournier, Alain
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sst Local Similarity 100.
Tches 88; Conservative
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MOLECULE TYPE: protein
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Sequence 12, Application US/08797689
Sequence 12, Application US/08797689
Sequence 12, Application US/08797689
Sequence 12, Application
APPLICANT: Flear, Reinhard
APPLICANT: Flear, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gearad
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
ITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STARE: PA
COUNTRY: USA
Sequence 2, Appli
Patent No. 5185259
Patent No. 5185259
Sequence 43, Appl
Sequence 38, Appli
Sequence 38, Appli
Sequence 38, Appli
Patent No. 5185259
Patent No. 5200340
Sequence 51, Appli
Sequence 51, Appli
Sequence 57, Appli
Sequence 67, Appli
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Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
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Sequence 17, Appli
Sequence 23, Appli
Sequence 53, Appli
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67, Appli
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US-08-811-949-63

US-09-618-869-10

US-09-811-949-61

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US-08-560-098A-50
US-08-883-795A-38
US-09-703-695A-4
  PCT-US91-01025A-2
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                     5520913-1
5200340-6
                                                                                   5185259-3
 RESULT 1
US-08-797-689-12
 Sequence 12, Appl
Sequence 12, Appl
Sequence 98, Appl
Sequence 98, Appl
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Sequence 12, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 37, Appl
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80, Appl
1, Appli
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65, Appl
51, Appl
16, Appl
39, Appl
                                                                  May 25, 2004, 14:48:05; Search time 6.0929 Seconds (without alignments) 745.636 Million cell updates/sec
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3: /cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-94-186-12
US-09-101-272G-73
US-08-09-741-83
US-08-09-720-012-83
US-08-05-00-098-44
US-08-05-00-098-44
US-08-06-00-098-44
US-08-08-70-24-2-24
US-08-08-70-18-18
US-08-153-79-18
US-08-153-79-18
US-09-101-75G-18
US-09-101-772G-90
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Maximum Match 100%
Listing first 75 summaries
                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Search completed: May 25, 2004, 15:03:40 Job time : 17.0421 secs
                                                                                                 VPDICANT: Cameron, Beatrice
NPPLICANT: Cameron, Beatrice
NPPLICANT: Blanche, Francis
TILE OF INVENTION: Abrogness Polypeptides, Nucleic Acids Encoding Them and Methods for
ITLE OF INVENTION: Using Them to Inhibit Angiogenesis
TILE OF INVENTION: Using Them to Inhibit Angiogenesis
TURRENT APPLICATION NUMBER: US/10/424,999
NRIOR APPLICATION NUMBER: 10/233,675
NRIOR APPLICATION NUMBER: 10/233,675
NRIOR PILING DATE: 2002-09-04
UNMER OF SEQ ID NOS: 70
OFTWARE: Patentin Version 3.2
LENGTH: 87
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PPLICANT: Cameron, Beatrice
PPLICANT: Branche, Francis
TILE OF INVENTION: Angiogenesis
TILE OF INVENTION NUMBER: US/10/425,000
URRENT PILING DATE: 2003-04-29
WICK FILING DATE: 2002-09-04
UMBER OF SEQ ID NOS: 105
UMBER OF SEQ ID NOS: 105
UMBER OF SEQ ID NOS: 105
UNDER OF OR SEQ ID NOS: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
O-THER PROSMATION: Human abrogen as secreted from pBA140 (abrogen N43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 3.2e-50;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
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quence 10, Application US/10424999
blication No. US20040052810A1
NERAL INFORMATION:
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98.8%;
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                             PPLICANT: Nesbit, Mark
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tches 85; Conserva
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US-10-233-675A-1

US-10-233-675A-1

Sequence 1. Application US/10233675A

Publication No. US20030228298A1

Publication No. US20030228298A1

GENERAL INFORMATION:

APPLICANT: Respit, Mark

APPLICANT: Brockstedt, Dirk

APPLICANT: Brockstedt, Dirk

TITLE OF INVENTION: Them To Inhibit Angiogenesis

TITLE OF INVENTION: Them To Inhibit Angiogenesis

FILE REPERENCE: ST01027

CURRENT APPLICATION NUMBER: US/10/233,675A

CURRENT PILING DATE: 2002-09-04

FRIOR PILING DATE: 2001-09-04

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 86
                                                                            TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for INTER OF INVENTION: Using Them to Inhibit Angiogenesis FILE REFERENCE: STO1027-A CURRENT APPLICATION NUMBER: US/10/424,999
CURRENT FILING DATE: 2003-04-29
PRIOR FULING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFFWARE: Patentin version 3.2
SEQ ID NO 1
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Pred. No. 3.2e-50;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: human derived abrogen US-10-233-675A-1
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US-10-424-999-1
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.8%;
Matches 85; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
        APPLICANT: Nesbit, Mark
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US-10-424-999-10
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APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for INVENTION: Using Them to Inhibit Angiogenesis
FILE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REFERENCE: ST01027-A
TURRENT APPLICATION NUMBER: US/10/424,999
SRIOR APPLICATION NUMBER: 10/233,675
RIOR APPLICATION NUMBER: 10/233,675
RIOR FILING DATE: 2002-09-04
WUMBER OF SEQ ID NOS: 70
SOFFWARE: Patentin Version 3.2
SQ ID NO 36
ELENGTH: 221
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SUBSTANTIANT US OF APPLICANTS

APPLICANT: Leenhouts, Cornelis J.

FITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way USRENT APPLICATION NUMBER: US/10/360,101

FILE REPRENCE: 2183-5673

FILE OF INVENTION NUMBER: US/10/360,101

PRIOR APPLICATION NUMBER: BP 02077060.8

PRIOR FILING DATE: 2003-02-04

SOFTWARE: Patentin version 3.1

SOFTWARE: Referit version 3.1

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: TrxA-Abrogen D43 fusion protein 0-424-999-36
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100.0%; Pred. No. 2.3e-50;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: sequence of urokinase 10-360-101-266
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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st Local Similarity
...heq 86; Conservat
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[0-360-101-266
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10-424-999-1
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Sequence 37, Application US/10424999

Sequence 37, Application No. US20040052810A1

Sequence 37, Application No. US20040052810A1

GENERAL INFORMATION:

APPLICANT: Nesbit, Mark

APPLICANT: Cameron, Beatrice

APPLICANT: Blanche, Francis

TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for TITLE OF INVENTION: USING Them to Inhibit Angiogenesis

FILE OF INVENTION: UNDER: US/10/424,999

CURRENT APPLICATION NUMBER: US/10/424,999

CURRENT APPLICATION NUMBER: 10/233,675

PRIOR APPLICATION NUMBER: 10/233,675

PRIOR APPLICATION NUMBER: 10/233,675

SPRIOR APPLICATION NUMBER: 10/233,675

SPRIOR APPLICATION OF 3.2

SEQ ID NO 37

LENGTH: 91
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TITLE OF INVENTION: Them To Inhibit Angiogenesis FILER REFERENCE: STOIO27
CURRENT APPLICATION NUMBER: US/10/233,675A
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/316,300
PRIOR APPLICATION NUMBER: 60/316,300
PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO SEC ID NOS TENGTH: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.8%; Score 499; DB 15;
Best Local Similarity 100.0%; Pred. No. 8.4e-51;
Matches 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: human derived fusion protein US-10-233-675A-9
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Publication No. US20040052810A1
GENERAL INFORMATION:
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US-10-424-999-37
                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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PPLICANT: Fong, Timothy

PPLICANT: Brockstedt, Dirk

TILB OF INVENTION: Abrogen Polypeptides, Mucleic Acids Encoding Them and Methods for
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PPLICANT: Cameron, Beatrice
PPLICANT: Cameron, Beatrice
PPLICANT: Cameron, Beatrice
PPLICANT: Cameron, Beatrice
PPLICANT: Blanche, Francis
TILE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
TILE OF INVENTION: Angiogenesis
TILE REPERENCE: ST01027-B
URRENT APPLICATION NUMBER: US/10/425,000
WRICH APPLICATION NUMBER: 10/233,675
RIOR APPLICATION NUMBER: 10/233,675
RIOR APPLICATION NUMBER: 10/233,675
UNGER OF SEQ ID NOS: 105
OPTWARE PATENTIN Version 3.2
Q ID NO 29
LENGTH: 87
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                                                                                                                                                                                                                                                                OTHER INFORMATION: Human abrogen as secreted from pMB063 (abrogen D43)
                                                                                                                                                                                                                                                                                                                                              ery Match 97.8%; Score 499; DB 12; Length 87; st Local Similarity 100.0%; Pred. No. 8.4e-51; tches 86; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.4e-51;
tive 0; Mismatches 0; Indels
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                            'RIOR APPLICATION NUMBER: 10/233,675 'RIOR FILING DATE: 2002-09-04
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     URRENT FILING DATE: 2003-04-29
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ORGANISM: Artificial Sequence
                                                                           UMBER OF SEQ ID NOS: 70
OFTWARE: Patentin version 3.2
Q ID NO 9.
LENGIH: 87
                                                                                                                                                                                         TYPE: PRT : : : : ORGANISM: Artificial Sequence
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st Local Similarity 100.
tches 86; Conservative
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0-425-000-29
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0-233-675A-9
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Sequence 22, Application US/10233675A

Sequence 22, Application US/10233675A

Publication No. US20030228298A1

SEQUENCE 22, Application No. US20030228298A1

SERBEAL INFORMATION:
APPLICANT: Nesbit, Mark

APPLICANT: Forg, Timothy

TITLE OF INVENTION: Them To Inhibit Angiogenesis
TITLE OF INVENTION: Them To Inhibit Angiogenesis

TITLE OF INVENTION: Them To Inhibit Angiogenesis

CURRENT APPLICATION NUMBER: US/10/233,675A

CURRENT FILING DATE: 2002-09-04

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Version 3.1

SEQ ID NO 22

LENGTH: 86
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Publication No. US20040052810A1
GENERAL INFORMATION:
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for TITLE OF INVENTION: USing Them to Inhibit Angiogenesis
FILE REFERENCE: ST01027-A
CURRENT APPLICATION NUMBER: US/10/424,999
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US-10-233-675A-22
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Pred. No. 8.3e-51;
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100.0%; Pred. No. c...
0; Mismatches
                                                                                                                                                                                                                                                                 OTHER INFORMATION: human derived abrogen
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                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 86
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Best Local Similarity 100.v
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US-10-233-675A-22
                                                                                                                                                                                                                                                                                                        US-10-233-675A-5
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Dilication No. US20040052777A1

GENERAL INFORMATION:

PPLICANT: Cameron, Beatrice

APPLICANT: Cameron, Beatrice

APPLICANT: Rancis

FILE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit

CITLE OF INVENTION: Angiogenesis

FILE OF INVENTION: Angiogenesis

FILE OF INVENTION: MUMBER: US/10/425,000

UNRENT FILING DATE: 2003-04-29

RIOR APPLICATION NUMBER: 10/233,675

PRIOR APPLICATION NUMBER: 10/233,675

WHORE REPERFORMER: 10/233,675

WHORE FILING DATE: 2002-09-04

WUMBER OF SEQ ID NOS: 105

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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OTHER INFORMATION: Human kringle domain ATF-Kringle (Abrogen)
(0-425-000-97
                                                                                                                                                           OTHER INFORMATION: Human kringle domain ATF-Kringle (Abrogen)
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    97.8%; Score 499; DB 12;
sst Local Similarity 100.0%; Pred. No. 8.3e-51;
atches 86; Conservative 0; Mismatches 0;
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                                                                                     ORGANISM: Artificial Sequence
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10-233-675A-5
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.0-425-000-97
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           LENGIH: 86
                                                                                                                            FEATURE:
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Sequence 62, Application US/10424999
Publication No. US20040052810A1
GENERAL INFORMATION:
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: USing Them to Inhibit Angiogenesis
TITLE OF INVENTION: USing Them to Inhibit Angiogenesis
FILE REFERENCE: ST01027-A
CURRENT APPLICATION NUMBER: US/10/424,999
CURRENT PILING DATE: 2003-04-29
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Version 3.2
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REFERENCE: STOL027-A
CURRENT APPLICATION NUMBER: US/10/424,999
CURRENT PILING DATE: 2003-04-29
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.2
LENGTH: 86
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                                                                                                                        Length 687;
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; FEATURE:
; OTHER INFORMATION: fusion protein human abrogen
US-10-233-675A-17
                                                                                                                        Query Match

98.0%; Score 500; DB 15
Best Local Similarity 98.9%; Pred. No. 6e-50;
Matches 86; Conservative 1; Mismatches
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US-10-424-999-5
US-10-424-999-5
Sequence 5, Application US/10424999;
Publication No. US20040052810A1
GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE;
; OTHER INFORMATION: Human abrogen
US-10-424-999-5
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ORGANISM: Artificial Sequence
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US-10-424-999-62
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blication No. US2004005277A1
NERAL INPORMATION
PPLICANT: Cameron, Beatrice
PPLICANT: Cameron, Beatrice
PPLICANT: Blanche, Francis
ITLE REFERENCE: STO1027B
ILLE REFERENCE: STO1027B
IURRENT APPLICATION NUMBER: US/10/425,000
URRENT FILING DATE: 2003-04-29
RIOR APPLICATION NUMBER: 10/233,675
RIOR PILLNG DATE: 2002-09-04
UMBER OF SEQ ID NOS: 105
CO ID NO 37
LENGTHARE: PatentIn version 3.2
CO ID NO 37
LENGTH: 687
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                              DB 12; Length 687;
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                                                                                          Indels
                          Score 500; DB 12; I
Pred. No. 6e-50;
1; Mismatches 0;
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OTHER INFORMATION: Human derived fusion protein
0-425-000-37
                                                                                                                                                                                                                                                                               61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
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ORGANISM: Artificial Sequence
                       Nexy Match 98.0%; st Local Similarity 98.9%; tches 86; Conservative
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ORGANISM: Artificial Sequence
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0-233-675A-17
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.0-425-000-37
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US-10-134-999-17

Sequence 17, Application US/10424999

Sequence 17, Application US/10424999

Sequence 17, Application US/10424999

Sequence 17, Application No. 1020040052810A1

SERVERAL INPORMATION:

APPLICANT: Nesbit, Mark

APPLICANT: Cameron, Bearrice

APPLICANT: Blanche, Francis

TITLE OF INVENTION: Using Them to Inhibit Angiogenesis

FILE REFERENCE: ST01027-A

CURRENT APPLICATION NUMBER: 10/207-A

FILE REFERENCE: ST01027-A

CURRENT APPLICATION NUMBER: 10/233,675

PRIOR FILING DATE: 2002-09-04

SOFTWARE: PATENTING OFFICE STORES ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGGKHNYCRNPDN 127
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                                                                                                                      1 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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            Pred. No. 2.8e-50;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                    128 RRRPWCYVQVGLKXLVQECMVHDCADGK 155
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                                                                                                                                                                                                                                                                                  61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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    98.98;
                                                 87; Conservative
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Best Local Similarity 98.9
Matches 87; Conservative
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            Best Local Similarity
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                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.6%; Score 508; DB 14; Length 431; larity 98.9%; Pred. No. 4.2e-51; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
0-247-671-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 RRRPWCYVQVGLKPLVQECMVHDCADGK 155
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OTHER INFORMATION: Xaa = Any Amino Acid
0-282-174-562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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URRENT FILING DATE: 2002-09-18
FRIOR PRPLICATION NUMBER: 60/323,784
PALOR FILING DATE: 2001-09-19
UMBER OF SEQ ID NOS: 186
COFTWARE: PERL PROGRAM
CONTWARE: PERL PROGRAM
LENGTH: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10282174
O. US20030224380A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEFAL INFORMATION:
NPELICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Wang, Xin
APPLICANT: Wang, Xin
                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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st Local Similarity
tiches 87; Conserv
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                                                                                                                                                                                                                                                                                                               Length 431;
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APPLICANT: MORTIS, David W.
APPLICANT: MORTIS, David W.
APPLICANT: BEGSIARD, ETIC K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ITLE REFERENCE: 5.29452001012.
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARES PRASTEED FOR WINDOWS VERSION 4.0
SEQ ID NO 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149, Application US/10247671
CENDICALION NO. US20030194721A1
CENDICAL INFORMATION:
APPLICANT: Mikita, Thomas
APPLICANT: Shiffman, Dov.
APPLICANT: Kaser, Matthew R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES BYPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
                                                                                                                                                                                                                                                                                                            100.0%; Score 510; DB 16;
100.0%; Pred. No. 2.4e-51;
ive 0; Mismatches 0;
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                                60/407,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i-10-087-192-594
Sequence 594, Application US/10087192
Publication No. US20020182586A1
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PRIOR FILING DATE: 2002-08-16
PRIOR PELLING DATE: 2002-08-28
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
SEQ ID NO 34
LENGTH: 431
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Best Local Similarity 100.
Matches 88; Conservative
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Matches 88; Conservative
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ORGANISM: Homo sapiens

US-10-411-049-34
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; ORGANISM: Homo sapiens
US-10-087-192-594
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ITLE OF INVENTION: ALPHA: 12003-04-09
INTERNY FILING DATE: 2001-10-10
INTOR APPLICATION NUMBER: US 60/328,523
RIOR FILING DATE: 2001-10-10
RIOR PLILING DATE: 2001-10-10
RIOR PLILING DATE: 2002-06-07
RIOR PLILING DATE: 2002-06-07
RIOR PLILING DATE: 2002-06-07
RIOR PLILING DATE: 2002-06-07
RIOR APPLICATION NUMBER: US 60/391,777
RIOR APPLICATION NUMBER: US 60/396,594
RIOR PLILING DATE: 2002-06-17
RIOR APPLICATION NUMBER: US 60/404,249
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                                                     PPLICANT: Hakes, David

PPLICANT: Chen, Xi

PPLICANT: Chen, Xi

ILLE OF LINVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND

ITLE OF INVENTION: GLYCOCONJUGATION OF G-GSF

ITLE REPERENCE: O4083-01-5054

URRENT APPLICANTON NUMBER: U3/10/410,962

URRENT FILING DATE: 2003-04-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 KRRPWCYVQVGLKPLVQECMVHDCADGK 155
                                                                                                                                                                                                                                          URREAT FILING DATE: 2003-04-09
RIOR APPLICATION NUMBER: US 60/328,523
RIOR PILING DATE: 2001-10-10
RIOR FILING DATE: 2001-10-10
RIOR FILING DATE: 2001-10-19
RIOR FILING DATE: 2001-10-19
RIOR FILING DATE: 2002-06-07
RIOR APPLICATION NUMBER: US 60/391,777
RIOR PILING DATE: 2002-06-25
RIOR PILING DATE: 2002-06-25
RIOR PILING DATE: 2002-06-25
RIOR PILING DATE: 2002-06-17
RIOR PILING DATE: 2002-06-16
RIOR PILING DATE: 2002-08-16
RIOR APPLICATION NUMBER: US 60/407,527
RIOR PILING DATE: 2002-08-16
RIOR PILING DATE: 2002-08-16
RIOR PILING DATE: 2002-08-16
UNBER OF SEQ ID NOS: 75
OPTWARE: PERCENTIN VERSION 3.2
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blication No. US20040082026A1
NERAL INFORMATION:
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128 RRRPWCYVQVGLKPLVQECMVHDCADGK 155
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; Sequence 1275, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Afar, Garasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Ginsberg, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/10410962
Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 88; Conservative
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CORGANISM: Homo sapiens
US-10-295-027-1275
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US-10-410-962-34
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                                                                                                                                                                                                            1 KTCYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
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PPLICANT: Marcay, Richard

PPLICANT: Marcay, Richard

PPLICANT: Wateon, Susan R.

PRICANTED OF INVENTION: Methods of Screening for Modulators of Cancer

ILLE REPRENCE: 01850-10125008

URRENT PILING DATE: 2002-11-13

PRIOR PILING DATE: 2001-11-13

PRIOR PILING DATE: 2001-11-15

PRIOR PILING DATE: 2001-11-15

PRIOR PPLICATION NUMBER: US 60/335,394

PRIOR PILING DATE: 2001-11-21

PRIOR PPLICATION NUMBER: US 60/334,393

PRIOR PILING DATE: 2001-11-21

PRIOR PPLICATION NUMBER: US 60/344,393

PRIOR PILING DATE: 2001-12-14

PRIOR PLING DATE: 2001-12-14

PRIOR PLING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-18

PRIOR PLING DATE: 2002-01-08

PRIOR PLING DATE: 2002-01-08

PRIOR PLING DATE: 2002-01-08

PRIOR PLING DATE: 2002-02-03

PRIOR PLING DATE: 2002-03-03

PRIOR PLING DATE: 2002-03-03

PRIOR P
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                                                                                                                                                         Gaps
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                                                               Nerry Match 100.0%; Score 510; DB 14; Length 431; st Local Similarity 100.0%; Pred. No. 2.4e-51; tches 88; Conservative 0; Mismatches 0; Indels 0.
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local Similarity 100.0%; Pred. No. 2.4e-51;
ltches 88; Conservative 0; Mismatches 0; Indels 0
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UBLICATION NO. US2003023250A1
UBPLICANT: Afar, Daniel
NPPLICANT: Afar, Daniel
NPPLICANT: Ginsberg, Wendy M.
NPPLICANT: Ginsberg, Wendy M.
NPPLICANT: Ginsberg, Wendy M.
NPPLICANT: Ginsberg, Wendy M.
NPPLICANT: Hevel, C.
NPPLICANT: Hevel, Park, C.
NPPLICANT: Mack, David H.
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ORGANISM: Homo sapiens
.0-295-027-414
10-131-985-21
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APPLICANT: Glymae, Richard.
APPLICANT: Glymae, Richard.
APPLICANT: Glymae, Richard.
APPLICANT: Marcay, Richard.
APPLICANT: Marcay, Richard.
APPLICANT: Marcay, Richard.
APPLICANT: Marcay, Richard.
APPLICANT: Marchay, Richard.
APPLICANT: Marchay, Richard.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Cancer.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer.
TITLE OF INVENTION: MUMBER: US 09/663,733
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR PILING DATE: 2001-11-13
PRIOR PRILING DATE: 2001-11-13
PRIOR PRILING DATE: 2001-11-21
PRIOR PRILING DATE: 2001-11-29
PRIOR PRILING DATE: 2001-11-29
PRIOR PRILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,214
PRIOR PRILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-02-13
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100.0%; Pred. No. 2.4e-51;
ive 0; Mismatches 0;
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Sequence 21, Application US/10131985
Publication No. US20030199440A1
GENERAL INFORMATION:
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; ORGANISM: Homo Sapiens
US-10-301-822-161
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ORGANISM: Homo sapiens
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TILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TILE OF INVENTION: OF CERVICAL CANCER
TILE REPERENCE: MRI-035
URRENT APPLICATION NUMBER: US/10/171,311
URRENT APPLICATION NUMBER: US 60/298,159
WRICH PILING DATE: 2001-06-13
WRICH APPLICATION NUMBER: US 60/298,155
WRICH APPLICATION NUMBER: US 60/298,155
WRICH APPLICATION NUMBER: US 60/335,936
WRICH PILING DATE: 2001-06-13
WRICH PILING DATE: 2001-01-14
WRICH FILING DATE: 2001-11-14
UWHER OF SEQ ID NOS: 238
UWHER PERSEQ FOR WINDOWS VERSION 4.0
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100.0%; Pred. No. 2.4e-51;
tive 0; Mismatches 0;
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UBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P00749
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(431)
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st Local Similarity 100.
tches 88; Conservative
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ORGANISM: Homo sapiens
0-171-311-184
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LENGTH: 43
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APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: MUSCHLOR GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: MOTHORS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERRAPY OF COLON CANCER
TITLE OF INVENTION: MOTHORS: 105 10/301, 922
CURRENT APPLICATION NUMBER: US 60/339, 971
PRIOR FILING DATE: 2002-01-21
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Score 510; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-51;
Matches 88; Conservative 0; Mismatches 0;
Sequence 161, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Milennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracv L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 RRRPWCYVQVGLKPLVQECMVHDCADGK 155
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APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: Huggins, Jonathan P
APPLICANT: Occleston, Nicholas L
TILE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT FILING DATE: 2002-04-25
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver: 2.1
LENGTH: 431

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APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                          Length 431;
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 510; DB 12; Best Local Similarity 100.0%; Pred. No. 2.4e-51; Matches 88; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEDDICATION NO. US20020193304A1
| Publication No. US20020193304A1
| GENERAL INFORMATION:
| APPLICANT: WADA, MANABU
| APPLICANT: WADA, MANKO
| TITLE OF INVENTION: AWTI-HIV AGENTS
| FILE REFERENCE: HAYAK-9
| CURRENT APPLICATION NUMBER: US/10/076,421
| PRIOR APPLICATION NUMBER: UP 2001-42655
| PRIOR FILING DATE: 2002-05-17
| PRIOR FILING DATE: 2001-02-20
| PRIOR FILING DATE: 2001-06-19
| WHERE OF SEQ ID NOS: 5
| SOFTWARE: PATCHIN VOR: 2.1
| SEQ ID NO 2.2
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PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 34
LENGTH: 431
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Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Monahan, John
APPLICANT: Kamackar, Shubhangi
APPLICANT: Glatt, Karen
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CRGANISM: Homo sapiens
US-10-076-421-2
                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-10-411-026-34
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US-10-076-421-2
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WERAL INFORMATION:
WPLICANT: Neose Technologies, Inc.
WPLICANT: DeFrees, Shawn
WPLICANT: DeFrees, Shawn
WPLICANT: DeFrees, Shawn
WPLICANT: Bayer, Robert
WPLICANT: Bayer, Bobert
WPLICANT: Bayer, Bobert
WPLICANT: Bayer, David
WPLICANT: Chen, Xi
FILLE OF INVENTION: WERTHODS
WERENERING: 040853-01-5053
WREENT APPLICATION NUMBER: US/10/411,026
WRIGH APPLICATION WUMBER: US 60/328,523
WRICH FILING DATE: 2001-10-10
WRICH FILING DATE: 2001-10-10
WRICH FILING DATE: 2002-06-07
WRICH FILING DATE: 2002-07-17
WRICH FILING DATE: 2002-08-16
                                                                                     PPLICANT: Haxes, David

(PPLICANT: Chen, Xi
(PPLICANT: Chen, Xi
(PPLICANT: Bowe, Caryn
(PPLICANT: Bowe, Caryn
(PTLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
(TILE OF INVENTION: ALPHA GALACTOSIDASE A
(TILE OF INVENTION: ALPHA GALACTOSIDASE A
(TILE PEPELGATION NUMBER: US, 10, 10, 10
(WRENT PPLICATION NUMBER: US, 60/328, 523
(WRENT APPLICATION NUMBER: US, 60/344, 692
(WRICH APPLICATION NUMBER: US, 60/394, 692
(WRICH APPLICATION NUMBER: US, 60/394, 777
(WRICH APPLICATION NUMBER: US, 60/394, 777
(WRICH APPLICATION NUMBER: US, 60/394, 594
(WRICH APPLICATION NUMBER: US, 60/394, 594
(WRICH APPLICATION NUMBER: US, 60/404, 249
(WRICH APPLICATION NUMBER: US, 60/404, 249
(WRICH APPLICATION NUMBER: US, 60/407, 527
(WUMBER OF SEQ ID NOS: 75
(WOMER OF SEQ I
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David
, Robert
, David
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ORGANISM: Homo sapiens
0-411-037-34
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48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
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APPLICANT: Wang, Jieyi
APPLICANT: Michaber, Vicki L.
APPLICANT: Henkin, Jack
APPLICANT: Henkin, Jack
APPLICANT: Severih, Richard A.
APPLICANT: Severih, Richard A.
APPLICANT: Severih, Thomas F.
APPLICANT: Ganli, Rohinton
APPLICANT: Johnson Jr., Robert W.
APPLICANT: Holzman, Thomas F.
TITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
FILE REPERENCE: 6310.US.Pl
CURRENT APPLICATION NUMBER: US/09/264,468B
CURRENT FILING DATE: 1999-03-05
FRIOR PRICATION NUMBER: US 09/036,361
FRIOR PRICATION NUMBER: US 09/036,361
FRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FasteSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 931
LENGTH: 931
                                                                                                                            Query March 100.0%; Score 510; DB 9; Best Local Similarity 100.0%; Pred. No. 2.38-51; Matches 88; Conservative 0; Mismatches 0;
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100.0%; Score 510; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.4e-51;
Matches 88; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(20)
OTHER INFORMATION: Leader sequence
NAME/KEY: VARIANT
LOCATION: (279)...(279)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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COTHER INFORMATION: Xaa = any amino acid
US-09-264-468B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09264468B Patent No. US20020106775A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-411-037-34

'Sequence 34, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
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US-09-264-468B-1
                               US-09-880-503-3
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PELICANT: HIGAZI, Abd Al-Roof
PELICANT: HIGAZI, Abd Al-Roof
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
ITLE PREPERENCE: 9596-331
URRENT PILING DATE: 2001-06-13
RIOR APPLICATION WUMBER: US/09/880,503
WRICK PILING DATE: 2000-06-20
UMBER OF SEQ ID NOS: 18
OFTWARE: PATENT OFTWER OTHER OFTWER OTHER OFTWER OFTWER OFTWER OFTWER OFTWER OFTWER OFTWER OFTWER OTHER OTHER
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100.0$; Score 510; DB 9;
st Local Similarity 100.0$; Pred. No. 2.3e-51;
tches 88; Conservative 0; Mismatches 0;
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tent No. US20020131964A1
NERAL INFORMATION:
                                                                                                  ORGANISM: Homo sapiens
0-264-049-2927
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ORGANISM: Homo sapiens
9-880-503-6
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ORGANISM: Homo sapiens
LENGTH: 337
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9-880-503-6
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9-880-503-3
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RESULT 13
US-10-166-698-6266

JOSTON NO. US20030109690A1

Publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

TITLE OF INVENTION: UNMBER: US/10/106,698

CURRENT FAPLICATION NUMBER: PCT/US00/26524

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR PILING DATE: 1999-09-29

PRIOR PILING DATE: 1999-10-3

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 6266

LENGTH: 337
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US-10-264-049-2927
| Sequence 2927, Application US/10264049
| Sequence 2927, Application US/10264049
| Publication No. US20040005579A1
| GENERAL INFORMATION:
| APPLICANT: Birse et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| FILE REFERENCE: PA133P1
| CURRENT APPLICATION NUMBER: US/10/264,049
| PRIOR APPLICATION NUMBER: PCT/US01/18569
| PRIOR PILING DATE: 2002-06-07
| PRIOR PILING DATE: 2000-06-07
| NUMBER OF SEQ ID NOS: 4360
| SOFFWARE: Patentin Ver. 3.1
| SEQ ID NO 2927
                                                                                                                                                                            Length 143;
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                                                                                                                                                                                                                              0; Indels
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100.0%; Score 510; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 88; Conservative 0; Mismatches 0;
                                                                                                                                                                      Query Match
100.0%; Score 510; DB 9;
Best Local Similarity 100.0%; Pred. No. 7.4e-52;
Matches 88; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
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                                                                                                                                                                                                                                                                                                                                                                                               61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
; SEQ ID NO 8
; LENGTH: 143
; TYPE: PRT
; CRGANIEM: Homo sapiens
US-09-880-503-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
) ORGANISM: Homo sapiens
US-10-106-698-6266
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atent No. US20020131964A1
BNERAL INFORMATION:
APPLICANT: OLUSE, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
FITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
FITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REPERBNCE: 9596-331
UNRENT FILING DATE: 2001-06-13
SRIOR PPLICATION NUMBER: US 60/212,847
SRIOR PPLICATION NUMBER: US 60/212,847
WUMBER OF SEQ ID NOS: 18
  PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                                                                                CORPOTER: Macintopy disk
COMPUTER: Macintosh
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/702,636
FILING DATE: 06-NOV-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-UAN-1992
ATTOMNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 1 (610) 454-3839
                                                                                                          ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 RRRPWCYVOVGLKPLVOECMVHDCADGK 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 138 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                        STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (610)
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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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Publication No. US20040086977A1
GENERAL INPORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 138;
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                                                                                                                                                                                                    CONTAINING SAID POLYPEPTIDES NUMBER OF SEQUENCES: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION

CURRENT APPLICATION DATA:

SOFTWARE: WOCK 5.1 (Patentin)

CURRENT APPLICATION NUMBER: US/10/702,536

FILING DATE: 07-Nov-2003

CLASSIFTCATION: 435

PRIOR APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-JAN-1997

FILING DATE: 31-JAN-1997

FILING DATE: 31-JAN-1997

FILING DATE: 31-JAN-1997

FILING DATE: 31-JAN-1993

APPLICATION NUMBER: FR 92/01064

APPLICATION NUMBER: PR 92/01064

FILING DATE: 31-JAN-1993

APPLICATION NUMBER: PR 92/01064

FILING DATE: 28-JAN-1993

ATTORNEY/ARRATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REPERBORE/COCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: protein
) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-702-536-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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US-10-702-636-12
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Matches
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                                                                                                                                                                          Fournier, Alain
Guitton, Jear-Dominique
Jung, Gerard
Xeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19426
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER MEACINCED;
OPERATING SYSTEM: System 7.1
SOFTWARE: WORD 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0237,624
FILING DATE: 10-Sep-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: FR 92/01064
FILING DATE: 38-JUL-1993
ATTORNEY/AGENT INFORMATION:
TELEBENOME: (610) 454-3899
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

ITYPE: amino acid
ITYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 RRRPWCYVQVGLKPLVQECMVHDCADGK 138
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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blication No. US20040086976A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                             quence 12, Application US/10237624 blication No. US20030082747A1 GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 10
0-702-536-12
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APPLICANT: flee, with the Fournier, Alain Guernier, Jean-Dominique Guitton, Jean-Dominique Guitton, Jean-Dominique Jung, Gerard Yeh, Patrisce Yeh, Patrisce TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, COMPOSITION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT MCATILLUSH
COPRATING
SOFTWARE: Word 5.1 (Patentin)
SOFTWARE: Word 5.1 (Patentin)
APPLICATION DATA: US/10/237,871
FILING DATE: 10-Sep-2002
CLASSIFICATION TO ATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UTL-1994
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-UTL-1994
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P38,619
REFERENCE/DOCKET NUMBER: 29-38,619
REFERENCE/DOCKET NUMBER: 3192006-US
TELECOMMUNICATION INFORMATION:
MEDICATION NUMBER: 28-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
111 RRRPWCYVQVGLKPLVQECMVHDCADGK 138
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 KRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                      Sequence 12, Application US/10237871
Publication No. US20030036172A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                RESULT 8
US-10-237-871-12
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHAMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
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100.0%; Pred. No. 7.1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER RELABBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,866
FILING DATE: 10-Sep-2002
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION NUMBER: US/8/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-UAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                            111 RRRPWCYVQVGLKPLVQBCMVHDCADGK 138
                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                  RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                   equence 12, Application US/10237866 blication No. US20030036171A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 138 amino acids
                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tery Match 100.
St Local Similarity 100.
(tches 88; Conservative
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Best Local Similarity 100.
Matches 88; Conservative
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COUNTRY: U
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                              Query Match
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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                             51 KTCYBGNGHFYRGKASTDIMGRPCLFWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNFDN 110
                                                                                                                                                                                                                                              1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                ö
                                                                                                                                             lery Match 100.0%; Score 510; DB 9; Length 138;
st Local Similarity 100.0%; Pred. No. 7.1e-52;
tches 88; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,667
FILING DATE: 10.5ep-2002
CLASSIFICATION EATH:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FF 92/01064
FILING DATE: 28-JUN-1993
ATTORREY/AGENT INFORMATION:
NAME: Smith Ph. D., Julie K.
REGISTRATION NUMBER: P39,619
FILING DATE: 28-JAN-1993
ATTORREY/AGENT INFORMATION:
NAME: Smith Ph. D., Julie K.
REGISTRATION NUMBER: P39,619
FERERENCE/DOCKET NUMBER: P39,619
REFERENCE/DOCKET NUMBER: P39,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                         111 RERPWCYVQVGLKPLVQECMVHDCADGK 138
                                                                                                                                                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
0-237-667-12
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cquence 12; Application US/10237667
bblication No. US2030022308A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454-3808
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Collegeville
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0-237-667-12
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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                     51 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 110
                                                                                                    1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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Length 138;
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100.0%; Score 510; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.1e-52;
Matches 88; Conservative 0; Mismatches 0;
100.0%; Score 510; DB 14;
100.0%; Pred. No. 7.1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 32-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P.38,619

REFERENCE/DOCKET NUMBER: P.38,619

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
COMPUTER: Macintosh
COMPUTER: Wacintosh
CORFATING SYSTEM: System 7.1
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                   0; Mismatches
                                                                                                                                                                                                                                          111 RRRPWCYVQVGLKPLVQECMVHDCADGK 138
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                                                                                                                                      61 RRRPWCYVQVGLKPLVQECMVHDCADGK
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(10) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/10237708
Publication No. US20030036170A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
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TELEPHONE: (610) 454-3839
TELEFATA: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-09-880-503-4
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 88; Conserva
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NERAL INFORMATION:
DEPLICANT: CINES,
DOUGLAS B

EPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION:
THEN REPERENCE: 9596-331
TURRENT APPLICATION NUMBER: US/09/880,503
TURRENT FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equence 4, Application US/09880503
ttent No. US20020131964A1
NDERAL INDOMENTION:
NDELAL INCOMMATION:
NPELICANT: CINES, Douglas B
NPELICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
TILE REPERENCE: 9596-331
URRENT APPLICATION NUMBER: US/09/880,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                          100.0%; Score 510; DB 9; Length 88; ilarity 100.0%; Pred. No. 4.3e-52; Conservative 0; Mismatches 0; Indels
TILE OF INVENTION: TISSUE CONTRACTABILITY
TILE REFERENCE: 9596-331
URRENT APPLICATION NUMBER: US/09/880,503
URRENT FILING DATE: 2001-06-13
RIOR APPLICATION NUMBER: US 60/212,847
RIOR FILING DATE: 2000-06-20
UMBER OF SEQ ID NOS: 18
OFTWARE: Patentin Ver: 2.1
LENGTH: 88
    TISSUE CONTRACTABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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OPTWARE: Patentin Ver. 2.1
O ID NO 9
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
9-880-503-9
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
9-880-503-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ery Match
st Local Similarity
tches 88; Conserv
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st Local Similarity
ttches 88; Conserv
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19-880-503-9
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19-880-503-4
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APPLICANT: Fleer, Reinhard

AppLICANT: Fleer, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                         48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                                    1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
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                                                                                                                                                                                                                                                                                                 Length 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: WORD 5.1 (Parentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31.-JAN-1997
APPLICATION NUMBER: PS/01064
FILING DATE: 31.-JAN-1994
APPLICATION NUMBER: PS/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PS/01064
FILING DATE: 28-JUN-1992
APPLICATION NUMBER: PS/01064
FILING DATE: 28-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P38,619
REFERRNCE/DOCKET NUMBER: P38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
CURRENT FILING DATE: 2001-06-13
PRICAR PAPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
LENGTH: 135
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Patent No. US20020151011A1
GENERAL INFORMATION:
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Sequence 3, Appli Sequence 34, Appli Sequence 34, Appl Sequence 24, Appli Sequence 184, Appli Sequence 114, Appli Sequence 21, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 564, Appli Sequence 562, Appli Sequence 567, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli

Sequence Seq

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FOR MODULATING MUSCLE CELL AND
              US-10-411-036-34
US-10-411-036-34
US-10-111-036-34
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US-10-233-675A-7
US-10-233-675A-27
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APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION:
RESULT 1
US-09-880-503-1
Sequence 12, Appl
Sequence 22, Appl
Sequence 2656, Ap
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1 KTCYEGNGHFYRGKASTDTM.....QVGLKPLVQECMVHDCADGK
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Homo sapiens,

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UX-S3 is one example of a plasminogen activator which differs from natural human pro-urokinase at positions 153 and 155. (Leu substituted by Asn; Pro substituted by Thr, respectively). The derivative has decreased susceptibility to thrombin compared to natural type pro-UK and higher specific activity. See also AAQ10168 and AAQ10169
                                                                                                                                                                                                                                                                                                                                                                                                                             KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                   New plasminogen activator almost identical to natural pro:urokinase - is thrombin resistant and used for prophylaxis-treatment of cerebral thrombosis or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                            1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pre-urokinase; thrombolytic; blood; plasmid; mutant; PUK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRRPWCYVQVGLKPLVQECMVHDCADGK 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR47956 standard; protein; 411 AA.
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/label= Loop_2
33. .42
/label= Loop_3
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/label= Loop_1
                                                                             18-JUN-1990; 90EP-00111471.
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/label= EGF
                                                                                                  89JP-00156302
                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.
88; Conservative
                                                                                                                                             Yasamura S, Nishi T,
                                                                                                                                                                    WPI; 1991-008678/02.
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                                                                                                                                                                                                                                                                                                                                          Sequence 411 AA;
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                                                                                                   19-JUN-1989;
                                                       02-JAN-1991.
                                 EP405285-A.
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Length 411;

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                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                              Mutant human presurokinase - by replacing specified aminoacid(s) in N-terminal for providing longer half-life in blood and higher thrombolytic ability.
                                                                                                                                                                                                                               Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or Tyr in the region ranging from residue 10 to 60 in the N-terminal of the human PUK by Thr, Pro or Ala. These mutants have a longer half-life in the blood and a higher thrombolytic ability. For examples see (AAR47956-
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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iive 0; Mismatches 0;
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                                                                                                                                                                                                  Disclosure, Page 3; 26pp; Japanese
 92JP-00030178
                                92JP-00030178
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 88; Conservative
                                                                  (GREC ) GREEN CROSS CORP.
                                                                                                WPI; 1993-277461/35.
                                                                                                                                                                                                                                                                                                                                     Sequence 411 AA;
20-JAN-1992;
                                 20-JAN-1992;
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New variants of human prourokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain, (ii) at least part of the first loop and at least part of the Second loop, or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and vary little tendency to cause spontaneous bleeding. The present sequence is that of the wild-type hPUK protein, including the EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent.
                                                                                                                                                                                                        Human; prourokinase; hPUK; variant; half-life; increase; EGF;
epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
                                    108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                   AAW13634 standard; protein; 411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1990; 90EP-00109472.
                                                                                                                                                     04-JUN-1997 (first entry)
                                                                                                                                                                               Human native prourokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GREC ) GREEN CROSS CORP.
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22-FEB-1990;
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10. .42 /label= EGF_domain /label= EGF_domain /label= "in Claimed variants, at least part of domain is deleted (see comments)"

20. .31 /label= second_loop 10. .19 /label= first_loop

33. .42 /label= third_loop

location/Qualifiers

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UK-T4 is one example of a plasminogen activator which differs from natural human pro-urckinase at positions 153 and 155 (Leu substituted by Ser, Pro substituted by Thr, respectively). The derivative has decreased susceptibility to thrombin compared to natural type pro-UK and higher specific activity. See also AAQ10168 and AAQ10170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New plasminogen activator almost identical to natural pro:urokinase - is thrombin resistant and used for prophylaxis-treatment of cerebral thrombosis or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                              pro-urokinase; UK-T4; plasminogen activator; myocardial infarction;
cerebral thrombosis.
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                                                                                                                                                                   Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).
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108 RRRPWCYVQVGLKPLVQBCMVHDCADGK 135
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                                                                                 AAR10057 standard; protein; 411
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Kawabe H;

Morita M,

Amatsuji Y, Kasai S, Hirose M,

89JP-00126433.

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KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHYCRNPDN 107 1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN

61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88

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The polypeptide is a deriv. of mature urokinase, designated UK-S3 which has 2 amino acid substns. which result in an N-linked glycosylation site giving the new protein improved stability and activity. See also AAROS113-17. (Updated on 25-MAR.2003 to correct PR field.) (Updated on 25-WAR. 2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide(s) with added carbohydrate chains - formed by modification of aminoacid sequence, used to improve physio:chemical properties and/or
                                               48 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDN
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/note= "old seq (Leu)"
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                                                                                       61 RRRPWCYVQVGLKPLVQECMVHDCADGK
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                                                                                                                                                                                              AAR05117 standard; protein; 411 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                   UK-S3 as encoded by pUKS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
es 88; Conservative
                                                                                                                                                                                                                                                                                                                                 Urokinase; glycosylation.
 88; Conservative
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/note= "c
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N-PSDB; AAQ04486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki K, Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                       25-MAR-2003
04-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-1990,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activities.
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Matches
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                                                                                                                                                               RESULT 46
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                                                                                                                   48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified pro-urokinase has a longer half-life in blood, and disolves thrombin without causing the spontaneous bleeding associated with urokinase. The modification puts an epidermal growth factor domain into the protein, containing the sequence Asn-X-Ser or Asn-X-Thr where X is any residue. Plasmid pHR24 is disclosed as containing the modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.
                                                                                       1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                            Gaps
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    .42
    label= Epidermal growth factor (EGF) domain

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                              Length 411;
                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 510; DB 2;
Pred. No. 9.2e-41;
                              DB 2;
                              Score 510; DB 2;
Pred. No. 9.2e-41
            100.0%; Scc...
100.0%; Pred. No...
0; Mismatches
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                                                                                                                                                                              108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                   88
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/label= Second loop
24...26
/label= Modified site
33...42
/label= Third loop
                                                                                                                                                   RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0. .19
label= First loop
                                                                                                                                                                                                                                                       AAR07903 standard; protein; 411 AA
                                                                                                                                                                                                                                                                                                                                                                            Thrombin; fibrin; bleeding; pHR24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amatsuji Y, Kasai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                               Human pro-urokinase variant.
                                                                                                                                                                                                                                                                                                                 21-FEB-1991 (first entry)
                                                            88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GREC ) GREEN CROSS CORP.
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                                              Similarity
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   Sequence 411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1989;
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                                                                                                                                                                                                                                                                                    AAR07903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanabe T.
                              ery Match
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Key Domain

Region

Region

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48 KTCYEGNGHFYRGKASTDINGRPCLPWNSATVLQQTYHAHRSDALQLGLGKGHNYCRNPDN 107
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                                                                                                                                                 1 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.
                                                                                                                       Gaps
      containing the sequence Asn-X-Ser or Asn-X-Thr where >
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                                                                                           411;
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/label= Epidermal growth factor (EGF) domain
                                                                                                                      Indels
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0
                                                                                      100.0%; Score 510, DB 2;
100.0%; Pred. No. 9.2e-41;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22. .24
/label= Modified site
33. .42
/label= Third loop
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                                                                                                                                                                                                                                                                                                                                                                                             Human pro-urokinase variant.
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                                                                                                                    88; Conservative
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/label= 1
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/label= 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amatsuji Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1990-350147/47.
                                                                                                       Local Similarity
                                                               Seguence 411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-350147/
N-PSDB; AAQ06133
      the protein,
any residue.
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Arimura H;
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                        By forming a precursor-lipid composite, the half-life of this thrombolytic agent in the blood may be increaced, exhibiting improved activity without abnormal acceleration of fibrinolytic activity. Compound is useful as a thrombolytic agent in treatment of cerebral thrombosis, myocardial infarction etc
                                                                                                                                                                                                                       KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKGKHNYCRNPDN 107
                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified pro-urokinase has a longer half-life in blood, and disolves thrombin without causing the spontaneous bleeding associated with urokinase. The modification puts an epidermal growth factor domain into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.
                                                                                                                                                                           Gaps
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                                                                                                                                                                          .
0
                                                                                                                                             Length 411;
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|label= Epidermal growth factor (EGF) domain
                                                                                                                                                                        Indels
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                                                                                                                                           Score 510; DB 2;
Pred. No. 9.2e-41;
; Mismatches 0;
                                                                                                                                                                                                                                                                            RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20. .31
/label= Second loop
27. .29
/label= Modified site
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/label= Third loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombin; fibrin; bleeding; pHR27
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                                                                                                                                          100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                          AAR07904 standard; protein; 411
Claim 3; Fig 1; 11pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                       88; Conservative
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N-PSDB; AAQ06135.
                                                                                                                                        ery Match
st Local Similarity
                                                                                                                Sequence 411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1990;
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Arimura H;
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                                                                                                                                                                                                                                                                                                                                                                                     AAR07904;
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Domain
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90JP-00207659

07-AUG-1990;

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                                                                                                                 Vector contg pro-urokinase encoding gene - includes mouse=1gG H chain E-
mu enhancer, enhancer contg. SV40, early phase promoter and SV40
                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                       The sequence is that of mature prourokinase having the sustitution mutations F157D and K1350. The sequence per se is not given in the specification, so the known sequence of prourokinase was used to demonstrate the mutant protein. The gene encoding prourokinase has been over-expressed by recombinant DNA technology and provides a method for the rapid, low cost produ. Of prourokinase, which is a low mol. Wt. plasminogen activator used for dissolving blood clots. See also AAR23794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...... purential cleavage site which generates the two-
chain form from the zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese Patent Application No.37119/84).
                                                                                                                                                                                                                                                                                                                                                                            1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombolytic agent; plasminogen activator activity; fibrin affinity;
                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                          Length 410;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                        100.0%; Score 510; DB 2;
100.0%; Pred. No. 9.2e-41;
ive 0; Mismatches 0;
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AAP50871 standard; protein; 411 AA.
                                                                                                                                                                   Claim 3; Page 1; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84EP-00306117.
                                      07-AUG-1990; 9 90JP-00207659
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                                                                                                                                                                                                                                                                                                                                 Similarity 100.
88; Conservative
                                                                                                                                          poly:adenylation site.
                                                                                        WPI; 1992-154820/19.
                                                                                                                                                                                                                                                                                     Sequence 410 AA;
                                                              (TOYJ ) TOSOH CORP.
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Disulfide-bond
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Disulfide-bond
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Disulfide-bond
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Disulfide-bond
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                                                                                                                                                                                                   Zymogen AAP50871 is the inactive precursor form of human urokinase. Urokinase zymogen is cleaved into the two-chain form composed of characteristic urokinase H (molecular w.c. of 30,000) and L (molecular w.c. of 30,000) chains when treated with catalytic amounts of plasmin. The patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a single chain molecular structure, and selective affinity for fibrin. It at thrombolytic agent which manifests its plasminogen activator activator activity on cleavage by proteolytic enzymes (e.g. plasmin) and has higher affinity for fibrin than known forms of urokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urokinase precursor-lipid composite - used as thrombolytic agent, having prolonged half-life in the blood, enhanced bio:availability and improved activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urokinase precursor, fibrinolysis, thrombolytic, cerebral thrombosis, myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 510; DB 1; Length 411; 100.0%; Pred. No. 9.2e-41; ive 0; Mismatches 0; Indels (
                                                                                                                                           New urokinase zymogen - useful as thrombolytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                    Suyama T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                         Disclosure; Page 12; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR06244 standard; protein; 411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tamanouchi K;
                                                                                    Mori K,
              83JP-00170354.
83JP-00195051.
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89JP-00121405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urokinase precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 88; Conservative
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                                                       (GREC ) GREEN CROSS CORP.
                                                                                    Arimura H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsuda H, Ueda Y,
                                                                                                               WPI; 1985-106530/18.
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                                                                                                                                                                                                                                                                                                                                                     Sequence 411 AA;
              13-SEP-1983;
17-OCT-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-1990;
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17-MAY-1989;
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                                                                                    Kasai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 42
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RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian unscide, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microanglopathies, surgically induced thrombotic invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, disorders, angiogenic disorders, tumour cell metastasis, glaucoma, charaction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sequence is human urokinase-type plasminogen activator (UPA) single chain urokinase (scupA) deletion mutant designated as scupA deltal36-143
                                                                                                                                                                                                                       Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; arroke, hypotensian, stroke, hypotensian, arroke, therobotic disordar; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome; scupA deltal36-143; single chain urokinase; mutent; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                             Human urokinase-type plasminogen activator scuPA delta136-143 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
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                                     AAE16547 standard; protein; 403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 22; Fig 1F; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-2001; 2001WO-US018976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-2000; 2000US-0212874P.
                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity 100.
88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200197752-A2.
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
Synthetic,
                                                                                                                                09-APR-2002
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                                                                                 AAE16547;
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st Local S:
tches 88
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KTCYEGNGHFYRGKASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNDDN 107

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RRRPWCYVQVGLKPLVQECMVHDCADGK 135 RRRPWCYVQVGLKPLVQECMVHDCADGK 88

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47 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vector contg. pro-urokinase encoding gene - includes mouse=IgG H chain E-mu enhancer, enhancer contg. SV40, early phase promoter and SV40 poly:adenylation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of mature prourokinase having the sustitution mutation F157D. The sequence per se is not given in the specification, the known sequence of prourokinase was used to demonstrate the mutant protein. The gene encoding prourokinase has been over-expressed by recombinant DNA technology and provides a method for the rapid, low cos produ. of prourokinase, which is a low mol. wt. plasminogen activator used for dissolving blood clots. See also AAR23795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 9.2e-41;
Matches 88; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substitution; animal; plasminogen activator; blood; clot.
                                                                                                                                                                                  Substitution; animal; plasminogen activator; blood; clot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 RRRPWCYVQVGLKPLVQECMVHDCADGK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prourokinase double mutant F157D, K135Q.
AAR23794 standard; protein; 410 AA
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                                                                                                                                                                                                                                                                                                                                                                    90JP-00207659
                                                                                                                                                                                                                                                                                                                                                                                                             90JP-00207659.
                                                                                            (first entry)
                                                                                                                                      Prourokinase mutant F157D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-154820/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 410 AA;
                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1990;
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                                                                                                                                                                                                                                Homo sapiens.
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                                                                                          03-NOV-1992
                                                                                                                                                                                                                                                                                                                        25-MAR-1992.
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                                              AAR23794;
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(revised)
(first entry)

location/Qualifiers

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Example 1; Page 10 and Fig 1; 34pp; German,
             Bifunctional urokinase variant M15.
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18t Local Similarity 100.
Atches 88; Conservative
                                                                                                                                                                         (CHEF ) GRUENTHAL GMBH
                                                                                                                                                                                                                                                                       correct PN field.)
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                                                                                                                                                                                                                                                                                 Sequence 397 AA;
                                                                 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
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Disulfide-bond
                                                                                                                                                      15-JUL-1993;
                                                                                                                                             01-DEC-1994.
                                                                                                                                                               15-JUL-1993;
                                                                                                                                    DE4323754-C1
25-MAR-2003
17-AUG-1995
                                     Synthetic
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93DE-04323754. 93DE-04323754

366. .378 /label= X1 379. .397 /label= Y1

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New variants of human prourokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain, (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while rectaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence represents a specific variant of hPUK which lacks EGF domain or the properties of the properties are specific variant of hPUK which lacks EGF domain the properties as those properties are part of the properties as those properties are properties as those the properties as those properties as those the properties as the properties as those the properties as the pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent.
                                                                                                                                                                                                                                    Human, prourokinase, hPUK, variant, half-life, increase, EGF,
epidermal growth factor domain, deletion, thrombolysis, fibrinolysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "residues 43-411 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirose M, Morita M,
                                                                                                                                                                              Human prourokinase variant lacking EGF domain loop 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .. .32
'note= "residues 1-32 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "corresponds to TAC codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 RRRPWCYVQVGLKPLVQECMVHDCADGK 125
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                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
AAW13637 standard; protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amatsuji Y, Kasai S,
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                                                                                                                  (first entry)
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Best Local Similarity 100.0
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N-PSDB; AAT61674.
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                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Synthetic.
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                                                            AAW13637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR6644-R66266 are specific examples of such derive. which have both improved ibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or birombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                          [. .365
|- .365
|Jabel= M4
|Inote= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                               fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urckinase; variant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R; Saunders DJ;
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9 97

> RRRPWCYVQVGLKPLVQECMVHDCADGK 88

N 61

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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
                                                                             "unglycosylated prourokinase (Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                                                                   Heinzel-Wieland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 10 and Fig 1; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                                                                                                                                                                                                                                                                                                                                                 Schneider J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRRPWCYVQVGLKPLVQECMVHDCADGK
                                              location/Qualifiers
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                                                                                                                                                                                                                                                                                   93DE-04323754.
                                                                                                                                                                                                                                                                                                       93DE-04323754.
                                                       1. .365
/label= M4
                                                                                                                                                                          106. .334
166. .377
1abel= X1
                                                                                                                                                                                                        378. .396
/label= Yl
    urokinase; variant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                           (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                                                                 Wnendt S,
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-015191/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 396 AA;
                                                                                      Disulfide-bond
Disulfide-bond
Disulfide-bond
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Disulfide-bond
Disulfide-bond
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Disulfide-bond
                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                   15-JUL-1993;
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                                                                                                                                                                                                                                       DE4323754-C1
                                                                                                                                                                                                                                                                                                                                               Steffens GJ,
Saunders DJ;
                                                                                                                                                                                                                                                            01-DEC-1994.
                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR66248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                              Key
Region
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Matches
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                                                                                                                                                                                                                                                                                                                                      improved
cardiac and
                                                                                                                                                                                                                                                                                                                                                                                               Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 examples of see features table). Sequences AAR66244-R66266 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, eag for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTCYBGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gabe
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrinolysis, thrombin inhibition; thrombolytic, anti-thrombotic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                 New bifunctional urokinase derivs and related plasmids - with fibrinolytic and thrombin inhibiting activities, for treating cerebral infarct, pulmonary embolism, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 395;
                                                                                                                                                                                                                                                                               Wnendt S, Schneider J, Heinzel-Wieland R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 510; DB 2;
100.0%; Pred. No. 8.9e-41;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 11 and Fig 1; 34pp; German.
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bifunctional urokinase variant M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR66246 standard; protein; 396 AA
                                                                                                                                                                                                                93DE-04323754
                                                                                                                                                                                                                                     93DE-04323754
                                                                                                         306. .334
366. .371
/label= X1
372. .395
/label= Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                               5. .67
                                                                                                                                                                                                                                                          (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                               WPI; 1995-015191/03.
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st Local Similarity
tches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 395 AA;
                             Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                15-JUL-1993;
                                                                                                                                                                       DE4323754-C1
                                                                                                                                                                                                                                    15-JUL-1993;
                                                                                                                                                                                                                                                                              Steffens GJ,
Saunders DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
17-AUG-1995
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Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derive. which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KTCYEGNGHFYRGRASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKGNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 510; DB 2; Length 396; 100.0%; Pred. No. 8.9e-41;
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AAR47902;

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Sequences (AAQS5711-72) are pro-urokinase derivatives. The products have an inserted sugar moeity having an amino acid substituted, depleted or inserted variant around the thrombin cleavage site. They also have a long half-life allowing them to be used in the treatment of thrombosis
                                                                           Pro-urokinase; half-life; thrombolytic; thrombosis; fibrinolytic; factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTCYEGNGHFYRGKASTDTMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                            KTCYEGNGHFYRGKASTDTMGRPCL PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                Novel human pro-urokinase derivs. having long half-life - with high thrombolytic activity, useful for treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urckinase; variant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 510; DB 2; Length 3 100.0%; Pred. No. 8.9e-41; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                                                                                 Disclosure, Page 14; 29pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifunctional urokinase variant M32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36265
AAR66265 standard; protein; 395 AA.
                                                                                                                                                                  91JP-00269615
                                                                                                                                                                                      17-0CT-1991; 3 9LJP-00269615
                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 100.
88; Conservative
                                                      Pro-urokinase derivative.
                                                                                                                                                                                                                             WPI; 1994-030907/04.
                                                                                                                                                                                                                                          N-PSDB; AAQ55771.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                         17-0CT-1991;
                                                                                                Homo sapiens
                                                                                                                      JP05336965-A
                               13-JUL-1994
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17-AUG-1995
                                                                                                                                            21-DEC-1993.
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                                                                                                                                                                                                                                                                                                                                                                                               lery Match
set Local S
ttches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR66265;
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後来のからなるとはずばなばればなばればなるまななないない。
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0; Gaps

Length 395;

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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
                                                                                                                                                                                                                                                                                                                                                                                                            Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such deriver, which have both improved fibrinollytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, and cerebral infarction and pulmonary about thrombosis, cardiac to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KTCYBGNGHFYRGKASTDTMGRPCL.PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 510, DB 2; Length 395; 100.0%; Pred. No. 8.9e-41; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R, Saunders DJ;
                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 11 and Fig 1; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bifunctional urokinase variant M29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR66262 standard; protein; 395 AA
                                                                                                                                                                                                                93DE-04323754.
                                                                                                                                                                                        93DE-04323754,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               urokinase; variant; mutein.
                                                                   366. .371
/label= X1
372. .395
/label= Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
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Best Local Similarity 100.
Matches 88; Conservative
                                                                                                                                                                                                                                          (CHEF ) GRUENENTHAL GMBH.
                                                                                                                                                                                                                                                                                                           WPI; 1995-015191/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 395 AA;
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                   DE4323754-C1
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17-AUG-1995
                                                                                                                                                              01-DEC-1994,
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                                                                     Region
                                                                                               Region
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New peptides (I) with fibrinolytic and anticoagulant activity comprise a plasminogen-activating amino acid sequence (A) fused at the N- and/or C- terminus to a thrombin and/or factor Xa inhibiting amino acid sequence (B). Excluded from the claims are (I) where (A) is Ser47 to Leu411 of unglycosylated urokinase linked at the C-terminus to sequences (i) to (iii): TI-RPP-12-GGGGGGDEEDERIAL PROPEXEPEREPERENCE (Iii) Where Tl= P or V; T2 = L or a bond; T3 = Q or T1-RPSERFEREIDEERK (Iii) Where Tl= P or V; T2 = L or a bond; T3 = Q or OH (A) is pref. (pro)urokinase; tissue plasminogen activator (tPA), bat-CC T1-RPSERFEREIDEERK (Iii) where T1= P or V; T2 = L or a bond; T3 = Q or OH (A) is pref. (pro)urokinase; and/or APSAC (anisolated plasminogen activator complex), septention; insertion and/or addn.); streptokinase activator complex), esp. prourokinase (411 amino acids) or streptokinase activator complex), esp. prourokinase (411 amino acids) or tis Ser9Arg to S27Pro or APSAC (anisolated plasminogen or tis derived from the human thrombin activities; or is derived from the human thrombin receptor, antistatin and/or the tick anticoagulant peptide. Most pref. Care the 65 amino acid hirudin sequence or one of the six sequences given in AAR99879 to AAR99884. Plasmids pwLT27 (MS1), pwS1 (MS1), pSS8 (M36) and pHWS6 (M31) contain the sequences encoding AAR99885 to AAR99888; respectively. The products were tested in human citrated plasma (5 microg in 200 microl 1:10 diluted plasma). The thrombin time was then 1.2, 3, 2.2, and 1.2 times greater, repectively, than in the absence of the
                                                                                                        Thrombin, factor Xa, anticoagulant, thrombolytic; plasminogen, urokinase, activator; streptokinase, staphylokinase, APSAC, antisolated plasminogen streptokinase activator complex; hirudin; hirulin, antistatin; pWL127; pWS1; pSE8; pHWS6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins with fibrinolytic and anticoagulant activity - useful
                                                                      M36: fibrinolytic and anticoagulant activity contg. protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 18; 59pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                               Wnendt S, Heinzel-Wieland R,
                                                                                                                                                                                                                                                                                                         95EP-00117316.
                                   27-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             (CHEF ) GRUENENTHAL GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombolytic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-240720/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 393 AA;
                                                                                                                                                                                                                                                                                                         03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                           17-NOV-1994;
                                                                                                                                                                                                                                                                     22-MAY-1996.
                                                                                                                                                                                                                                   EP712934-A2
                                                                                                                                                                                                 Synthetic.
   AAR99885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric protein contg. plasminogen activating sequence and thrombin-
inhibiting sequence - useful as thrombus-specific thrombolytic agent with
rapid action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1 describes the prodn. of plasmids pSE1 and pSE9 contg. a DNA encoding a chimeric protein with fibrinolytic and thrombin-inhibiting properties. pSE1 encodes the protein given in AAR99597 and pSE9 encodes the protein given in AAR99596
                                                                                              3 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKRNYCRNPDN
                                                                       1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Thrombin, inhibition, thrombus, thrombolysis, chimeric protein, plasminogen activating sequence, fibrinolysis, infarction, angina pectoris, deep vein thrombosis.
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   Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wnendt S, Steffens GJ, Janocha E, Heinzel-Wieland R;
100.0%; Score 510; DB 2;
100.0%; Pred. No. 8.8e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                            88
                                                                                                                                                                  RRRPWCYVQVGLKPLVQBCMVHDCADGK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                            61 RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                             Chimeric protein M37 encoded by pSE9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 19-20; 37pp; German.
                                                                                                                                                                                                                                                                   AAR99596 standard; protein; 393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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tery Match 100.
st Local Similarity 100.
tches 88; Conservative
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st Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                       AAR99596;
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Steffens GJ;

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                                                                       1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                        3 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                    ..
0
100.0%; Score 510; DB 2; Length 393; 100.0%; Pred. No. 8.8e-41;
                                  0; Indels
                                    0; Mismatches
                                                                                                                                               61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                  63 RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                      AAR47902 standard; protein; 395 AA.
                   100.08;
                                    88; Conservative
                                                                                                                                                                                                                                      RESULT 32
AAR47902
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RRRPWCYVQVGLKPLVQECMVHDCADGK

AAR99885 standard; peptide; 393 AA

LT 31

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Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R6656 are specific examples of such derivs. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activities or thrombin inhibitors. The proteins are useful as thrombolytic agents, egg for treatment of arterial occlusions, deep vein thrombolytic agents, and carebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                        1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                                                                                                                      KTCYEGNGHFYRGKASTDTWGRPCLFWNSATVIQQTYHAHRSDALQLGLGKGNYCRNPDN 61
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
4. .85
                                                                                                                                                                                                                                                                                                                                                                                                   fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
                                                                                                                                                  ,0
                                                                                                                             Length 393;
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                                                                                                                                                Indels
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0
                                                                                                                          100.0%; Score 510; DB 2;
100.0%; Pred. No. 8.8e-41;
iive 0; Mismatches 0;
                                                                                                                                                                                                                   61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                                                                                                                     RRRFWCYVQVGLKPLVQECNVHDCADGK 89
                                                                                                                                                                                                                                                                                                                                                                              Bifunctional urokinase variant M17.
                                                                                                                                                                                                                                                                         ILT 28
;6250
AAK66250 standard; protein; 393 AA.
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279. .295
306. .334
366. .372
/label= Xl
373. .393
/label= Yl
                                                                                                                                                                                                                                                                                                                                                                                                                urokinase; variant; mutein.
                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                   set Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHEF ) GRUENTHAL GMBH
                                                                                                       Sequence 393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
Disulfide-bond
Disulfide-bond
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17-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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Region
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WPI; 1995-015191/03

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inhibiting sequence - useful as thrombus-specific thrombolytic agent with
rapid action.
New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
                                                                                     Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derive. Which have both improved fibrinollytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1 describes the prodn. of plasmids pSE1 and pSE9 contg. a DNA encoding a chimeric protein with fibrinolytic and thrombin-inhibiting properties. pSE1 encodes the protein given in AAR99597 and pSE9 encodes the protein given in AAR99596
                                                                                                                                                                                                                                                                                                                            1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombin; inhibition; thrombus; thrombolysis; chimeric protein; plasminogen activating sequence; fibrinolysis; infarction; angina pectoris; deep vein thrombosis.
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                                                                                                                                                                                                                                                           Length 393;
                                                                                                                                                                                                                                                                                           Indels
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                                                           Example 1; Page 10 and Fig 1; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                       61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric protein M38 encoded by pSE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR99597 standard; protein; 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95EP-00118050.
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                   Sequence 393 AA;
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                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                   KTCYEGNGHFYRGRASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
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                                                                            Length 393;
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                                                                           100.0%; Score 510; DB 2;
100.0%; Pred. No. 8.8e-41
ive 0; Mismatches 0
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                                                                                                                                                                                        61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
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                                                                                                                                                                                                        RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                Bifunctional urokinase variant M11.
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366. .374
/label= X1
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/label≃ Y1
                                                            Ouery Match
Best Local Similarity 100.
اونان B8; Conservative
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Saunders DJ;
                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-015191/03.
                                                Sequence 393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
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22-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                              AAR66244;
                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
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                                                                                                                                                                                                                                                         RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derive. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
                                            1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                2 KTCYBGNGHFYRGKASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "unglycosylated prourokinase (Ser47-Leu411)"
                                                                                                                                                                                                                                                                                                                        fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
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Saunders DJ;
                   0; Indels
     100.0%; Pred. No. 8.8e-41; cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 10 and Fig 1; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibrinolytic and thrombin inhibiting activerebral infarct, pulmonary embolism, etc.
                                                                                                    RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                    Location/Qualifiers
1. .365
/label= M4
                                                                                                                                                                                               AAR66252 standard; protein; 393 AA
                                                                                                                                                                                                                                                                                              Bifunctional urokinase variant M19.
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279. .295
306. .334
366. .372
/label= X1
373. .393
/label= Y1
                                                                                                                                                                                                                                                                                                                                        urokinase; variant; mutein
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     Similarity 100.
88; Conservative
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Disulfide-bond
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17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                           AAR66252;
    st Local &
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Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac acerebral infarct, pulmonary embolism, etc.
                                                                                                                                                                                                                                          'note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                       fibrinolysis, thrombin inhibition, thrombolytic, anti-thrombotic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heinzel-Wieland R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lot Match 100.0%; Score 510; DB 2; st Local Similarity 100.0%; Pred. No. 8.8e-41; tches 88; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                     Location/Qualifiers
                                                                                                              Bifunctional urokinase variant M20.
                       AAR66253 standard; protein; 393 AA
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/label= M4
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279. .295
306. .334
366. .372
/label= X1
373. .393
/label= Y1
                                                                                                                                                    urokinase; variant; mutein
                                                                        25-MAR-2003 (revised)
17-AUG-1995 (first entry)
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Saunders DJ;
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                                                 AAR66253;
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Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244.R66266 are specific examples of such derivs. which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, eag for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac scerebral infarct, pulmonary embolism, etc.
                                                                                                                                                                                                                                                          1. .365
|Tabel= M4
|note= "unglycosylated prourokinase(Ser47-Leu411)"
                                                                                                                                                                                   fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
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89
             RRRPWCYVQVGLKPLVQECMVHDCADGK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schneider J,
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                             Bifunctional urokinase variant M16.
                                                                               AAR66249 standard; protein; 393 AA
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/label= X1
373. .393
/label= Y1
                                                                                                                                                                                                 urokinase; variant; mutein
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                                                                                                                             (revised)
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Saunders DJ;
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17-AUG-1995
                                                                                                                                                                                                                        Synthetic.
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                                                                                                     AAR66249;
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100.0%; Score 510; DB 2; Length 393;

Sequence 393 AA;

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Gaps

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Indels

Length 393;

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KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61

1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN

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Query Match

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Location/Qualifiers
1. 365
1. abel 1. M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
4. 85
                                                               fibrinolysis, thrombin inhibition, thrombolytic; anti-thrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R; Saunders DJ;
                                      urokinase variant M18.
                                                                                                                                                                                                                                                                                                                                                                                                                          93DE-04323754
                                                                             urokinase; variant; mutein.
                                                                                                                                                                                                                                                                                                                                373. .393
/label= Y1
(revised)
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Les 88; Conservative
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                                       Bifunctional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KTCYBGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
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                                                                                          /note= "unglycosylated prourokinase(Ser47-Leu411)"
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                                                     Location/Qualifiers
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  urokinase; variant; mutein.
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/label= M4
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st Local Similarity 100.
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                                                                                                                   Disulfide bond
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                             Synthetic
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
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             'note= "unglycosylated prourokinase(Ser47-Leu411)"
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Pred. No. 8.8e-41;
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| abel = X1
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Saunders DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
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Pred. No. 8.8e-41;
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1. .365
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/label= X1
372. .392
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nes 88; Conservative
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
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/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
4. .85
25. .67
102. .233
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100.0%; Pred. No. 8.9e-41;
tive 0; Mismatches 0;
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/label= X1
372. .392
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                                                                                                                                                                                                                           Schneider J, Heinzel-Wieland R;
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100.0%; Pred. No. 8.8e-41;
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                                                                                          New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
                                                                                                                                                                          Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such deriva. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                               2 KICYEGNGHEYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 61
                                                                                                                                                                                                                                                                                                                                                                                       1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKGHNYCRNPDN 60
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    .365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"

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                         Wnendt S, Schneider J, Heinzel-Wieland R;
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100.0%; Pred. No. 8.8e-41;
ive 0; Mismatches 0;
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366. .371
/label= X1
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Best Local Similarity 100.
Matches 88; Conservative
(CHEF ) GRUENENTHAL GMBH.
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                          Steffens GJ,
Saunders DJ;
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc. 1 KTCYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60 2 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDN 61 Gaps l. .365 |label= M4 /note= "unglycosylated prourokinase(Ser47-Leu411)" fibrinolysis, thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein. 0 0; Indels Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland Saunders DJ; 100.0%; Score 510; DB 2; 100.0%; Pred. No. 8.8e-41; ive 0; Mismatches 0; 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88 RRR PWCYVQVGLKPLVQECMVHDCADGK Location/Qualifiers Bifunctional urokinase variant M22. Ş AAR66255 standard; protein; 392 15-JUL-1993; · 93DE-04323754 93DE-04323754 102. .233 143. .159 151. .222 247. .316 279. .295 306. .334 312. .392 /label= x1 (revised) (first entry) ery Match 100. st Local Similarity 100. tches 88; Conservative .85

ö Bifunctional urckinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such deriva: which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombolytic agents, and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.) 9 61 2 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGLGKHNYCRNPDN 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN Gaps /note= "unglycosylated prourokinase(Ser47-Leu411)" 4..85 25..67 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein. 0 100.0%; Score 510; DB 2; Length 392; 100.0%; Pred. No. 8.8e-41; ive 0; Mismatches 0; Indels (Heinzel-Wieland R; 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88 Schneider J, 62 RRRPWCYVQVGLKPLVQECMVHDCADGK Location/Qualifiers AAR66259 standard; protein; 392 AA Bifunctional urokinase variant M26 93DE-04323754 93DE-04323754 366. .371 /label= X1 372. .392 /label= Y1 (revised)
(first entry) 1. .365
/label= M4 Query Match
Best Local Similarity 100.
Matches 88; Conservative Wnendt S, (CHÉF) GRUENENTHAL WPI; 1995-015191/03 Sequence 392 AA; Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond 15-JUL-1993; 15-JUL-1993; Steffens GJ, Saunders DJ; DE4323754-C1 25-MAR-2003 17-AUG-1995 01-DEC-1994 Synthetic. AAR66259; Key Region Region Region RESULT 16 AAR66259 ¥888888888¥& ò

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2 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 61
                                                            1 KTCYBGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
ch
1 Similarity 100.0%; Pred. No. 8.8e-41;
88; Conservative 0; Mismatches 0:
                                                                                                                                62 RRRPWCYVQVGLKPLVQECMVHDCADGK 89
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17-AUG-1995
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           2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 61
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
4. .85
                                                                                                                                                                                                                                                    fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
Saunders DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 11 and Fig 1; 34pp; German.
                                       REREWCYVQVGLKPLVQECMVHDCADGK 88
                                                       Bifunctional urokinase variant M27.
                                                                                                                                   AAR66260 standard; protein; 392 AA.
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151. .222
279. .295
306. .334
366. .371
372. .392
/label= X1
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17-AUG-1995 (first entry)
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Region

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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
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                                                                                                                                                                                                                                                                                                     fibrinolysis, thrombin inhibition; thrombolytic; anti-thrombotic;
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AAR66264 standard; protein; 392 AA.
                                                                                                                                                                    Bifunctional urokinase variant M31.
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151. .222
279. .316
279. .334
306. .331
/label= x1
/label= x1
                                                                                                                                                                                                                                           urokinase; variant; mutein.
                                                                                              (revised)
(first entry)
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and
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                                                            fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerebral infarct, pulmonary embolism,
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306. .371 /label= X1

372. .390 /label= Y1

93DE-04323754. 93DE-04323754

/note= "unglycosylated prourokinase(Ser47-Leu411)"

Location/Qualifiers

1. .365 /label= M4

.80

urokinase variant M12.

(revised)
(first entry)

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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
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                                                                                                      Bifunctional urokinase variant M14.
                      AAR66247 standard; protein; 390 AA
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306. .334
366. .371
/label= X1
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/label= Y1
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Matches 88; Conservative
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Saunders DJ;
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Length 390; 0; Indels

100.0%; Score 510; DB 2; 100.0%; Pred. No. 8.8e-41; iive 0; Mismatches 0;

88; Conservative

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Similarity

etc.

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2 KICYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGKHNYCRNPDN

88 89

RRRPWCYVQVGLKPLVQECMVHDCADGK RRRPWCYVQVGLKPLVQECMVHDCADGK

61 62

note= "unglycosylated prourokinase(Ser47-Leu411)"

Location/Qualifiers

Synthetic.

.. .365 |abel= M4

306. .334 365. .366 /label= X1 /note= "peptide bond" 366. .386 /label= Y1

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New bifunctional urokinase derive and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                        Steffens GJ, Wnendt S, Saunders DJ;
                                                                                                                                                                                                                                                                                                                                                                                       (CHEF ) GRUENENTHAL GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-015191/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 386 AA;
                                                                           Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
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Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                   15-JUL-1993;
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Region
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Schneider J, Heinzel-Wieland

93DE-04323754.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of human prounokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence represents a specific variant of hPUK which lacks loops 1 and 2 of the EGF domain; the sequence does not appear in the specification and has been created using the wild-type hPUK sequence and the junction sequence after deletion, both of which are given (in Fig 1 and on page 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KTCYBGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent.
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                                           Human, prourokinase; hPUK; variant; half-life; increase; EGF;
epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawabe H;
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0
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               Human prourokinase variant lacking EGF domain loops 1 and 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                          /note= "residues 33-411 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirose M, Morita M,
                                                                                                                                                                         "residues 1-10 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 510; DB 2;
100.0%; Pred. No. 8.7e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                         /note= "corresponds to TAC codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRRPWCYVQVGLKPLVQECMVHDCADGK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR66245 standard; protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanabe T, Amatsuji Y, Kasai S,
Airmura H;
                                                                                                                                                                                                                                                                                                                                        90EP-00109472.
                                                                                                                                                                                                                                                                                                                                                                       89JF-00126433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page; 22pp; English.
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Best Local Similarity 100.
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                            389
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'note≖
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-350146/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 389 AA;
                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                          18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     respectively)
                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                       18-MAY-1989;
22-FEB-1990;
                                                                                                                                                                                                                                                                                                         22-NOV-1990.
                                                                                                                                                                                                                                                                          EP398361-A
                                                                                                              Synthetic
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Region
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ID AAR6
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AC AAR6
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Location/Qualifiers

deleted"

87US-00008795.

Kalyan NK;

Lee SL,

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Human prourokinase variant lacking entire EGF domain.
                                                                                                                                                                                                                                                                              AAW13635 standard; protein; 378 AA
                                                                                          (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                    Claim 1; Page ?; 26pp; English.
                                                                         29-JAN-1988; 88US-00150267
                      Homo sapiens; (engineered)
                                                                                                              WPI; 1995-043464/06.
                                                                                                                                                                                                Sequence 365 AA;
                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                  30-JAN-1987;
                                                                                                                                                                                                                                                                                                 04-JUN-1997
                                                               27-DEC-1994.
                                                       US5376547-A.
                                                                                                                                                                                                                                                                                                                                      Synthetic.
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st Local S
tches 88
                                                                                                    Hung PP,
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(ii) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the same properties as those of hPUK variant and urckinase while retaining the same properties as those of hPUK variant and urckinase while retaining the and very little tendency to cause spontaneous bleeding. The present sequence represents a specific variant of hPUK which lacks the entire EGF commain; the sequence does not appear in the specification and has been created using the wild-type hPUK sequence and the junction sequence after deletion, both of which are given (in Fig 1 and in Fig 2(3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of human prourokinase (hPUK) comprise a hPUK deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinclytic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                   /note= "residues 43-411 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                             Hirose M, Morita M,
                                         /note= "residues 1-9 of native hPUK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 510; DB 2;
100.0%; Pred. No. 8.5e-41;
ive 0; Mismatches 0;
                                                                                                                               /note= "corresponds to TAC codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 RRRPWCYVQVGLKPLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RRRPWCYVQVGLKPLVQECMVHDCADGK
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR66266 standard; protein; 386 AA
                                                                                                                                                                                                                                                                                                                                                                                                               ω,
                                                                                                                                                                                                                                                                                                                                                                                                             Amatsuji Y, Kasai
                                                                                                                                                                                                                                                                                                     89JP-00126433.
90JP-00042020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 22pp; English.
                                                                                                                                                                                                                                                           90EP-00109472.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
...-rhes 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                     (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-350146/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT61672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 378 AA;
                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      respectively)
                                                                                                                                                                                                                                                              18-MAY-1990;
                                                                                                                                                                                                                                                                                                     18-MAY-1989;
22-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
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                                                                                                                                                                                                                  22-NOV-1990.
                                                                                                                                                                                                                                                                                                                                                                                                             Tanabe T,
Airmura H;
                                                                                                                                                                          EP398361-A.
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Region
                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid residues 1-46 contain the EGF region of human urokinase. Deletion of this region results in a plasminogen activator with reduced affinity for liver cell membranes; the mutant protein is not cleared from the circulation as rapidly as is wild-type tPA. The specification only gives the sequence around the deletion and not the full-length sequence of "delta 1-46 urokinase"; the sequence in AAR86854 has been obtained by amending a previously disclosed wild-type human urokinase sequence (from W09501427) according to the description given in Example 3. (Updated on 25-WAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise
                  Human; des-epidermal growth factor homologous plasminogen activator; uPA; liver membrane; reduced affinity; EGF homologous; thrombosis; thrombolytic; increased half-life; urokinase.
                                                                                                                                                                                             'note= "amino acids 1-46 of wild-type urokinase have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified plasminogen activator cpds. - having regions removed to reduce affinity for liver membranes and increase circulation half-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prourokinase; hPUK; variant; half-life; increase; EGF; epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
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9 74

88

Similarity 88; Conserv

N 61 RRRPWCYVOVGLKPLVQECMVHDCADGK

(first entry)

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AAH32943 to AAH37195 and AAG73514 to AAG7778B represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAH7789 represent sequences used in the exemplification of the present invention. N. B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                             Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 7707-7708; 9803pp; English.
     Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to 1052, 7921 and 7922
Ruben SM, Barash SC,
                                                                                                             WPI; 2001-235357/24.
                                                                                                                                                           N-PSDB; AAH34897
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Sequence 337. AA;

ö .; 0 100.0%; Score 510; DB 4; Length 337; 100.0%; Pred. No. 7.6e-41; ive 0; Mismatches 0; Indels 0 88; Conservative nery Match ast Local Similarity tches

1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60

61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88

Ö 'n

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134 RRRPWCYVQVGLKPLVQECMVHDCADGK 161

11795 RAHXAXAXIXXXXXXXXXXXXXXXXXXXXXXXXXX

ABP41795 standard; protein; 337 AA.

ABP41795;

Human ovarian antigen HVVCB79, SEQ ID NO:2927.

22-AUG-2002 (first entry)

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; utinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 10q24.

WO200200677-A1

03-JAN-2002.

07-JUN-2001; 2001WO-US018569

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA; Birse CE,

2002-147878/19.

N-PSDB; ABQ54872

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 11; SEQ ID NO 2927; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP41228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also concendences of the invention and polymucleotides 99% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen.

The invention of the invention of the invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen.

The sequences of the invention comprising human ovarian antigen.

The sequences of the invention of the sequence and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic or oplycyptic ovary syndrome, ovarian cystes, and dysmeorichees, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and vaginatory disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and unimary system disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndromy and sorders (e.g., chlamydia, HIV, toxoplasmosis, ophoritis and unimary system disorders. Neurological disorders, gastrointestinal disorders of polymucleotides may also be used in screening for compounds which condulate ovarian antigen expression or activity. The polymucleotides may curtain antigen expression or activity. The polymucleotides may confirm any polymosis, drug argeting and phenotyping. The present confirmation of individuals and in forensic analysis, and the confirmation of polymosis, drug argeting and prepare antibodies useful in disease diagnosis, drug argeting and prepare antibodies useful in disease human ovarian antigen of the invention. Note: The sequence data for this patent did neterionic format directly from WIPO certification, but was

Sequence 337 AA;

. Length 337; Indels Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e-41;
Matches 88; Conservative 0; Mismatches 0;

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AAR68854 standard; protein; 365 RESULT 7

(revised) AAR68854; AAR68854
ID AAR6
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AC AAR6
XX
DT 16-C
DT 25-N
XX
XX
DT 22-N
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DE DElt

(first entry) 16-OCT-2003 25-MAR-2003 22-NOV-1995

Delta 1-46 urokinase.

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The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uph). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occludions, thrombotic microrangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (uPA) amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 1D; 117pp; English
13-JUN-2001; 2001WO-US018976
                                                                                               20-JUN-2000; 2000US-0212874P
                                                                                                                                                                                         (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                             Cines DB, Higazi AA;
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N-PSDB; AAD27078.
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1 KTCYEGNGHPYRGKASTDTMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60
                                                                                        0; Gaps
                                       100.0%; Score 510; DB 5; Length 135; 100.0%; Pred. No. 3.2e-41; ive 0; Mismatches 0; Indels (
                                                                                        88; Conservative
                                         ery Match
st Local Similarity
Sequence 135 AA;
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AAE16549 standard; protein; 143 AA AAE16549;

(first entry) 09-APR-2002

Human uPA amino terminal fragment (ATF) and connecting peptide.

Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; stroke; hypotension; anglogenic disorder; pulmonary fibrosis; aethma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; ATF; male impotence

Homo

WO200197752-A2

13-JUN-2001; 2001WO-US018976.

20-JUN-2000; 2000US-0212874P.

(UYPE-) UNIV PENNSYLVANIA

Cines DB, Higazi AA;

WPI; 2002-122240/16. N-PSDB; AAD27082 Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.

Claim 24; Fig 1H; 117pp; English

The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occludions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, upulmonary fibrosis, asthma, timmour cell angiogenesis, tumour cell metastasis, glaucoma, disorder, male impotence, respiratory discress syndrom, tumour cell such as asthma, adult respiratory discress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sespiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sespent casociated with chronic intrapulmonary fibrin formation. The present temminal fragment (APF) and connecting peptide

Sequence 143 AA;

0; Gaps Length 143; 0; Indels 100.0%; Score 510; DB 5; 100.0%; Pred. No. 3.4e-41; tive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 88; Conservative

48 KTCYZGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107 9 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN d

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AAG75492 RESULT

AAG75492 standard; protein; 337 AA

AAG75492;

03-SEP-2001

Human colon cancer antigen protein SEQ ID NO:6256.

Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 10.

WO200122920-A2.

05-APR-2001.

28-SEP-2000; 2000WO-US026524

99US-0157137P. 29-SEP-1999; 03-NOV-1999;

(HUMA-) HUMAN GENOME SCI INC

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The invention relates to a composition comprising one or more domains of urckinase-type plasminogen activator (uPA). The composition is used to endoulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypotension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metaetasis, glaucoma, dabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory discress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (uPA) kringle
                                                                                                                                                                                                                                                                                                                              Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urckinase-type plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1, FigilA, 117pp, English.
                                                                                                        .3-JUN-2001; 2001WO-US018976.
                                                                                                                                            20-JUN-2000; 2000US-0212874P.
                                                                                                                                                                                  (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                 Cines DB, Higazi AA;
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                          WO200197752-A2.
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0; Indels lery Match 100.0%; Score 510; DB 5; Length 88; st Local Similarity 100.0%; Pred. No. 2.2e-41; trches 88; Conservative 0; Mismatches 0; Indels Sequence 88 AA;

1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 60 1. XTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGHGHVGRNPDN 60

RRRPWCYVQVGLKPLVQECMVHDCADGK 88 RRRPWCYVQVGLKPLVQECMVHDCADGK 88 61

Ø Α AAE16550 standard; protein; 96 AA.

AAE16550;

Human uPA kringle and connecting peptide.

MAHXAXDXDXXXXXXXXX

09-APR-2002 3 (first entry)

Human, urokinase-type plasminogen activator, uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; uncrovascular occlusion; angiogenic disorder; pulmonary fibrosis; atthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; male impotence.

Homo sapiens

40200197752-A2

The invention relates to a composition comprising one or more domains of urckinase-type plasminogen activator (uPA). The composition is used to endothelial cell or tissue. The composition is used to endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, pulmonary fibrosis, asthma, tumour cell andiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory discress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (uPA) kringle and Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator. Claim 25; Fig 11; 117pp; English 20-JUN-2000; 2000US-0212874P. 13-JUN-2001; 2001WO-US018976. (UYPE-) UNIV PENNSYLVANIA. Cines DB, Higazi AA; 2002-122240/16. connecting peptide N-PSDB; AAD27083

1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60 1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKGNYKCRNPDN 60 0; Gaps Query Match 100.0%; Score 510; DB 5; Length 96; Best Local Similarity 100.0%; Pred. No. 2.3e-41; Matches 88; Conservative 0; Mismatches 0; Indels 8

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AAE16545 standard; protein; 135 AA. RESULT 3

09-APR-2002 (first entry)

AAE16545;

Human urokinase-type plasminogen activator amino terminal fragment (ATF).

Human; urokinase-type plasminogen activator; uPh; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthmattumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine concraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; ATF; male impotence

Homo sapiens,

WO200197752-A2

27-DEC-2001

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Aby1795 Human col
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ALIGNMENTS

Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome. Human urokinase-type plasminogen activator (uPA) kringle. AAE16542 standard; protein; 88 AA (first entry) 09-APR-2002 AAE16542; RESULT 1
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1 SNELHQVPSNCDCLNGGTCV.....QVGLKPLVQECMVHDCADGK 135
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ALIGNMENTS

ALIGNMENTS	
1 inogen activator (EC 3.4.21.73) precursor [validated] - human nate names: cellular plasminogen activator; urokinase; urokinase-type p ins: urokinase-type plasminogen activator chain A; urokinase-type plasm	swinog ogen a
n rorm C.Species: Homo sapiens (man) C.Date: 17-Dec-1982 #Bequence revision 04-Dec-1986 #text_change 15-Sep-2000 C.Accession: A00931; 152209; JT0102; A37561; 138102; S65783; A37562; A37563; A .64 R.Kiccio, A.; Grimaldi, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.	.64; A
Nucleic Acids Res. 13, 2759-2771, 1985 A;Title: The human urokinase-plasminogen activator gene and its promoter. A;Reference number: A00931; MUID:85215647; PMID:2987867 A;Accession: A00931	
A,Molecule type: DNA A,Residues: 1-431 <ric> A,Residues: 1-431 <ric> A,Gross-references: GB:X02419, NID:g37601; PIDN:CAA26268.1; PID:g1834524 A,Cross-references: GB:X02419, NID:g37601; PIDN:CAA26268.1; PID:g1834524 A;Note: the authors translated the codon ATG for residue 214 as Ile R;Nagamine, Y.; Pearson, D.; Grattan, M.</ric></ric>	
Biochem. Biophys. Res. Commun. 132, 563-569, 1985 A;Title: Exon-intron boundary sliding in the generation of two mRNAs coding for porcir A;Reference number: IS2209; MUID:86050639; PMID:3933505	orcir

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A; Molecule type: protein
A; Residues: 21-34 cRAB-
R; ii. X; Boxman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.
submitted to the Brookhaven Protein Data Bank, July 1993
A; Reference number: A5125; PDB:1KDU
A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NW, res
R; ii. X.; Smith, R.A.G.; Dobson, C.M.
B; ochemistry 31, 9562-9571, 1992
B; ii. M. Sequential (1)H NMs assignments and secondary structure of the kringle loma
A; Title: Sequential (1)H NMs assignments and disulfide bond assignments by (1)H-NM; A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NM; R; Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Ol. iicz
submitted to the Brookhaven Protein Data Bank, January 1994
A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NM; R; R; Ragragon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobs, C.; R; Spragon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobs, C.; Submitted to the Brookhaven Protein Data Bank, July 1995
A; Reference number: A66058; PDB:1LMW
A; Reference number: A66058; PDB:1LMW
A; Reference number: A66058; PDB:1LMW
C; Comment: This enzyme is found in urine in a high molecular mass form, consist of C; Comment: Urokinase-type plasminogen activator proteolytically activates plasm 10ges
C; Comment: Urokinase-type plasminogen activator proteolytically activates plasm 10ges
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A; Cross-references: 1973, 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
A; Introns: 1973, 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
A; Introns: 1973, 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
C; Function:
A; Description: proteolytically activates plasminogen
A; Pathway: fibrinolysis
C; Gyperfamily: urokinase-type plasminogen activator; EGF homology; kringle hom ogy; C; Superfamily: urokinase-type plasminogen activator, single chain form #sta
F; 21-43//Product: urokinase-type plasminogen activator chain A #status experim
F; 21-43//Product: urokinase-type plasminogen activator chain B #status experim
F; 11-62/Domain: EGF homology eEGF>
F; 71-151/Domain: kringle homology eEGF>
F; 71-151/Domain: trypsin homology ergy plasminogen activator chain B #status experim ral
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F; 115-413/Product: urokinase-type plasminogen activator chain B #status experimental
F; 13-413, 23-51, 23-62, 70-151, 91-133, 122-146, 168-299, 209-225, 217-288, 313-382, 345-1, 37-413/Product experimental
F; 117-413/Product extended experimental
F; 118-113/Cleavage site: His, Asp. Ser #status experimental
F; 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 12-17, 1
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100.0%; Pred. No. 3.3e-64;
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Best Local Similarity 100.
Matches 135; Conservative
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A,Molecule type: protein
A,Molecule type: protein
A,Residues: 156-176;179-193, 'T',195,'T',197-224 <SCH>
R,Steffens, G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
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A,Molecule type: protein
A,Recession: A35689
A,Mote: identification of a fucose and attempt to determine its attachment site
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A; Ratus: preliminary
A; Rolecule type: mRNA
A; Ratus: preliminary
B; Cooim. Biophys. Acta 1293, 17, 215-385, °C',387-429, °V',431 «JAC>
A; Cross-references: EMBL:X02760; NID:935297; PIDN:CAA26535.1; PID:935298
B; Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, B; Cochim. Biophys. Acta 1293, 83-89, 1996
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A; Residues: 21-140, 'L',142-213, 'I',215-431 «YOS>
A; Cross-references: EMBL:D11143; NID:91311467; PIDN:BAA01919.1; PID:91199928
A; Cross-references: EMBL:D1143; NID:91311467; PIDN:BAA01919.1; PID:91199928
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A; Cross-references: EMBL:D1143; NID:91311467; PIDN:BAA01919.1; PID:91199928
A; Cross-reference number: A37562; MUD:83055084; PMID:674869
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               A;Accession: I52209
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosidus: 145-161
A;Cross-references: GB:K03027; NID:g340174; PIDN:AAA61257.1; PID:g340175
A;Cross-references: GB:K03027; NID:g340174; PIDN:AAA61257.1; PID:g340175
A;Title: Molecular cloning of cDNA coding for human preprourokinase.
A;Title: Molecular cloning of cDNA coding for human preprourokinase.
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A;Residues: 1-213,'1', 215-431 cNAG2>
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A; Residues: 66-431 «VER»
A; Craches: 66-431 «VER»
A; Craches: 66-431 «VER»
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DNA 4, 139-146, 1985
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A; Reference number: 138102; MUID:85203359; PMID:3888571
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u-plasminogen activator (EC 3.4.21.73) precursor - rat
N.Alternate names: plasminogen activator, urokinase-type; urinary plasminogen
C;Species: Rattus norvegicus (Norvay rat)
C;Date: 18-Oct-1989 #sequence revision 10-Feb-1995 #text_change 18-Jun-1999
C;Accession: S24604, I60186; I53472, S18932
R;Rabbani, S.A.
S:Rabbani, S.A.
A;Reference number: S24604
A;Reference number: S24604
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A; Residues: 1.15, 'H'. 17-23,'G',25-331,'N',333-432 <RAB>
A; Cross-references: EMBL: K65651; ND:957456; PIDN:CAA46601.1; PID:957457
A; Experimental source: tissue kidney
R;Henderson, B.R.; Tansey, W.P.; Phillips, S.M.; Ramshaw, I.A.; Kefford, R.F.
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A;Title: Transcriptional and posttranscriptional activation of urokinase plasm
A;Reference number: 160186; MUID:92233409; PMID:1568219
                                                                                                                                                                                                                                                                                                                                                              u-plasminogen activator (EC 3.4.21.73) precursor - bovine
Nylternate names: uPA
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-0ec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: JNO560
R;Kraetzschmar, J:; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
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A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning A;Reference number: JNO560; MUID:9316119; PMID:8385052
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A, Residues: 1-433 <RRNA

A, Residues: 1-433 <RRNA

A, Cross-teferences: GB:L03546; NID:g163800; PIDN:AAA51419.1; PID:g163801

C, Superfamily: urokinase-type plasminogen activator; EGF homology; kringle hom

C, Keywords: g1ycoprotein; heterodimer; hydrolase; kringle; serine proteinase

F;1-20/Domain: signal sequence #status predicted <81G>

F;21-179/Product: plasminogen activator chain A #status predicted <MA1>

F;21-179/Product: urokinase-type plasminogen activator chain A #status predict

F;33-64/Domain: EGF homology <RRG>

F;31-153/Domain: EGF homology <RRG>

F;181-433/Product: plasminogen activator chain B #status predicted <MA2>

F;181-421/Domain: trypsin homology <RRG>

F;181-421/Domain: trypsin homology <RRG>

F;170-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status pre

F;226,277,378/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                        81 RGKANTNTGGRECLPMNSATVLLNTYHAHRPDALQLGLGKHNYCRNPDNQRRPWCYVQVG 140
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.larity 73.0%; Pred. No. 6.7e-45;
Conservative 13; Mismatches 22;
           RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGI
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                                                                                                                                               LKPLVQECMVHDCADGK 135
                                                                                                                                                                                    Best Local Similarity
Matches 100; Conserv
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              59
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C'Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C'Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C'STOMOMA:: signal sequence #status predicted <SIGNS
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F;72-153/Domain: EGF homology <EGF>
F;190-442/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
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F;150-430/Domain: trypsin homology <TRY>
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F;255,286,387/Active site: His, Asp, Ser #status predicted
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F; 69-150/Domain: kringle homology <EGF>
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F; 178-421/Apaduct: plasminogen activator chain B #status predicted <BCH>
F; 178-421/Apaduct: plasminogen activator chain B #status predicted <BCH>
F; 178-421/Apaduct: plasminogen activator chain B #status predicted <BCH>
F; 178-421/Apaduct: plasminogen activator chain B #status predicted <BCH>
F; 187-223,274,378/Active site: His, Asp, Ser #status predicted
F; 324/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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C;Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
C;Accession: A00932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiNagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucledic Acids Res. 12, 9525-9541, 1984
A.;Title: CDNA and gene nucleotide sequence of porcine plasminogen activator.
A;Reference number: A00932; MUID:85087954; PMID:6096832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHELHQESGASNCGCLNGGKCVSYKYFSNIQRCSCPKKFQGEHCEIDTSQTCFEGNGHSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SREL-QVPSDCGCLNGGTCMSNKYFSSIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 713.5; DB 1; Length 433;
Pred. No. 4.9e-57;
4; Mismatches 6; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.7%; Score 608; DB 1; Length 442; 78.1%; Pred. No. 1.6e-47; ive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the Protein Sequence Database, December 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      u-plasminogen activator (EC 3.4.21.73) precursor - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: annotation; correction to residue 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: A00332
A,Molecule type: DNA
A,Residues: 1-240, "H',242-442 <NAG1>
A,Experimental source: kidney cell line LLC-PK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 QRVQECMVHNCADGK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.9%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           il Similarity 78.1%;
107; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local
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Matches
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C. Species: Megaderma lyras C. 5.4.21.08) preductor - Talse Vample Dat Newsqueet.
C. Species: Megaderma lyras C. 5.4.21.08) preductor - Talse Vample Date Newsqueet.
C. Species: Megaderma lyras C. 5.20.099 #text_change 10-Sep-1999
C. Accession: A34369
A. Totale: Isolation, Characterization, and cDNA cloning of a vample bat saliva pla A,Tete: Isolation, Characterization, and cDNA cloning of a vample bat saliva pla A,Reference number: A34369 MUD:90036867; PMID:2509450
A,Reference number: A34369 MUD:90036867; PMID:2509450
A,Reference number: A34369
A,Reference number: A34369
A,Residues: 1477 cGAR>
A,Residues: 1477 cGAR>
A,Residues: 1477 cGAR>
A,Residues: 1211 maxy
A,Molecule type: mRNA
A,Residues: 1211 can arrivator maxy
A,Residues: 1210 companies grantus predicted cSIG>
F,12-10 formain: signal sequence #status predicted cSIG>
F,12-10 formain: signal sequence #status predicted cSIG>
F,12-36 formain: EGF homology cRGP>
F,12-10 formain: EGF homology cRGP>
F,12-209 formain: EGF homology cRGP>
F,12-209 formain: trypsin homology cRGP>
F,12-209 formain: tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderm. C;Species: Megaderma lyra
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                               B #status predic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 RPCLAWNAPAVLQKPYNAHRPDAISLGLGRGHYCRNPDNQKRPWCYVQIGLRQFVQECMV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t-plasminogen activator (BC 3.4.21.68) alpha-2 precursor - common vampire bat N;Alternate names: tissue plasminogen activator C;Species: Desmodus rotundus (common vampire bat) C;Species: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F,71-152/Domain: kringle homology «KRG»
F,180-431/Product: urokinase-type plasminogen activator chain B #status pres
F,180-421/Domain: trypsin homology «TRY»
F,180-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status F,226,277,378/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 QCHTVPVKSCSELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                               SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 ŚNCGCQNGGVCVSYKYPSRIRRCSCPRKFQGEHCEIDASKICYHGNGDSYRGKANTDIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV
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                                                                                                                                                                                                                                                                                                                                                              23; Indels
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46.3%; Pred. No. 6.8e-23;
tive 17; Mismatches 50;
                                                                                                                                                                                                                                                                  , DB 1;
4.2e-42;
                                                                                                                                                                                                                                                                  Query Match
69.1%; Score 548; DB
Best Local Similarity 71.7%; Pred. No. 4.2e
Matches 91; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 LKPLVQECMVHDCA 132
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 HDCSLSK 156
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dates: 30.5ep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A29420; A24615
B;Ochemistry 26; 8270-8279, 1987
A;Title: The murine urokinase-type plasminogen activator gene.
A;Reference number: A29420; MUID:88163489; PMID:2831940
A;Residues: 1-433 -CBG3
A;Residues: 1-433 -CBG3
A;Cosse-references: GB:MIJ922; NID:920226; PIDN:AAA40539.1; PID:9202297
B;Belin, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher, E.U. J. Blochem. 1446, 225-222, 1985
A;Cosse-references: GB:MIJ922; NID:95129; PIDN:CAA26231.1; PID:955128
A;Reference number: A24615; MUID:85179474; PMID:2985383
A;Reference number: A24615; MUID:85179474; PMID:2985383
A;Residues: 1-433 -CBG3
A;Accession: A4485
A;Residues: 1-433 -CBG3
A;Accession: A24615
A;A
                                                                                                                                 A)Cross-references: EMBL:X63434; NID:g57465, PIDN:CAA45028.1; PID:g57466
A)Experimental source: strain Fischer 344; tissue mammary
A,Kagno, P.; Cassano, S.; Degen, J.; Kessler, C.; Blasi, F.; Rossi, G.
FX,Ragno, B.; Dogen, J.; Ressler, C.; Blasi, F.; Rossi, G.
A,Title: The receptor for the plasminogen activator of uroxinase type is up-regulated in A;Reference number: I53472; MUID:92339549; PMID:1321734
A,Accession: I53472
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ajgene: upA
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C;Superfamily: urokinase-type plasminogens; kringle; serine proteinase
C;Keyworsis: glycoprotein; heterodimer; hydrotes; kringle; serine proteinase
C;Keyworsis: glycoprotein; heterodimer; hydroted <SIG;
F;1-19/Domain: signal sequence #status predicted <ACH>
F;20-177/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F;70-151/Domain: kringle homology <RRG>
F;70-420/Domain: kringle homology <RRG>
F;179-420/Domain: trypsin homology <RRY>
F;179-420/Domain: trypsin homology <RRY>
F;255,276,377/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 RPCLPWNSATVLOOTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 SNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 SNCGCQNGGVCVSYKYPSSIRRCSCPKKFKGEHCEIDTSKTCYHGNGQSYRGKANTDTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:X66907; NID:g396200; PIDN:CAA47356.1; PID:g938279
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.0%; Score 571; DB 1; Length 43
Best Local Similarity 77.2%; Pred. No. 3.5e-44;
Matches 98; Conservative 8; Mismatches 21; Indels
              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 HDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 QDČSLSK 155
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A/Cross-references: GDB:119496; OMIM:173370
A/Cross-references: GDB:119496; OMIM:173370
A/Cross-references: GDB:119496; OMIM:173370
A/ADP position: 8p12-8p12
A/ADP position: 8p12-8p12
A/ADP position: 8p12-8p12
A/ADP position: 8p12-1; 122/1; 180/2; 211/1; 268/2
C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I
C/Superfamily: tissue plasminogen activator predicted a/ADP
F/1-23/Domain: signal sequence #status predicted a/ADP
F/1-23/Domain: propeptide #status predicted a/ADP
F/1-27/Domain: BGF homology a/ADP
F/1-27/Domain: Kinpale homology a/ADP
F/1-27-208/Domain: kringle homology a/ADP
F/21-201/Domain: kringle homology a/ADP
F/21-201/Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                 t_plasminogen activator precursor, inactive endothelial splice form - human NyAlternate names: tissue plasminogen activator (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Spacession: 17-May-1996 #text_change 22-Jun-1999 (Spacession: 138098; Sol6/8 # $1000 K. Nyalelor Acids Res. 18 1086, 1990 (Spacession: 138098; MID:190192128; PMID:1969145 (PLAT) cDNA obtained from hareference number: 138098; MUID:90192128; PMID:1969145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 gchsvpvkscseprcfndgrcggalyfsdf-vcgcpegfagkcceidtratcyedggisy
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40 CQCLNGGTCITYRFFSQIKRCLCPEGYGGLHCEIDTNSICYSGNGEDYRGMAEDP----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X13097; NID:g35282; PIDN:CAA31489.1; PID:
C;Comment: For the main splice form, see PIR:UKHUT. This form prob
                                                                                                         71 CLPWNSATVLQ-OTYHAHRSDALQLGLGRGHNYCRNPDNRRRPWCYVQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch
1 Similarity 46.3%; Pred. No. 1.9e-22;
63; Conservative 13; Mismatches 55; Indels
                                                                                                                                                           96 CLYWDHPSVIRWGDYHADLKONALQLGLGKGHYCRNPNGRSRPWCYTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-291 <SIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LKPLVQECMVHDCADG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 GKYSSEFCSTPACSEG 211
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Best Local Si
Matches 63;
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A.Residues: 1-434 <LES.
C.Superfamily: urokinase-type plasminogen activator; BGF homology; kringle homology; try C; keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F.1-21/Domain: signal sequence #status predicted <SIG>
F.1-21/Domain: signal sequence #status predicted <AGH>
F.1-21/Domain: RF homology <RGF>
F.3-17/Domain: RF homology <RRG>
F.3-17/Domain: kringle homology <RRG>
F.79-158/Domain: kringle homology <RRG>
F.13-416/Domain: tryppsin homology <TRV>
F.13-428/Domain: tryppsin homology <TRV>
F.162-296,202-218,210-285,310-379,342-358,369-397/Disulfide bonds: #status predicted
F.17,272,373/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA

A, Residues: 1-477 < KRA.

A, Residues: 1-477 < KRA.

A, Residues: 1-477 < KRA.

A, Cross-references: GB:M63989, NID:g166074; FIDN:AAA31593.1; FID:g166075

C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C, Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

C, Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F; 12-21/Domain: stonal sequence #status predicted < RO.

F; 37-477/Product: plasminogen activator alpha-2 #status predicted <PLA.

F; 87-120/Domain: EGF homology < EGF.

F; 87-120/Domain: Kringle homology < RG.

F; 87-120/Domain: kringhe homology < RG.

F; 88-120/Domain: kringhe homology < RR.

F; 88-120/Bonain trypsin homology < RR.
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           R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Gene 105, 229-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat A;Reference number: JS0597; MUD:92039036; PMID:1937019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136
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NyAlternate names: uPA
C.Species: Gallus gallus (chicken)
C.Species: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 335.5; DB 2; Length 477; Pred. No. 6.8e-23; 17; Mismatches 50; Indels 5;
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R)Leslie, N.D.; Kessler, C.A.; Bell, S.M.; Degen, J.L.
J. Biol. Chem. 265, 1339-1344, 1990
A)Title: The chicken urokinase-type plasminogen activator gene. A;Reference number: A35005; MUID:90110185; PMID:2295632
A;Accession: A35005
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ilarity 54.2%;
Conservative 1
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1 Similarity 46.3%;
62; Conservative 1'
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Best Local Similarity
Matches 62; Conserv
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Best Local S
Matches 58
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C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted <8IG>
F;2-36/Domain: propeptide #status predicted <PRO>
F;2-36/Domain: propeptide #status predicted <PRO>
F;3-7-411/Product: plasminogen activator beta #status predicted <PLA>
F;41-74/Domain: BGF homology <BGF>
F;82-165/Domain: kringle homology <RR>
F;82-165/Domain: kringle homology <RR>
F;180-425/Domain: kringle homology <RR>
F;280-425/Domain: kringle homology <RR
F;48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.4%; Score 328.5; DB 2; Length 431;
larity 47.6%; Pred. No. 2.7e-22;
Conservative 16; Mismatches 48; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 59; Conserv
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A; Residues: 33-45;311-320 <POH>
A; Residues: 33-45;311-320 <POH>
A; Residues: 33-45;311-320 <POH>
A; Reperimental source: uterus
A; Note: in the uterus, cleavage of the activation peptide may also occur after 3-G1:
A; Note: in the uterus, cleavage of the activation peptide may also occur after 3-G1:
B; Nan Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
J. Biol. Chem. 261, 14214-14218, 1886
A; Richerence number: A37567; MUID:8703361; PMID:3021732
A; Contents: annotation; fibrin binding site
A; Reference number: A37568; MUID:8716761; PMID:3030730
A; Reference number: A37568; MUID:8716761; PMID:3030730
A; Rottens: annotation; fibrin binding site
A; Reference number: A60902; MUID:89044681; PMID:3142086
A; Contents: annotation; identification and pharmacokinetic properties of human tis 3-ty
A; Reference number: A60902; MUID:89044681; PMID:3142086
A; Contents: annotation; novel forms of expressed recombinant t-PA
A; Reference number: A60902; MUID:8046481; PMID:3142086
A; Contents: annotation; novel forms of expressed recombinant t-PA
A; Title: Cloning of cDNA coding for human tissue-type plasminogen activator an its
A; Reference number: A544645; MUID:86284200; PMID:3090401
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 251-358 <EDL>
A;Experimental source: melanoma cells
A;Experimental source: melanoma cells
B;Pohl, G; Kallstrom, M; Bergadorf, N; Wallen, P; Jornvall, H.
B;Pohl, G; Kallstrom, M; Bergadorf, N; Wallen, P; Jornvall, H.
A;Title: Tissue plasminogen activator: peptide analyses confirm an indirectly differences.
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Ajaccession: A54645
Ajaccession: A54645
Ajaccession: L562 GIRR>
Ajaccess-references: GB:M15518; NID:g190031; PIDN:AAA60111.1; PID:g190032
Ajacces parse of this sequence were confirmed by peptide sequencing
Ajacces: parse of this sequence, were confirmed by peptide sequencing
R;Reddy, V. B.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
DNA 6, 461-472, 1987
Mill: Expression of human uterine tissue-type plasminogen activator in mous
A;Pitcher number: 160110; MUD:88054470; PMID:2824147
A;Accession: 160110
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A;Contents annotation; melanoma cells, partial sequence of residues 36-562, a. R;Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H. FBS Lett. 168, 29-32, 1894
A;Title: Differences between uterine and melanoma forms of tissue plasminogen A;Reference number: A91322; MUID:84158956; PMID:6538514
R;Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.

Nucleic Acids Res. 16, 5695, 1988

Nucleic Acids Res. 16, 5695, 1988

A;Fitle: Nucleotids sequence of the tissue-type plasminogen activator cDNA from A;Feference number: S02125; MUID:88262579; FMID:3133640

A;Accession: S02125

A;Actual: translation not shown

A;Status: translation not shown

A;Residues: 1-562 <ASA>

A;Accession: Expression: RNA

A;Residues: 1-562 <ASA>

A;Accession: Expression in Bscherichia coli of finger-domain lacking tissue-type pa;Residue: pa;Residue: 189, 145-149, 1985

A;Reference number: A91343; MUID:85285620; PMID:3896853

A;Accession: A91343;
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A;Residues: 1.38, 'G', '86-433,'E', 435-562 <KAG>
A;Respentantal source: Detroit 562 cells; ATCC 138
A;Experimental source: Detroit 562 cells; ATCC 138
B;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephso:
Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
A;Title: Isolation of CDNA sequences coding for a part of human tissue plasmin
A;Reference number: A93951; MUID:83169656; PMID:6572897
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A; Molecule type: mENA A; Molecule type: mENA A; Molecule type: mENA A; Molecule type: mENA A; Residues: 1-562 < RES > A; Residues: 1-562 < RES > A; Cross-references: GB:M18182; NID:g340176; PIDN:AAA36800.1; PID:g340177
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L-plasminogen activator (EC 3.4.21.68) precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accesion: A29941; S48205; S48206 S;Rickles, R.J.; Darrow, A.L.; Strickland, S. J. Biol. Chem. 263, 1563-1569; 1988 A; Musculus Musculus cloning of complementary DNA to mouse tissue plasminogen ac A;Reference number: A29941; MUID:88087303; PMID:2826484 A;Reference number: A29941; MUID:88087303; PMID:2826484 A;Reference number: A29941; MUID:88087303; PMID:2826484 A;Reference number: B2941; MUID:88087303; PMID:2826484 A;Reference musculus type: many A;Residues: 1-559 cRIC> A;Reference musculus type: many A;Reference musculus type: MUID:39010076; PMID:7523120 A;Reference number: S48205 A;Accession: S48205 A;Accessio
                            A; Residues: 1-379; "KK."

A; Residues: 1-379; "KK."

A; Residues: 1-379; "KK."

A; Cross-references: GB:M23697; NID:g530159; PIDN:AAA1812.1; PID:g530160

C; Superfamily: tissue plasminagen activator; EGF homology; fibronectin type I
C; Keywords: fibrinolysis: glycoprotein; hydrolase; kringle; serine proteinase
E;1-17/Domain: signal sequence #status predicted <RG>
E;1-17/Domain: signal sequence #status predicted <RG>
F;30-308/Product: t-plasminogen activator fastatus predicted <AGH>
F;30-559/Product: t-plasminogen activator chain A #status predicted <AGH>
F;31-208/Domain: kringle homology <KR1>
F;21-208/Domain: kringle homology <KR2>
F;21
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A,Molecule type: protein
A,Residues: 33-37, X,39-40 <LIJ>
A,Accession: S48205
A,Molecule type: protein
A,Accession: S48207
A,Accession: S48206
A,Accession: Signal sequence #status predicted <SIC>
F,117/Domain: propeptide #status predicted <AMT>
F,30-559/Product: t-plasminogen activator #status predicted <AMT>
F,30-559/Product: t-plasminogen activator chain A #status predicted <ACH>
F,30-559/Product: Tolasminogen activator chain A #status predicted <ACH>
F,31-57/Domain: GGP homology <GGR>
F,31-7205/Domain: Kringle homology <KR1>
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Matches 62
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A/Cross-references: GDB:119496; OMIM:173370
A/Cross-references: GDB:119496; OMIM:173370
A/Cross-references: GDB:119496; OMIM:173370
A;Map position: 8p12-8p12, 8p12/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 510
A;Map position: 9p12-8p12, 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 510
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C;Keywords: fibrinolysis; glycoprotein; hydrolaes; Kringle; plasma; Serine proteinase F;1-23/Domain: propeptide # status predicted <RGO-F;23-52/Domain: propeptide # status predicted <RGO-F;33-52/Product: t-plasminogen activator chain A #status experimental <ACH>F;33-52/Product: t-plasminogen activator chain A #status experimental <ACH>F;31-50/Domain: fibronectin type I repeat homology <RGO-FF;11-526/Domain: kringle homolo
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A,Cross-references: GB:M11890; NID:g339837; PIDN:AAA61213.1, FID:g339839
A;Cross-references: GB:M11890; NID:g339837; PIDN:AAA61213.1, FID:g339839
C;Comment: Cleavage by plasmin or trypsin produces two chains held together by a single C;Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. It C;Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.
R;Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D. J. Biol. Chem. 260, 11223-11230, 1985
A;Title: Isolation and characterization of the human tissue-type plasminogen activator A;Reference number: I55232; MUID:85289338; PMID:3161893
A;Accession: I55232
A;Accession: I55232
A;Accession: Lossianinary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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46.3%; Pred. No. 3.3e-22;
ive 14; Mismatches 54; Indels 5
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A)Gene: GDB:HGFAC; HGFA; HGFAP
A)Cross-references: GDB:9954514
A;Map position: 4p16-4p16
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;213-294/Domain: kringle homology <KR2>
F;309-559/Product: -_plasminogen activator chain B #status predicted <BCH>
F;309-559/Product: -_plasminogen activator chain B #status predicted <BCH>
F;309-553/Pomain: trypsin homology <TRX>
F;38-68,66-75,83-94,88-105;107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-</br>
F;309-86,75,83-94,88-105;107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-</br>
F;308-309/Cleavage site: carbohydrate (Asn) (covalent) #status predicted
F;308-309/Cleavage site: Arg-11e (Asn) (apsemin trypsin) #status predicted
F;355,404,510/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 HOVPSN-CD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCRIDKSKTCYEGNGHFY
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                                                                                                                                                                                                                                                                                    Query Match
39.8%; Score 315.5; DB 1; Length 559;
Best Local Similarity 44.5%; Pred. No. 4.9e-21;
Matches 61; Conservative 15; Mismatches 56; Indels 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKYTTEFCSTPACPKGK 209
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C;Becies: Homo sapiens (man)
C;Date: 21-Sep-193 #sequence_revision 25-Aug-1995 #text_change 08-Dec-2000
C;Date: 21-Sep-1993 #sequence_revision 25-Aug-1995 #text_change 08-Dec-2000
C;Date: 26s, 10024-10028, 1993
J; Miyazawa, K.; Shimomura, T.; Kitamura, A.; Kondo, J.; Morimoto, Y.; Kitamura A; Mitle: Molecular cloning and sequence analysis of the cDNA for a human serin d coagulation factor XII.
A;Reference number: A46688; MUID:93252878; PMID:7683665
A;Accession: A46688; MUID:93252878; PMID:7683665
A;Accession: A46688
A;Molecule type: mRNA
A;Residues: 1-655 aMIY
A;Cross-references: DBW:D14012; MID:g219680; PIDN:BAA03113.1; PID:g219681
A;Cross-references: DBW:D14012; MID:g219680; PIDN:BAA03113.1; PID:g219681
A;Aross-references: DBW:D104012; MID:g219680; PIDN:BAA03113.1; PID:g219681
A;Arose: sequence extracted from NCBI backbone (NCBIN:131227, NCBIP:131228)
A;Note: sequence extracted from NCBI backbone (NCBIN:131227, MCBIP:131228)
A;Note: parts of the sequence, including the amino ends of the heavy and light main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V.Fauthway: tissue repair and regeneration
A.Description: activates hepatocyte growth factor by specific proteolytic clea ge
A.Pathway: tissue repair and regeneration
C.Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat omo:
C.Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat predicted cSIG>
F;1-34/Domain: Bigran sequence #status predicted cSIG>
F;104-197/Domain: Eibronectin type I repeat homology cIF2>
F;164-197/Domain: EGF homology cEG3>
F;286-279/Domain: EGF homology cEG3>
F;286-367/Domain: EGF homology cEG3>
F;286-367/Domain: EGF homology cEG3>
F;286-555/Product: hepatocyte growth factor activator light chain #status expe
F;408-655/Product: hepatocyte growth factor activator heavy chain #status expe
F;408-651/Domain: trypsin homology cTRY>
F;408-651/Domain: trypsin homology cTRY>
F;408-651/Domain: trypsin homology cTRY>
F;408-651/Domain: trypsin homology cTRY>
F;408-651/Domain: trypsin site: carbohydrate (Asn) (covalent) #status pr icte
F;408-61/Domain: trypsin site: carbohydrate (Asn) (covalent) #status pr icte
F;164-175,169-186,188-197,202-230,228-237,245-256,250-267,269-278,286-367,307-
Å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 YWNSHLLLQETYNMFWEDAETHGIAEHNFCRNPDGDHKPWCFVKVNSEXVKWEYCDVTVC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 CLNGGICVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
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molog

72

8;

Indels

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A.Cross-references: GB M31315; NID:g182291; PIDN:AAA70225.1; PID:g182292
R.Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGill.
J. Biol. Chem. 260, 13666-13676, 1985
J. Title: Characterization of human blood coagulation factor XII cDNA. Predicting A.Reference number: A00930; MUID:86033830; PMID:3877053
A.Accession: A00930
A.Residues: 14-332, S., 334-615 <CO2>
A.Cross-references: GB:M11723; NID:g180358; PIDN:AAA51986.1; PID:g180359
A.Cross-references: GB:M1723; NID:g180358; PIDN:AAA51986.1; PID:g180359
A.Cross-references: GB:M1023; NID:g180358; PMID:3011063
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Cybecles: Homo sapiens (man)
Cybecles: 17-Nov-1985 #sequence revision 30-Jun-1991 #text change 08-Dec-2000
CyAccession: A29411; A26814; A00930; A25191; A22248; A21037
R;Cool, D.E.; MacGillivray, R.T.A.
J. Biol. Chem. 262, 13662-13673, 1987
A;Title: Characterization of the human blood coagulation factor XII gene. Intro
A;Reference number: A29411; MUID:88007593; PMID:2888762
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A,Residues: 1-615 <COO.
A,Residues: 1-615 <COO.
A,CCOS-CEETENCES: GB:MJ7466, GB:J02807; NID:g180355; PIDN:AAB55450.1; PID:g18
A;Cross-ceetences: GB:MJ7466, GB:J02807; NID:g180355; PIDN:AAB55450.1; PID:g18
B;Tripod1, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.
Nucleic: Acids Res. 14, 3146, 1986
A;Title: cDNA sequence coding for human coagulation factor XII (Hageman).
A;Reference number: A26814; MUID:86176794; PMID:3754331
C;Species: Cavia porcellus (guinea pig)
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C;Accession: 228941
R;Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.;
Biochim. Biophys. Acta 1159, 113-121, 1992
A;Title: Primary structure of guinea-pig Hageman factor: sequence around the CA;Reference number: $28991; WUID:93003367; PMID:1390917
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-603 <85N.
A; Residues: 1-603 <85N.
A; Cross-references: EMBL.X68615; NID:949578; PIDN:CAA48600.1; PID:949579
A; Cross-references: EMBL.X68615; NID:949578; Fibronectin type I repeat
C; Keywords: hydrolage: serine proteànase thomology <1F2>
F;46-87/Domain: fibronectin type I repeat homology <FB1>
F;134-169/Domain: Efbronectin type I repeat homology <FB1>
F;177-208/Domain: Efbronectin type I repeat homology <FB1>
F;16-294/Domain: kringle homology <FRS>
F;359-597/Domain: trypsin homology <FRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 RWAS----BATYRNMTAEQALRRGLGHHTFCRNPDNDTRPWCEVWMGNRLSWEYCDLAQC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||| |: | |- VEGHHLCDCPMGYTGPFCDLDTTASCYEGRGVSYRGMARTTVSGAKCQ 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
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A;Residuses: 146-378,'G',380-615 <QUE>
A;Cross-references: BB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361
R;McMullen, B.A.; Pujikawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.4%; Score 257; DB 2; Length 603; 40.8%; Pred. No. 1e-15;
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A;Molecule type: mRNA
A;Residues: 4-615 <TRI>
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A;Residues: 1-560 <CHO>
A:Residues: 1-560 <CHO>
A;Exper-imental source: plasma
A;Exper-imental source: plasma
A;Note: parts of this sequence, including the amino ends of the mature chains, were dete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: JC4795.
JChoi-Miura, N. H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tomita, M. Slochem. 119, 1157-1165, 1996.
JTitle: Purification and characterization of a novel hyaluronan-binding protein (PHBP)
                                                                                                                                                                                            7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CMVHDC 131
                                                                                                                                                                                                                                                                                                                                      242 HTACLSSPCINGGTC-----HIUATGTTVCACPPGFAGRICNIEPDERCFIGNGT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                          5 HOVPSNCDCLNGGTCVSNKYFSNIHW-----CNCPKKFGGQHCEIDKSKTCYEGNGH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 FYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 GYRGVASTSASGLSCLAWNSDLLYQELHVDSVGAAALLGLGPHAYCRNPDNDERPWCYV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasma hyaluronan-binding protein precursor - human NyAlternate names: hepatocyte growth factor activator-like protein; PHBP NyContains: serine proteinase (EC 3.4.21.-) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: 15-Oct_1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 CONCATCSRHKRRSKF-TCACPDQFKGKFCEIG-SDDCYVGDGYSYRGKMRRTVNQHACL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLNGGT CVSNKY FSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                            Gaps
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N;Alternate names: Hageman factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                     Length
                                                                                                                                                                                       Indels
             F;447,497,598/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: JC4795; MUID:96425001; PMID:8827452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.5%; Score 257.5; DB 1;
42.1%; Pred. No. 8.5e-16;
tive 18; Mismatches 49;
                                                                                                                                                                                            42;
                                                                                                                                                   2e-16
                                                                                                Score 260.5; I
Pred. No. 5.2e-
8; Mismatches
                                                                                           ch 32.8%;
l Similarity 43.7%;
52; Conservative
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les 51; Conserv
                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: JC4795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
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coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
NyAlternate names: Hageman factor (activated)
Cipecies: Bos primingenius taurus (cativated)
Cipate: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
Cyaccession: $45281; A61329
Rishibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Rishibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Riceference number: $45281; MUID: 94242782; PMID: 8186251
A; Molecule type: mRNA
A; Molecule to a tresidue 203 as Deu
B; Molecule type: mRNA
A; Molecule to and ATC for residue 505 as Deu
B; Molecule type: mRNA
A; Molecule to and characterization of bovine factor XII (Hageman factor)
A; Molecule type: MUID: 77182112; PMID: 861210
A; Molecule type: MUID: 77182112; PMID: 861210
A, Residues: 1-394 «KRA»
A, Rocosar Ferences: GB: K63990, NID:g166078; PIDN:AAA31595.1; PID:g166079
A, Grosar Ferences: GB: K63990, NID:g166078; PIDN:AAA31595.1; PID:g166079
A, Note: the authors translated the codon ATC for residue 75 as Thr
C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I
C, Reywords: fibrinolysis; glycoprocien; hydrolase; kringle; serine proteinase
F; 1-21/Domain: signal sequence #status predicted <PRO>
F; 2-36/Domain: propeptide #status predicted <PRO>
F; 2-126/Domain: propeptide #status predicted <PRO>
F; 37-384/Product: plasminogen activator gamma #status predicted <PLA>
F; 45-126/Domain: trypsin homology <TRY>
F; 413-388/Domain: trypsin homology <TRY>
F; 45-126, Ge-108, 97-121, 131-262, 174-190, 182-251, 276-351, 308-324, 341-369/Disulfi, F; 45-126, Ge-108, 97-121, 131-262, 174-190, 182-251, 276-351, 308-324, 341-369/Disulfi, F; 45-126, Domain: site: His Ser (Plasmin) #status predicted
F; 315/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: A61329
A, Accession: A61329
A, Molecule type: protein
A, Residues: 10-16, 'X', 18-19;525-550 <FUJ>
A, Residues: 10-16, 'X', 18-19;525-550 <FUJ>
C, Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat
C; Keywords: blood coagulation; fibrinolyais; glycoprotein; hydrolase; monomer;
F;37-78/Domain: Eibronectin type II repeat homology <1F2>
F;125-16/Domain: Eibronectin type I repeat homology <FB1>
F;207-28/Domain: Eibronectin type I repeat homology <FB1>
F;350-58/Domain: Eibronectin type I repeat homology <FB1>
F;550-58/Domain: Erypsin homology <IRX-
F;550-58/Domain: Erypsin homology <IRX-
F;551/Active site: Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 TDIMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.1%; Score 223; DB 2; Length 394; 44.3%; Pred. No. 8.2e-13; ive 13; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDNRRRPWCYVQVGLKPLVQECMVHDCA 132
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Matches 46; Conserv
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Matches 39; Conserv
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C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Superfamily: coagulation; fibrinolysis; glycoprocein; hydrolase; kringle; plasma; BF;1-19/Domain: signal sequence #status predicted <SIG>
F;20-372,373-61S/Product: coagulation factor XIIa, alpha form #status experimental <AL2>
F;36-130/Domain: EGF homology <EG1>
F;36-130/Domain: EGF homology <EG2>
F;178-259/Domain: EGF homology <EG3>
F;178-259/Domain: Edr homology <ERG>
F;28-356/Region: proline-rich
F;28-356/Region: proline-rich
F;36-136/Product: coagulation factor XIIa, beta form #status experimental <B12>
F;373-609/Domain: trypsin homology <FRY>
F;38-100/L04-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-296
F;299-305/328,328,329,337/Binding site: carbohydrate (Ann) (covalent) #status experimental
F;299-305,328,329,337/Binding site: carbohydrate (Ann) (covalent) #status predicted
F;309,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;309,305,328,328,329,337/Binding site: carbohydrate (Thr) #status predicted
F;309,305,328,328,329,337/Binding site: carbohydrate (Thr) #status predicted
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NiAlternate names: tissue plasminogen activator
C;Species tesmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: JS0600
R;Kraetzschmar, J, ; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 223-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des A;Accession: JS0600
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
R;Mesidues: 354-362;373-615 <FUJ>
R;Mesidues: 354-362;373-615 <FUJ>
R;Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A;Title: O-linked fucose is present in the first epidermal growth factor domain of facto A;Title: O-linker annotation; carbohydrate binding site
C;Genetics:
             J. Biol. Chem. 260, 5328-5341, 1985
A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated Ha
A;Reference number: A22248; MUID:85182674; PMID:3886654
A;Accession: A22248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:F12
A;Cross-references: GDB:119892; OMIM:234000
A;Cross-references: GDB:119892; OMIM:234000
A;Map position: 5G34-5gter
A;Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma
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                                                                                                                                                                               A,Molecule type: protein
A,Residues: 20-379 «MCM»
R,Fulikawa, K.; McMullen, B.A.
7. Holl. Chem. 259, 10924-10933, 1983
A,Title: Amino acid sequence of human beta-factor XIIa.
A,Reference number: A21037; MUID:83291041; PMID:6604055
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A;Title: Multiple members of the plasminogen-apolipoprotein(a) gene family ass
A;Reference number: I52415; MUID:92207924; PMID:1554698
A;Accession: I52415
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R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning of the linked A; Reference number: A47233; MUID:93087573; PMID:1454851
X',4396-4401 <EAT>
R;Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.;
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A;Title: S' control regions of the apolipoprotein(a) gene and members of the A;Reference number: A47277; MUID:93165698; PMID:7679504
A;Recession: A47277
                                                                                                                                                                                                                                                                   A;Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ
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A;Note: several genes closely linked on chromosome 6 are identical in the
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A)Cross-references: GB:M86878, NID:g178782; PIDN:AAA51749.1; PID:g553186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M90078; NID:g178786; PIDN:AAA35547.1; PID:g553188 A;Cross-references: GB:M90078; NID:g178786; PIDN:AAA35547.1; PID:g553188 A;Accession: A47233
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R;Ichinose, A.
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A;Cross-references: GDB:120699; OMIM:152200
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F;256-333/Domain: Kringle homology <RR3>
F;370-447/Domain: Kringle homology <RR4>
F;484-561/Domain: Kringle homology <RR5>
F;588-675/Domain: Kringle homology <RR5>
F;598-675/Domain: Kringle homology <RR5>
F;826-903/Domain: Kringle homology <RR7>
F;826-903/Domain: Kringle homology <RR8>
F;940-1017/Domain: kringle homology <RR8>
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                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-16 <RES>
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A, Residues: 1-16 <RE5>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 08-Dec-2000
C;Accession: 500657; A28017; Ā47277; 160906; A47233; 152415; 165286
R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, B.Y.; Fless, G.M.; Scang Mature 330, 132-137, 1987
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A,ROLECULE LYBORE MRNA
A,ROLECULE LYBORE MRNA
A,ROLECULE LYBORE AMCLA
A,ROLECULE LYBORE AMCLA
A,ROLECULE LYBORE AMCLA
CORGETTER ACTOR
R,EBECON, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A,Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A,Reference number: A28017; MUID:87204109; PMID:3472206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: FlyBase:FBgn0010407
C;Superfamily: Drosophila neurotrophic receptor ror; kringle homology; protein kinase ho
C;Keywards: AFP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyros
F;237-310/Domain: kringle homology «KRG»
F;314-338/Domain: transmembrane #status predicted «TML»
F;408-677/Domain: protein kinase homology «KIN»
F;408-677/Domain: protein kinase homology «KIN»
F;416-424/Region: protein kinase APD-binding motif
F;45,63,129,144,250/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 20-21,'P',23-34;177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-31
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A,Reference number: S00657; MUID:88039109; PMID:3670400
A,Accession: S00657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN-RRRPWCYVQVGLKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKA

    fruit fly (Drosophila melanogaster)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-685 «MIL»
A;Cross-references: GB:L20297; NID:g348103; PIDN:AAA28860.1; PID:g348104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: A48289
R;Wilson, C.; Goberdhan, D.C.I.; Steller, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7109-7113, 1993
A;Title: Dror, a potential neurotrophic receptor gene, e
A;Reference number: A48289; WUID:93348222; PMID:8394009
A;Accession: A48289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.3%; Score 169; DB 1;
28.8%; Pred. No. 9.7e-08;
cive 27; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains: protein-tyrosine kinase (EC 2.7.1.112)
Species: Drosophila melanogaster
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCQKLPQHKDCLSLGITI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVQECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.8
Matches 38; Conservative
                                                 VQECMVHDC 131
                                                                                                                                         WNYCRLAPC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: FlyBase:bsk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212
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                                                 123
                                                                                                                               279
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Dissmin (EC 3.4.21.7) precursor - goat (fragments)
NiAlterrate names: plasminogen
NiAlterrate names: plasminogen
C;9pecies: Capra aegaquence_revision 28-oct-1994 #text_change 12-May-1995
C;Accession: C61545
R;Schaller, J; Rckii, E.E.
Enzyme 40, 63-69, 1988
A;Catuctural aspects of the plasminogen of various species.
A;Reference number: A61545; MUD:89005015; PMID:3168975
A;Accession: C61545
A;Accession: C61545
A;Residues: 1-123 <SCH>
C;Superfamily: plasmin, kringle homology; plasminogen-related protein precurso nom C;Superfamily: plasmin, kringle homology <KR4>
F;41-118/Domain: kringle homology <KR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 KKPGGO-----HCEIDKSKTCYEGNGHFYRGKASTDIMGRPCLPWNSAIV--LQQTYH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 KKLAGRSVEDCAAKCE-EBAQDCYHGNGQSYRGTSSTTVTGRKCQSWSMIPHRHQKTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
20.2%; Score 160; DB 2; Length 123;.
Best Local Similarity 34.5%; Pred. No. 1.5e-07;
Matches 38; Conservative 17; Mismatches 35; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 AHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYPNAGLIM-----NYCRNPDADKSPWCYT---TDPRVRWBFCNLKKCSB 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 38.9
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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A921869

Apolipopotein(a) (BC 3.4.21.-) - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Accession: A32869; A30848
B;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Accession: A32869; MUID:89174660; PMID:3942073
A;Accession: A1280 c/MM
A;Residues: 1-1420 c/MM
A;Residues: 1-1420 c/MM
A;Residues: 1-1420 c/MM
A;Residues: GB:Jd4635; NID:g342072; PIDN:AAA36833.1; PID:g342073
C;Superfamily: apolipoprotein(a); kringle homology c/R2>
C;Keywords: hydrolase; kringle homology c/R2>
F;50-127/Domain: kringle homology c/R2>
F;276-585/Domain: kringle homology c/R3>
F;276-585/Domain: kringle homology c/R3>
F;26-697/Domain: kringle homology c/R3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1068 CYHGHGGSYRGTFSTTVTGRTCQSWSSMTPHQHKRTPENHPNDDLTM-----NYCRNPDA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 CYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 PCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 NIHW--CN---CP-----KKFGGOHCEIDKSKT---CYEGNGHFYRGKASTDIMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

20.3%; Score 161; DB 2; Length 1420;
Best Local Similarity 40.9%; Pred. No. 9.4e-07;
Matches 36; Conservative 9; Mismatches 31; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 162.5; DB 1; Length
; Pred. No. 1.8e-06;
12; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 RRRPWCYVQVGLKPLVQE--CMVHDCAD 133
                                                                                  KR284
KR294
KR304
                           KR26>
                                                                                                                                                             KR31>
                                                                                                                                                                                                              KR33
                                                                                                                                                                                                                                          < KR34>
                                                       homology
                                                                                                                                                                                                                                                                                                                                                                F;4328-4541/Domain: trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.1%;
Matches 41; Conservative 1:
     kringle b
                                                                                                                                                                                                                                                                                                               kringle b
                                                                                                                                                                                                                                       kringle h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3856 LTQC 3859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 VHDC 131
F;2764-2841/Domain: K
F;2878-2955/Domain: K
F;292-306/Domain: K
F;3220-3297/Domain: K
F;3334-3411/Domain: K
F;348-3525/Domain: K
F;362-639/Domain: K
F;362-639/Domain: K
                                                                                                                                                                                                                                                                                                                  4124-4201/Domain:
                                                                                                                                                                                                                                    F;3782-3859/Domain:
F;3896-3973/Domain:
F;4010-4087/Domain:
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46 KSKTCYEGNGHPYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL----QLGLGKHN 100
                                                                                                                                                                                                                                                                                                                                      33 KVQECYHGNGQSYRGT8STTITGRXCQSWSSWT-----PHRHEKTPEHFPEAGL-TMN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurotrophic receptor ror1 precursor - human
N;Contains: protein-tyrosine kinase (BC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 30-Sep.1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C;Accession: A45082
                                                                                                                                                                                                                                                                                    18; Gaps
                                                                                                                                                                                                                                                          Length 120;
                                                                                                                                                                                                                                                     20.1%; Score 159; DB 2; Length 120
38.9%; Pred. No. 1.8e-07;
tive 8; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                           101 YCHNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
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10mol

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A,Accession: 803736
A,Molecule type: protein
A,Rossidues: 27-83 cBRU>
A,Rossidues: 27-83 cBRU>
A,Rossidues: 27-83 cBRU>
C,Function:
A,Description: dissolves the fibrin of blood clots; acts as a proteolytic fact; in a the walls of the graafian follicle; also activates the urokinase-type plasm. gen be the walls of the graafian follicle; also activates the urokinase-type plasm. G,Superfamily: plasmin, kringle homology; plasminogen-related protein predicted c.SiG>
C,Roywords: duplication; fibrinolysis; glycoprotein, bydrolase; kidney; kringl. F;1-26/Domain: signal sequence #status predicted c.SiG>
F;8-103/Domain: signal sequence #status experimental c.RO>
F;27-812/Product: plasminogen #status experimental c.RO>
F;104-583,584-812/Product: plasmin #status experimental c.RO>
F;104-583,584-812/Product: plasmin #status experimental c.RO>
F;192-266/Domain: kringle homology c.RR3>
F;192-266/Domain: kringle homology c.RR3>
F;282-359/Domain: kringle homology c.RR3>
F;282-359/Domain: kringle homology c.RR3>
F;284-812/Domain: plasmin chain B #status experimental c.BCH>
F;584-812/Domain: plasmin chain B #status experimental c.BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 706-743, 78, 745-812 < MAL
A,Ecsidues: 706-743, 78, 745-812 < MAL
A,Cross-references: GB:K02935; NID:9163551; PIDN:AAA30714.1; PID:9163552
B,Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Mann: Br. J. Blochen. 114, 465-470, 1991
A,Title: Comparison of the primary structure of the N-terminal CNBr fragments of the number: S03735; MUID:91212097; PMID:7238497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein A;Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH> R;Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH> R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W. Blochemistry 23, 4243-4250, 1984 A;Ritle: Characterization of a complementary deoxyribonucleic acid coding for A;Title: Characterization of a complementary deoxyribonucleic acid coding for A;Reference number: 145961; MUID:85023311; PMID:6148961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: mRNA
A, Residues: 1-812 -8BER-
A, Cross-references: BMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963
A, Experimental source: liver
A, Bxperimental source: liver
B, Note: it is uncertain whether Met-1 or Met-8 is the initiator
R, Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer
Bir. J. Biochem: 149, 267-278, 1985
A, Title: Complete amino acid sequence of bovine plasminogen. Comparison with h.
A, Reference number: A25835; MUID:88203906; PMID:3846532
                                                                                                                                                                                                             78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mid-ternate names: plasminogen
Nighternate names: plasminogen
Cispecies: Bos primidenius taurus (cattle)
Cispecies: Bos primidenius taurus (cattle)
Cispecies: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
Cispecession: S450646, A25835; I45961; S03736
Siberglund, L.; Andersen, W.D.; Petersen T.E.
Submitted to the EMBL Data Library, May 1994
A; Reference number: S45046
A; Reference number: S45046
                                                                                                                                                                                          20 KKLAGRSVEDCAAKCE-EEAQDCYHGNGQGYRGTSSTTVTGRKCQSWSSMIPHRHQKTPE
                                                                                                                                                      35 KKFGGQ-----HCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATV--LQQTYH
                                                                                           15;
                                Length 460;
                                   DB 2;
                                   19.9%; Score 157.5; DB 2; 38.2%; Pred. No. 7.6e-07; ive 13; Mismatches 27;
                                                                                                                                                                                                                                                                                  114
                                                                                                                                                                                                                                                                                                                  86 AHRSDALQLGLGKHNYCRNPDNRRRPWCY
                                                                 Similarity 38.29
                                                                                                 34;
                                   Query Match
Best Local S:
Matches 34
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S.Superfamally: neutrotrophic receptor ror; immunoglobulin homology; kringle homology; pro
C.Superfamally: neutrotrophic receptor ror! #status predicted cs1G>
F)1-23/Domain: signal sequence #status predicted cs1G>
F)24-93/Product: neutrotrophic receptor ror! #status predicted cMAT>
F)24-93/Product: neutrotrophic receptor ror! #status predicted cMAT>
F)22-133/Domain: immunoglobulin homology ckRG>
F)313-391/Domain: kringle homology ckRG>
F)44-425/Domain: transmembrane #status predicted cfMI>
F)47-55/Domain: protein kinase homology ckRN>
F)47-55/Domain: protein kinase homology ckRN>
F)47-65,184,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
R;Masiakowski, P.; Carroll, R.D.
J. Biol. Chem. 267, 26181-26190, 1992
A;Tille: A novel family of cell surface receptors with tyrosine kinase-like domain.
A;Reference number: A45082; MUID:93100347; PMID:1334494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 DETSSVPKPRDLCRDECEILENVLCQTEYIFARSNPMILMRLKLPNCEDLPQPESPEAAN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 CIRIGIPMADPINKNHKCYNSTGVDYRGTVSVTKSGRQCQPWNS----QYPHTHTFTAL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NELHQVP-----BNCDCLNGGTCVSNKYFS-----NIHWCNC-----PKKFGGQH 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-----EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Gaps
                                                                                                                                                                                                                          PID:9337465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                A;Cross-references: GB:M97675; NID:g337464; PIDN:AAA60275.1; A;Note: sequence extracted from NCBI backbone (NCBIP:120916)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.0%; Score 158.5; DB 2 Best Local Similarity 29.7%; Pred. No. 1.1e-06; Matches 43; Conservative 14; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - sheep (fragments)
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                                                                                                                                                                                                                                                                                                                      A,Gene: GDB:NTRKR1
A,Cross-references: GDB:136453
                                                                                                                                                                                          A; Residues: 1-937 < MAS>
                                                                                                                                                                   A; Molecule type: mRNA
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plasmin (EC 3.4.21.7) precursor [validated] - human plasmin (EC 3.4.21.7) precursor [misnomer] NyAlternate names: plasminogen precursor [misnomer] NyAlternate names: plasminogen precursor [misnomer] NyContains: anajoretatin; microplasmin; plasminogen C;Species: Homo sepiens (man) C;Date: 24-Apr.1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000 C;Date: 24-Apr.1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000 C;Date: 24-Apr.1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000 C;Accession: A35229 Mill; 1990 A;Peterson, T.B.; Martzan, M.R.; Ichinose, A.; Davie, E.W.

J. Biol. Chem. 265, 6104-6111, 1990 A;Peterson anumber: A35229 MID: 90202079; PMID: 2318848 A;Reference number: A35229 MID: 90202079; PMID: 2318848 A;Residues: 1-810 <PET-A;Cross-references: GB: UDS286; GB: M34276; NID: 9190064; PIDN: AAA60113.1; PID: 93: 026 A;Residues: 1-810 <PET-A;Cross-reference: leuvicoyte; lung fibroblast A;Residues: GB: UDS286; GB: M34276; NID: 9100064; PIDN: AAA60113.1; PID: 93: 026 A;Rejaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Ottoleng, S. Biochem: Biophys: Res: Commun. 173: 1013-1018, 1990 A;Reference number: 152242; MUID: 91097523; PMID: 2268308

A;Reference number: 152242; MUID: 91097523; PMID: 2268308
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Matches 34,
                                Query Match
Best Local S:
Matches 44
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A; Residues: 450-790 <a href="Mailto:MAR">Molecule type: protein
A; Residues: 450-790 <a href="Mailto:MAR">Molecule type: protein
A; Residues: 450-790 <a href="Mailto:Mar.">Molecule type: protein
A; Residues: 450-790 <a href="Mailto:Mar.">Molecule type: protein:Mar.</a>
C; Function: dissolves the fibrin of blood clots; acts as a proteolytic factor in a vans the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A; Pathway: fibrinolysis; glycoprotein; hydrolase; kidney; kringle: plasminogen #status predicted <a href="Mailto:Mar.">Molecule:Mailto:Mar.</a>
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasminogen-related protein precursor homology (fragment) <a href="Mailto:Fill-T77">Fill-T77</a>
F; 1-79</a>
Cp. Product: plasminogen-related protein precursor homology (fragment) <a href="Mailto:Fill-T77">FILL-T77</a>
F; 1-77</a>
F; 1-77</a>
Comain: Aringle homology <a href="Mailto:KRZ">KRZ</a>
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F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
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A, Accession: S03733
A, Receive type: protein
A, Residues: 1-560 excus
B, Erunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M. B, Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, A, Reference number: S03735; MUID: 81212097; PMID: 7238497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: protein
A, Residues: 1-57 c & Rickli, E.B.
R, Marti, T.; Schaller, J.; Rickli, E.B.
Eur. J. Biochem. 149, 279-285, 1985
A, Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A, Reference number: A25834; MUID: 85203907; PMID: 3846533
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N;Contains: miniplasminogen
N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03733; S03737; AZ5834
R;Schaller, J; Marti, T; Roesselet, S.J.; Kaempfer, U; Rickli, E.B.
Fibrinolysis 1, 91-102, 1987
A;Ttle: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of P; Reference number: S03733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 NRIPENFPCKNLEENYCRNPNGEKAPWCYTIN--SEVRWEYCTIPS-----CESSPLST 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 BRMDVPVPPBQTPVPQDCYHGNGQSYRGTSSTTITGRKCQSWSS-----MTPHRHLKTPE 421
                                                                                                                                                                                                                                                                                                                                                                                                                              5 HQVPSNCDCLN------GGTCVSNKYFSNIHW--CNCPKKFGGQHCEIDKSKT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                              (covalent) #status experimental
(covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                               54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 DALOLGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                   19.7%; Score 156; DB 1; Length 812; 28.3%; Pred. No. 1.7e-06; Live 12; Mismatches 53; Indels
                                              bonds: #status predicted
$\frac{13.5}\sinding site: carbohydrate (Asn) (covalent) #status e.
F;36F\sinding site: carbohydrate (Ser) (covalent) #status e.
F;624,667,762/Active site: His, Asp, Ser #status predicted
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Plasmin (EC 3.4.21.7) precursor - chicken (fragment)
NiAlternate names: plasminogen
Cippecies: Gallus gallus (chicken)
Cipate: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C;Accession: A60140
R;Gyenes, M., Patthy, L.
Biochim. Biophys. Acta 832, 326-330, 1985
A;Title: The kringle 4 domain of chicken plasminogen.
A;Reference number: A60140
A;Molecule type: protein
A;Reference number: A60140
A;Molecule type: protein
A;Residues: 189 cGYE
A;Residues: 189 cGYE
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precurso
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine pro
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasmin kringle bomology cKRG>
F;6-83,Cp-66,55-78/Pisulfide bonds: #status predicted
F;39/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                  345 APVPPEQTPVAQDCYRCNGESYRCTSSTTITCRKCQSW-----VSMTPHRHEKTPGNFPN 399
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                                                                                       Gaps
                                                                                       46;
                                                                                                                                                                      5 HOVPSNCDCLNGGTCVSNKYFSN----IHWC-NCPKKFGGQHCEIDK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 LGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 AGL-TMNYCRNPDADKSPWCXT---TDPRVRWEYCNLKKCSE 437
                                                                                   56;
ch 19.5%; Score 155; DB 1. Similarity 27.2%; Pred. No. 2e-06; 44; Conservative 16; Mismatches
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A. Hille: Structure of the omega-aminocarboxylic acid-binding sites of human pl minocarboxylic acid-binding sites of human pl minocarboxylic acid-binding sites of knumber: A5282; WID: 821539
A. McOntentes annocarboxylic acid binding sites
B. Wali, Z.; Patthy. L.
J. Biol. Chem. 259, 1660-1369, 1984
A. Willie: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are ssent annocarboxylic acid binding sites of human plasminogen. Arginines 32 and 34 are ssent annocarbox biology. B. McGa. S.; Sal. S.; McGa. S.; Mc
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RyWu, T. P.: Padmarabhan, K.; Tulinsky, A.; Mulichak, A.M.
Blochemistry 30, 10589-10594, 1991
A.Title: The refined structure of the epsilon-aminocaproic acid complex of hum. pla
A.Title: The refined structure of the epsilon-aminocaproic acid complex of hum. pla
A.Fontents: annotation, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Wes cook
Ride Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Wes cook
Biochemistry 31, 270-279, 1992
A.Title: Crystal structure of the kringle 2 domain of tissue plasminogen activ. or a
A.Fitle: Crystal structure of the kringle 2 domain of tissue plasminogen activ. or a
A.Fitle: Crystal structure of the kringle 2 domain of tissue plasminogen activ. or a
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A, Contents: annotation; conformation by (1) H-NMR, residues 103-181
R; Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A; Reference number: A65804; PDB:1HPK
A; Contents: annotation; conformation by (1) H-NMR, residues 103-181
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R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
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1r. J. Biochem. 221, 927-937, 1994
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A;Molecule type: protein
A;Residues: 20-60, 0', 51-71, E', 73-85,87-100 <WI2>
B;Wiman, B:; Wallen, P;
Fur. J. Blochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha A;Reference number: A04626; MUID:76043692; PMID:126863
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Ajrosestion: 292-471, D', 473-810 cMAL2)
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A,Residues: 581-810 <W11>
R;Wiman, B.; Wallen, P.
Bur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid" and "lysine" forms of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. L. C. C. L. W. K.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A; Title: Studies on the active center of human plasmin. Partial amino acid sequence a A; Reference number: A92048; MUID: 62234739; PMID: 4240117
A; Contents: annotation; active site
R; Trexler, M.; Vali, Z.; Patrhy T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The histidine loop of
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Eur. J. Biochem. 76, 129-137, 1977

Faritile: Primary structure of the B-chain of human plasmin. A;Reference number: A04627; MUID:77225245; PMID:142009

A;Accession: A04627
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A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Modecule type: protein
A; Reaidues: 483-507, E', 509-604 < W13>
R; Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
G. Biol. Chem. 248, 1631-1633, 1973
A; Title: The primary structure of human plasminogen. II.
A; Reference number: Ag2125; WUID:73149248; PMID:4694729
A; Contents: annotation; active site
R; Groskopf, W.R.; Summaria, L.; Robbins, K.C.
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A; Residues: 20-71, E', 73-76 <BRU>
R; Sottrup-Jensen, L.; Petersen, T.E.; Magnusson,
submitted to the Atlas, July 1977
A; Reference number: A00929
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A;Status: preliminary
A;Olecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross references: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfemily: plasmin; kringle homology; plasminogen-related protein precursor c;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine protein precursor homology <PLPH>
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine protein precursor homology <PLPH>
F;1-96/Domain: signal sequence #status predicted <SIG>
F;103-181/Domain: kringle homology <KR1>
F;385-262/Domain: kringle homology <KR2>
F;375-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR4>
F;481-661/Jo3-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352, i-33
B;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352, i-33
B;622,665,760/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 HSDAPVIVPPEQTPVVQECYQGNGQTYRGTSSİTITGKKCQPWTSMRPHRHSKTPENYPD 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 ------CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmin (EC 3.4.21.7) precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 GYRGKKATTVTGTPCQEWAA-----QEPHSHRIFTPETNPRAGLEK-NYCRNPDGDVGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 NPDADKGPWCFTTDPSVRWEYCNLKKCSGTEGSVAAPPPVAQLPDAETPSEEDCMFGNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 QVPSNCDCLN-------GGTCVSNKYFSNIHW--CNCPKKFGGQHCBIDKSKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                       precursor homology <PLPH>
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R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Accession: B32869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        .8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                           BB
                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 153.5;
; Pred. No. 2.8e
12; Mismatches
                          C;Keywords: hydrolase; serine proteinase F;1-96/Domain: plasminogen-related protein F;103-181/Domain: kringle homology «KR1>F;185-262/Domain: kringle homology «KR2>F;275-352/Domain: kringle homology «KR3>F;379-456/Domain: kringle homology «KR4>F;480-61/Domain: kringle homology «KR5>F;80-61/Domain: kringle homology «KR5>F;80-61/Domain: kringle homology «KR5>F;80-61/Domain: kringle homology «KR5>F)582-803/Domain: trypsin homology «TRX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 ADLTM---NYCRNPDGDKGPWCY 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 LOLGLGKHNYCRNPDNRRRPWCY 114
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Best Local Similarity 2,...
Local 39, Conservative
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Best Local Similarity
Matches 45; Conserv
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A; Pathway: fibrinolysis
C; Superfamily: plasmin, kringle homology; plasminogen-related protein precursor homology
C; Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
F; 1-96/Domain: plasminogen-related protein precursor homology «PLPH»
F; 1-96/Domain: plasminogen-related protein precursor homology «PLPH»
F; 1-96/Domain: plasminogen #status experimental «PRO»
F; 20-810/Product: plasmin matter experimental «PRO»
F; 79-466/Product: angiostatin #status experimental «MAT»
F; 77-466/Product: plasmin matter experimental «MAT»
F; 77-466/Product: plasmin matter experimental «CHA»
F; 78-262/Domain: kringle homology «KR1»
F; 18-262/Domain: kringle homology «KR3»
F; 275-352/Domain: kringle homology «KR3»
F; 377-444/Domain: kringle homology «KR3»
F; 377-444/Domain: kringle homology «KR3»
F; 377-444/Domain: kringle homology «KR3»
F; 378-360,580,581-810/Product: microplasmin #status experimental «WMT»
A;Reference number: S43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Bur. J. Biochem. 221, 939-499, 1994
A;Title: Sclution structure of the epsilon-aminohexanoic acid complex of human plasminog
A;Reference number: A58817; MUID:94237158; PMID:8181476
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many ot
C;Comment: Plasminogen is convexted to plasmin by plasminogen activators (see PIR:UKHU a
C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af
C;Comment: Plasmin is formed by autolytic cleavage of plasmin under artificial cond
C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. Te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pissmin (EC 3.4.21.7) precursor - western European hedgehog
Cispecies: Erinaceus europaeus (western European hedgehog)
Cispecies: Erinaceus europaeus (western European hedgehog)
Cispecies: Erinaceus europaeus (western European hedgehog)
Ciscession: 146260
Ciscession: 146260
Ciscession: 164260
Cisc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 PTAPPELTPVVQDCYHGDGQSYRGTSSTTTTGKKCQSWSS-----MTPHRHQKTPENYPN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 HOVPSNCDCLNGGTCVSNKYFSN----IHWCNCP-KKFGGQHCEI---DKS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 28.0
45; Conservative
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A;Gene: GDB:PLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
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Matches 4
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A, Accession: $48203
A, Accession: $48203
A, Accession: $48203
A, Molecule type: protein
A, Residues: $2-27 < Li2>
C, Comment: Plasminogen is converted into plasmin by plasminogen activators, be c; comment: Plasminogen is converted into plasmin by plasminogen activators, be c; comment: Plasminogen is converted into plasmino by plasminogen activators, be activation plasminogen is converted into plasminogen coft the inhibitor, en activation involves also removal of the activation peptide.
C, Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angion of plasminogen treating solid tumors.
C, Punction: alsolves the fibrin of blood clots; acts as a proteolytic fact in a site walls of the graafian follicle; also activates the urokinase-type plasm as the walls of the graafian follicle; also activates the urokinase-type plasm and pathona; in plasminogen-related protein precursor homology companies in angiogenesis inhibitor; blood; tuplication; fibrinolysis; glycopro (F;1-56/Domain: plasminogen-related protein predicted cARD>
F;20-96/Domain: activation peptide #status predicted cARD>
F;20-96/Domain: activation peptide #status predicted cARD>
F;37-444,Domain: chain A #status predicted cARD>
F;37-444,Domain: kringle homology cRRD>
F;37-444,Domain: kringle homology cRRD>
F;37-454,Domain: kringle homology cRRD>
F;38-805/Domain: kringle hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmin (EC 3.4.21.7) precursor - mouse
N; Contains: anglostatin; plasminogen
C; Species: Mus musculus (house)
C; Species: Mus musculus (house)
C; Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C; Accession: A38514; S48202; $38203
R; Pbegen, S.U.F.; Bell, 1990
A; Title: Characterization of the CDNA coding for mouse plasminogen and localiz
A; Reference number: A38514; MUID: 9184812; PMID: 2081600
A; Accession: A38514
A; Molecule type: mRNA
A; Residues: 1-812 < DECA
A; Residues: 1-812 < DECA
A; Residues: 1-812 < DECA
A; Cross-references: GB: J04766; NID: 9200402; PIDN: AAAS0168.1; PID: 9200403
R; Lijnen, H:R; van Hoef, B:; Beelen, V:; Collen, D.
B; U: J: Bicchem: 224, 863-871, 1994
A; Title: Characterization of the murine plasma fibrinolytic system.
A; Reference number: $48202; MUID: 95010076; PMID: 7523120
299 NCMRIGIPAERLGRYH------QCYNGSGMDYRGTASTTKSGHQCQPW--ALQHPHSHH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;78-79/Cleavage site: Glu-Aan (atromelysin 1) #status predicted
F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;466-467/Cleavage site: Thr-val (stromelysin 1) #status predicted
F;501-582/Cleavage site: Arg-val (plasminogen activator) #status experimental
F;501-582/Cleavage site: Arg-val Asp, Ser #status predicted
                                                                                                                                                                                                  86 AHRSDALQLGLGKHNYCRNPDNRRR-PWCYVQVGLKPLVQECMVHDCA 132
                                                                                                                                                                                                                                                                            350 LSSTDFPELG-GGHAYCRNPGGQMEGPWCFTQ-NKNVRMELCDVPSCS 395
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18.5%; Score 147; DB 1; Length 81
Best Local Similarity 26.4%; Pred. No. 1.1e-05;
Matches 42; Conservative 21; Mismatches 56; Indels
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A/Map position: 6p21-6p21

A/Map position: 6p21-6p21

A/Map position: 6p21-6p21

A/Map position: 6p21-6p21

C/Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringle homology; procycledin; kringle; phosphotraneferase; transmembrane protein; tyros F;1-27/Domain: signal sequence #status predicted <SIG>
F;18-937/Product: neurotrophic receptor ror2 #status predicted <MAI>
F;7-137/Domain: immunoglobulin homology <IMM>
F;316-394/Domain: transmembrane #status predicted <TMN>
F;412-484/Domain: protein kinase homology <IMN>
F;471-753/Domain: protein kinase APP-binding motif
F;70,188;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein precursor homology
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C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C; Accession: B45082 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
R; Masiakowski, P.; Carroll, R.D.
J; Biol. Chem. 267, 26181-26190, 1992
A; Title: A novel family of cell surface receptors with tyrosine kinase-like domain. A; Reference number: A45082; MUID: 93100347; PMID: 1334494
                                                            A/3022

Plasmin (EC 3.4.21.7) precursor - rat (fragment)

C.Species: Rattus norvegicus (Norway rat)

C.Species: Rattus norvegicus (Norway rat)

C.Jate: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999

C.Jate: 28-Feb-1992 #sequence_revision 05-Feb-1993 #text_change 16-Jul-1999

A.Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a recept A.Feference number: A40522; MUID:91250378; PMID:1645711

A.Feference number: A40522; MUID:91250378; PMID:1645711

A.Status: preliminary

A.Gress-references: GB:M62832; NID:9206215; PIDN:AAA41884.1; PID:9554488

A.Gross-references: GB:M62832; PIDN:AAA41884.1; PID:9554488

A.Gross-references: GB:M62832; PIDN:AAA41884.1; PI
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A;Residuss: 1-943 <MAS>
A;Residuss: 1-943 <MAS>
A;Cross-references: GB:M97639; NID:g337466; PIDN:AAA60276.1; PID:g337467
A;Note: sequence extracted from NCBI backbone (NCBIP:120918)
C;Genetics:
A;Gene: GDB:NTRKR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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18.7%; Score 148; DB 2; Length 943;
Best Local Similarity 34.3%; Pred. No. 9.9e-06;
Matches 37; Conservative 12; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
19.2%; Score 152; DB 2; Length 169;
Best Local Similarity 32.2%; Pred. No. 1e-06;
Matches 39; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurotrophic receptor ror2 precursor - human
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B45082
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A;Molecule type: protein
A;Residues: 230-247;288-291,'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-3 :326-3
A;Experimental source: plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Gene: GDB:MST1; D3F15S2; DNF15S2; HGFL
A/Cross-references: GDB:128833; OMIM:142408
A/MSD position: 3p21-3p21.3
A/MSD position: 2p21-3p21.3
A/MSD position: 2p21-3p21.3
A/MSD position: 2p21-3p21.3
A/MSD position: 2p21-3p21.3
C;Complex: disulfide-bonded heterodimer of chains derived from the same precur: C;Complex: disulfide-bonded heterodimer of chains derived from the same precur: C;Complex: display: hepatocyte growth factor; kringle homology
C;Keywords: duplication; glycoprotein; growth factor; kringle; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>F;19-483,484-711/Product: macrophage-stimulating protein 1 #status predicted 
F;110-166/Domain: kringle homology <KR2>F;110-166/Domain: kringle homology <KR2>F;23-364/Domain: kringle homology <KR2>F;370-448/Domain: kringle homology <KR3>F;370-448/Domain: trypsin homology <KR3>F;484-711/Domain: beta chain #status predicted <BGH>F;370-263,283-361,304-343, 7-35F;55-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343, F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: protein
A, Residues: 1-33;34-117 <SCH>
A, Residues: 1-33;34-117 <SCH>
A, Residues: 1-33;34-117 <SCH>
B, Schaller, U.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A, Title: Complete amino acid sequence of equine miniplasminogen.
A, Recession: S17527; MUID: 92052077; PMID: 1946332
A, Molecule type: protein
A, Rocession: S17627
A, Molecule type: protein
A, Rocession: S17627
A, Molecule type: protein
A, Residues: 118-455 <SC2>
C, Superfamily: plasmin, kringle homology; plasminogen-related protein precurse C, Reywords: fibrinolysis: glycoprotein; hydrolase; kringle; plasmin profession; hydrolase; kringle; plasmin esting profession; hydrolase; kringle; plasmin estingle; plasmin estingle; plasmin estingle; plasmin estivation peptide (fragment) #status experimental <APT>
F;1-33/Domain: activation peptide (fragment) #status experimental <APT>
F;1-17,118-225,226-455/Product: plasmin (fragments) #status experimental <APT>
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A;Cross-references: GB:L11924; NID:G398037; PIDN:AAA59872.1; PID:G398038
A;Note: authors translated the codon TTT for residue 623 as Leu; parts of this R;Skeel, A; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, J. Exp. Med. 173, 1227-1234, 1991
A;Title: Macrosphage stimulating protein: purification, partial amino acid sequal, R;Reference number: A61395; MUID:91217635; PMID:1827141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 ATVLQQTYHAHRSDALQLGLG--KHNYCRNPDNRRRPWCYVQVGLKPLVQBC----MVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 -----QIPHQHRFTPEKYACKDLRENFCRNPDGSEAPWCFT---LRPGMRAAFCYQIRRC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disamin (EC 3.4.21.7) precursor - horse (fragments)
NiAlternate names: plasminogen
NiContains: miniplasminogen
NiContains: miniplasminogen
O(species: Equus caballus (domestic horse)
C(species: Equus caballus (domestic horse)
C(species: A61545; 817527
C(species)
C(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 WC-NCPKKFGGQHCEIDK-----SKTCYEGNGHFYRGKASIDIMGRPCLPWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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18.2%; Score 144; DB 1; Length 711;
Best Local Similarity 27.0%; Pred. No. 1.8e-05;
Matches 33; Conservative 19; Mismatches 44; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 Ap 133
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Macrophage-stimulating protein 1 precursor - human

C; Specesion: A4031; May-1994 #sequence revision 14-Nov-1997 #text_change 18-Jun-1999

C; Accession: A4031; B40331; A47136; A61395

R; Han, S; Stuart, L.A.; Degen, S.J.F.

Biochemistry 30, 9768-9780, 1991

A; Title: Characterization of the DNF15S2 locus on human chromosome 3: identification of A; Reference number: A40331 MUID:92002016; PMID:1655021

A; Accession: A40331

A; Molecule type: DNA

A; Residues: 1-711 < HAI>
A; Molecule type: BNA

A; Residues: B40331

A; Molecule type: MRNA

A; Residues: 1-711 < HAI>
A; Cross-references: GB:M74179

A; Cross-references: GB:M74179

A; Cross-references: GB:M74179

A; Cross-references: GB:M74179

A; Cross-references: GB:M74178; NID:9183976; PIDN:AA50165.1; PID:9183977

B; Yoshimura, T; Yuhki, N; Wang, M; H; Skeel, A; Leonard, E.J.
J; Biol: Chem. 268, 15461-15468, 1993

A; Title: Cloning, sequencing, and expression of human macrophage stimulating protein (MS A; Residues: A47136; MUID:93340141; PMID:8393443

A; Residues: 1-12, C', 14-622, F', 624-711 < YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 STALQSSPVAEVNRGHLTHWCYVNSGTQYEGTVAQTSSGKQCAPWIDST--SRDFNVHRF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A) Reference number: Z19029
A) Reference number: Z19029
A) Reference number: Z19029
A) Accession: T18840
A) Status: prefilminary; translated from GB/EMBL/DDBJ
A) Residues: 1-806 «WIL>
A) Residues: 1-806 «WIL>
A) Cross-references: EMBL:Z35595; PIDN:CAA84639.1; GSPDB:GN00020; CESP:C01G6.8
A) Experimental source: clone C01G6
C) Genetics: CSP:C01G6.8
A) Residues: CSP:C01G6.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                            43 -----EIDK---SKTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRS 89
                                                                                      308 NRTPENFPCKN----LEENYCRNPDGETAPWCYTTDSQLRWEYCEIPSCESSASPDQSDS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C01G6.8 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T18840
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                                                                                                                                                                                                   ---KICYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
18.2%; Score 144.5; DB 2; Length 8(
Best Local Similarity 25.5%; Pred. No. 1.8e-05;
Matches 42; Conservative 25; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 -EMNYCRNPDGDKGPWCYT---TDPSVRWBYCNLKRCSE 456
                                                                                                                                                                                                                                                                                                                                                                                                            97 GKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Map position: 2
A,Introns: 36/3; 170/3; 217/3; 636/3; 760/1
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Gaps

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455; DB 2; Length F,37-114/Domain: kringle homology <KR4>
F,118-455/Product: miniplasminogen #status experimental <MIN>F,126-205/Domain: kringle homology <KR5>
F,226-455/Domain: plasmin chingle #status experimental <BCH>F,226-445/Domain: trypsin homology <RR>
F,226-448/Domain: trypsin homology <RR>
F,265-448/Domain: trypsin homology <RR>
F,267,310,405/Active site: His, Asp, Ser #status predicted

Gaps 13; Indels Ouery Match
17.8%; Score 141.5; DB 2;
Best Local Similarity 33.7%; Pred. No. 2.1e-05;
Matches 33; Conservative 15; Mismatches 37;

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OHCEIDKSKTCYEGNGHFYRGKASTDIMGRPCLPWNSATV--LQQTYHAHRSDALQLGLG 97 40 28 g ઠે

KHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133 --NYCRNPDGDKGPWCYT---TDPSVRWEFCNLRKCSE 98 84

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hepatocyte growth factor precursor [validated] - human N'Alternate names: hepapoietin A; scatter factor C; Species: Homo sapiens (man) (c) Species: Homo sapiens (man) (c) Species: Homo sapiens (man) (c) Species: 17-40g-1992 #sequence revision 17-Aug-1992 #text_change 08-Dec-2000 (c) Accession: JH0579; JU0333; A41140; B3677; A33677; A33512; A39006; PH0114; A37796; S06 R: Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S. Gene 102, 213-219; 1991 A; Title: Organization of the human hepatocyte growth factor-encoding gene. A; Reference number: JH0579; MUID: 91340155; PMID:1831432

A;Accession: JH0579
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DBU-1D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
A;Note: the authors translated the codon GAA for residue 662 as Gly
B;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JU0333

A,Accession. Junuaci: UU0333
A,Accession. August: UU0333
A,Accession. Boba
A,Rocession. Acad. SE2>
A,Rocession. Acad. SE2>
A,Title: Evidence for the identity of human scatter factor and human hepatocyte growth farmaticle: Evidence for the identity of human scatter factor and human hepatocyte growth farmaticle: Evidence for the identity of human scatter factor and human hepatocyte growth farmanear. Ad1140
A,Rocession: A41140
A,Rocession: A41140
A,Molecule type: mRNA
A,Molecule typ

A,Molecule type: mRNA A,Residues: 1-728 <SE3> A;Cross-references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032 A,Accession: A36677

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A; Experimental source: leukocyte
R; Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
B; Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
A; Mitle: Molecular commun. 163, 967-973, 1988
A; Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte growth factors and sequence analysis of cDNA for human hepatocyte g

A;Status: not compared with conceptual translation A;Molecule type: mRNA

A;Molecule type: mRNA A;Residues: 1-728 <MIY> A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846

epatc R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast derived mitogen is a variant or lepa A;Reference number: A39006; WID:91110540; PMID:1824873
A;Accession: A39006
A;Molecule type: mRNA
A;Residues: 1-161,167-728 - RUB>
A;Experimental source: embryonic lung
R;Yosshiyama, Y.; Arakaki, N.; Naka, D; Takahashi, K.; Hirono, S.; Kondo, J.; Caya B; Cosshiyama, Y.; Arakaki, N.; Naka, D; R; Kober, D; R; Kondo, J.; Caya B; Cosshiyama, Y.; Arakaki, N.; Naka, D; R; Kober, Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both n. Lve A;Reference number: PH0114, MUID:91207365; PMID:1826837
A;Rossidues: 32-43,53-58 - KVS>
A;Roperimental source: plasma
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2018, 1990
A;Title: Scatter factor: molecular characteristics and effect on the invasiven. For A;Reference number: A37796; MUID:91035621; PMID:2146276
A;Rossidues: A37796; MUID:91035621; PMID:2146276

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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 161-166 <SHI>
A; Residues: 161-166 <SHI>
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A; Map position: 7q21.1-7q21.1
A; Map position: 7q21.1-7q21.1
C; Complex: disulfide-bonded heterodimer of chains derived from the same precur: C; Function:

lle; Ÿ, A,Description: stimulates mitosis of hepatocytes and other cells A,Note: does not have proteinase activity C,Superfamily: hepatocyte growth factor; kringle homology; trypsin homology C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer;

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C; Accession: 151283
R; Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
Mech. Dev. 49, 123-131, 1995
A; Title: Molecular cloning of Xenopus HGF CDNA and its expression studies in X: pus A; A; Accession: 151283; MUID:95267690; PMID:7748783
A; Reference number: 151283; MUID:95267690; PMID:7748783
A; Reference number: 151283; MUID:95267690; PMID:7748783
A; Accession: 151283
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Cross-references: GB:577422; NID:998932; PIDN:AAB34354.1; PID:998933
A; Cross-references: GB:577422; NID:998932; PIDN:AAB34354.1; PID:998833
A; Cross-references: GB:577422; NID:998932; PIDN:AAB34354.1; PID:998833
A; Molecule type: mRNA
A; Roule to authors' translation for residue 458 (Thr) is inconsistent with th: C; Function: stimulates mitosis of hepatocytes and other cells
A; Note: does not have proteinase activity
C; Function:
A; Description: stimulates mitosis of hepatocytes and other cells
A; Note: does not have proteinase activity
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F; A2-477, A79 = TO9; Product: hepatocyte growth factor alpha chain #status predicted cACH>
F; A18-779 Domain: kringle homology ckR2>
F; A18-779 Domain: kringle homology ckR2>
F; A18-779 Domain: kringle homology ckR2>
F; A18-770 Domain: hepatocyte growth factor beta chain #status predicted caCH>
F; A18-770 Domain: trypsin homology ckR2>
F; A18-770 Domain: trypsin homol
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Nylternate names: hepatocyte growth factor-like protein
Cygecies: Wis musculus (house mouse)
Cybate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
Cyacession: A40332; B40332
Rybean, S.U.P.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991
A;itle: Characterization of the mouse cDNA and gene coding for a hepatocyte g. vth
A;Reference mumber: A40332; MUD:9202017; PMID:1832957
A;Accession: A40332
A;Molecule type: DNA
A;Residues: 1-716 abgs
A;Accession: B40332
A;Molecule type: DNA
A;Residues: 1-716 abgs
A;Accession: B40332
A;Accession: B403333
A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LHQ-VPSNCDC--LNGGTCVSNKYFSNIHWC-----NCPKKFGGQHCEIDKSKTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 141; DB 1;
29.2%; Pred. No. 3.4e-05;
iive 12; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 RPWCYVQVGLKPLV--QECMVHDC 131
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42; Conser
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C;Species: dallus gallus (chicken)
C;Species: dallus gallus (chicken)
C;Accession: 151285
C;Accession: 151285
R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin
A;Reference number: 151285
A;Reference number: 151285
A;Gession: 151285
A;Reference number: MNA
A;Residues: 1411 cSTR
A;Molecule type: mRNA
A;Residues: 1411 cSTR
A;Coss references: GB:S77480; NID:g998675; PID:g998676
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
F;204-279/Domain: kringle homology cKR>
F;206-374/Domain: kringle homology cKR>
F;206-374/Domain: kringle homology cKR>
                                                                                                                                                                                                                                                                                                                                                                                 experimen
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>
F:32-494/Domain: alpha chain #status experimental <ACH>
F:22-94/Domain: alpha chain #status experimental <ACH>
F:318-206/Domain: kringle homology <KR2>
F:305-383/Domain: kringle homology <KR3>
F:305-383/Domain: kringle homology <KR4>
F:395-728/Domain: kringle homology <KR4>
F:495-728/Domain: beta chain #status experimental <BCH>
F:495-728/Domain: trypsin homology <FR4>
F:395-Modified site: pyrrolidomology <FR4>
F:324,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted F:487-604/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GNGKNYMGNLSQTRSGLTCSMWDKN---MEDLHRHIFWEPDASKL---NENYCRNPDDDA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 NSATVLQQTYHAHR--SDALQLGLGKHNYCRNPDNRRRPWCY----VQVGLKPLVQBCM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
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hepstcoyte growth factor precursor - clawed frog
N/Alternate names: hepspoietin A; scatter factor
C/Species: Xenopus sp. (clawed frog)
C/Species: Xenopus sp. (clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEHDMTPENFKCKDLRENYC-RNPDGSESPWCFTTDPNIRVGYCSQ1PNCDMSHGQDCYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NELHQVPSNCDC--LNGGTCVSNKYFSNIHWC-----NCPKKFGGQ--HCEIDKSKTCYE
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30.3%; Pred. No. 3.1e-05;
ive 12; Mismatches 64
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37; Conservative
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AjStatus: preliminary
AjMolecule type: protein
AjMolecule type: Aj Behrens, J.; Gherardi, E.; Birchmeier, W.
Aj Biol. Chem. 270, 830-836, 1995
AjTitle: Characterization of the scatter factor/hepatocyte growth factor gene
AjMolecension: I48758; MUID:95122532; PMID:7822318
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A) Reference number: $4521

A) Accession: $45521

A) Accession: $45521

A) Accession: $45521

A) Cocur type: mRNA

A) Residues: 1-53, 4", 555-728 <LI2>
A) Coster, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.

R) Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.

A) This Cocur to and characterization of biologically active scatter fact.

A) Reference number: $17173; MUID:91354223; PMID:1831975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Afforced type: protein
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence revision 26-May-1994 #text change 16-Jun-2000
C;Date: 03-Mar-1993 #sequence revision 26-May-1994 #text change 16-Jun-2000
C;Accession: JC2117; PC2064; A60185; S44416; S45521; S11773; S10966; I48758; J
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J
Biochem. Biophys Res Commun. 199, 772-779, 1994
A;Title: Identification of mouse mammary fibroblast-derived mammary growth factorer number: JC2117; MUID:94183257; PMID:8135822
                                                                                                            391 DCYRGNGKNYMGNLSKTRSGLTCSMWDKN---MEDLHRHIFWEPDASKL---TKNYCRNP
           TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH----RSDALQLGLGKHNYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-728 <BAS2>
A,Cross-references: GB:D10212; NID:g220435; PIDN:BAA01064.1; PID:g220436
A,Experimental source: fibroblast, COS-1 cell
A,NOTE: submitted to JIPID, May 1993
A,Accession: PC2064
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A,Residues: 496-517, 77, 519 <COF>
R,Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A,Title: Hepatocytes and scatter factor.
A;Reference number: $10966; MUID:90326152; PMID:2142751
                                                                                                                                                                                                                                                                                                                               470
                                                                                                                                                                                                                                                                                                                         445 DDDAHGPWCYTG---NPLVPWDYCPISRC
                                                                                                                                                                                                                              106 - DNRRRPWCYVQVGLKPLV - - QECMVHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatocyte growth factor precursor
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A, MoLecule type: mRNA
A, Residues: 1.728 < LIU>
A, Cross-references: EMBL:X72307
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A;Note: does not have proteinase activity
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Superfamily: hepatocyte growth factor growth factor; heterodimer; kringle; pyn
B;1-32/Domain: signal sequence #status predicted <&IGs
F;56-495/Porduct: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;26-207/Domain: kringle homology <KR2>
F;36-394/Domain: kringle homology <KR3>
F;36-347/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;392-470/Domain: kringle 
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A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
Bur. J. alochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur
A;Reference number: S13211; MUID:91031482; PMID:2146117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; Nakamur
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Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of
A;Reference number: A35644; MUID:90222197; PMID:2139229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Accession: S13211
A/Status: preliminary
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-728 <0KA>
A/COSS-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDITPENFKCKDLRENYC-RNPDGAESPWCFTTDPNIRVGYCSQIPK-----CDVSSGQ 390
F;191-268/Domain: kringle homology <KR2>
F;290-370/Domain: kringle homology <KR3>
F;370-457/Domain: kringle homology <KR4>
F;484-711/Domain: kringle homology <KR4>
F;484-711/Domain: beta chain #stauts experimental <BCH>
F;489-709/Domain: trypsin homology <TRY>
F;789-709/Domain: crypsin homology <TRY>
F;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WCYTINESVEF--QSCGI---KTCREAVCVLCNGEDYRGEVDVTESGRECQRWD----L 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WC---NCPKKFGGQHCEIDKSKTCYEG-----NGHFYRGKASTDTMGRPCLPWNSATVLQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternate names: hepapoietin A; scatter factor
Species: Rattus norvegicus (Norway rat)
Date: 28-Sep-1990 #sequence revision 18-Nov-1992 #text_change 21-Jul-2000
Accession: A35644; S13211
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                                                                                                                                                                                                                                                                                                                                                                             17.5%; Score 139; DB 1; Length 716; 39.6%; Pred. No. 5.1e-05; ive 4; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OHPHSHPFQPEKFLDKDL-KDNÝCRNPDGSERPWCY 252
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nes 38; Conservative
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A;Molecule type: mRNA
A;Residues: 1-728 <TAS>
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A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-30 <res> A,Gross-references: EMBL:X81630; NID:g673451; PIDN:CAA57286.1; PID:g673452 C,Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Punction: S;Description: stimulates mitosis of heperocytes and other cells A,More: Adoes not have profeines activity</res>	Db 168 WCYTTNRSVRFOSCGIKSCREAUCUWCNGEDYRGEVDVTESGRECQRWDLQHPHS 222 QY 82 QTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCY 114 Db 223 HPFHPEKFPDKALKDNYCRNPDASERPWCY 252
	RESULT 49 T18518 apolipoprotein(a) - western European hedgehog (fragment) C;species: Erinaceus europaeus (western European hedgehog) C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999 C;Accession: T18518 R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, 10.; Fc R;Lawn, R.M.; 270, 24004-24009, 1995 A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog a) lipopx
496-728/Domain: hepatocyte growth factor beta chain #status predicted <bch 496-719="" <try="" domain:="" homology="" trypsin=""> 33/Modified bomain: trypsin homology <try> 33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #stat 295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted 488-607/Disulfide bonds: #status predicted Query Match 17.5%; Score 139; DB 1; Length 728; Best Local Similarity 28.9%; Pred, No. 5.2e-05;</try></bch>	A, Reference number: 146259; MUID:96025/78; FMID:759259/ A, Accession: T18518 A, Accession: T18518 A, Residues: 1-2869 < LAWA A, Residues: 1-2869 < LAWA A, Residues: T2869 < LAWA A, Residues: EMBL:033170; NID:g1046358; PID:g1046359; PIDN:AAC48522.1 A, Experimental source: liver C, Comment: The lipoprotein Lp(a), a major inherited risk factor for atheroscle sis, c
Matches 43; Conservative 11; Mismatches 5/; Indels 58; Gaps 11; Qy S HQV-PSNCDCINGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSK 48	ent apolipopioceinta). Query Match Best Local Similarity 30.8%; Pred. No. 0.00028; Matches 32; Conservative 8; Mismatches 47; Indels 17; Gaps 4
QY 49 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNP 105	QY 19 CVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYBGNGHFYRGKASTDIMGRP 70
Qy 106 -DNRRRPWCYVQVGLKPLVQECMVHDC 131	QY 71 CLPMNSATVLQQTYHAHRSDALQLGKGKHYYCRNPDNRRRPWCY 114
RESULT 48 JC5061 macrophage-stimulating protein 1 precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000	RESULT 50 \$33879 plasmin precursor - lamprey (fragments) N;Alternate names: plasminogen N;Alternate perconyzontidae gen. sp. (lamprey) C;Bpcies: Petronyzontidae gen. sp. (lamprey)
Cyfactestain: Uccommin. 2270. Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu, N. Biochem. Biophys. Res. Commun. 227, 273-280, 1996 A.; Title: Wolecular cloning of rat macrophage-stimulating protein and its involvement in A.; Reference number: JCSO61, MUID:97011126; PMID:8858136 A. Accession: JCSO61, MUID:97011126; PMID:8858136	cid sequence of 1
A, Nolecule - type: mana, A, Residues: 1-716 <0HS> A; Residues: 1-716 <0HS> A; Cross-references: EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PID:g1669719 C; Complex: disulfade-bonded heterodimer of chains destived from the same precursor C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology C; Keywords: duplication; glycoprotein; growth factor; kringle	A;Scatus: preliminary A;Molecule type: protein A;Molecule type: protein A;Molecule type: protein A;Molecule type: plasmin; Xingle homology; plasminogen-related protein precurso nomolo C;Superfamily: plasmin; Kringle homology; plasminogen-related protein precurso nomolo F;81-146/Domain: kringle homology <rr3></rr3>
F;1-31/Domain: signal sequence #status predicted <sig> F;12-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <amt> F;32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ach> F;110-186/Domain: kringle homology <krii></krii></ach></amt></sig>	Query Match Best Local Similarity 30.7%; Pred. No. 5e-05; Matches 31; Conservative 7; Mismatches 41; Indels 22; Gaps 3
F;191-26B/Domain: Kringle nomology <kk12> F;292-370/Domain: kringle homology <kk13> F;379-457/Domain: kringle homology <kr14> F;379-457/Domain: macrophage-stimulating protein 1 beta chain #status predicted <bch></bch></kr14></kk13></kk12>	OY 34 PKKFGGQHCEIDKSKTCYBGNGHFYRGKASTDIMGRPCLPWNSATVLQOTYHAHRSDALO 93
F;489-709/Domain: trypsin homology <try> F;72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted</try>	QY 94 LGLGKGHYCRNPDNRRRPWCYVQVGLKPLVQBCMVHDCADG 134
Query Match 17.4%; Score 138; DB 1; Length 716; Best Local Similarity 36.6%; Pred. No. 6.3e-05; Matches 34; Conservative 6; Mismatches 37; Indels 16; Gaps 5;	Db 116 CQGLVSNYCRNPDGEKLPWCYTTEYCNVPSCTGG 149 Search completed: May 25, 2004, 14:58:29

Search completed: May 25, 2004, 14:58:29 Job time : 8.80894 secs

30 WC---NCPKKFGGQHCEIDKSKTCYEG----NGHFYRGKASTDTMGRPCLPWNSATVLQ 81

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SwissProt_42:*

Database :

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PLMN MACMU	PLMN RAT	KRM2 HUMAN	ROR2 HUMAN	ROR2 MOUSE	PLMN MOUSE	KRM2 MOUSE	HGFL_HUMAN	HGF HUMAN	PLMN CANFA	HGFL MOUSE	HGF MOUSE	HGF_RAT	PLMN PETMA	THRE MOUSE	THRB HUMAN	ROR2 DROME	PLMN SHEEP	NOTC_XENLA	THRB_BOVIN	THRB_RAT	JAG2_HUMAN	NTC2 HUMAN	JAG1_BRARE	PGCA_CHICK	PLMN HORSE	JAG3_BRARE	PGCN_HUMAN	NTC2_MOUSE	CRBH_HUMAN	DLL4_MOUSE	NTC1 HUMAN	NOTC_DROME	WIF1 HUMAN	DLL3 HUMAN	JAG2_RAT	NTC2 RAT	NTC1 RAT	CLR1 HUMAN	CRB DROME	4.	NTC1_MOUSE
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ALIGNMENTS

complete amino acid sequence of low molecular mass urokinase

Tue May 25 15:05:07 2004

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TISSUELLURE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDILINE=6520359; Pubmed=3888571;
Jacobs P., Cravador A., Loriau R., Brockly F., Colau B., Chuchana P.,
Van Elsen A., Herzog A., Bollen A.,
"Molecular cloning, sequencing, and expression in Escherichia coli of
human preprourokinase CDNA.";
DNA 4:139-146(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Reference of the property of the E.L., Poel C.L., Yi Steder M.J., Carrington D.P., Chung M.-W., Lee K.L., Foel C.L., Yi Nickerson D.A., Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-83055084; Pubmed-6754569;
Gunzler W.A., Steffens G.J., Otting F., Kim S.-M.A., Frankus E.,
                                                                                                                 MEDLINE-86056954; PubMed=2415429;
Nagai M., Hiramatsu R., Kaneda T., Hayasuke N., Arimura H.,
Nishida M., Suyama T.;
Molecular cloning of cDNA coding for human preprourokinase.";
Gene 36:183-188(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 156-176 AND 179-224.
MEDLINE=83003608; PubMed=6749491;
Schaller J', Nick H., Rickli E.E., Gillessen D., Lergier W., Studer R.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 81:4727-4731(1984)
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Biotechnology 3:923-929(1985).
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SEQUENCE OF 158-410. MEDLINE=83055099; PubMed=6754572; Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe

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X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 159-411.
MEDLINB=20266327; Pubmed=10805774;
Speatl S., Jacob U., Arroyo de Prada N., Sturzebecher J., Wilhelm O.G., Bode W., Magdolen V., Huber R., Moroder L.;
E(4-aminomethyl)phenyljumaintaine derivatives as nonpeptidic highly selective inhibitors of human urokinase.";
Proc. Natl. Acad. Sci. U.S.A. 97:5113-5118(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93003110; PubMed=1327118;
Li X., Smith R.A.G., Dobson C.M.;
"Sequential IH NMR assignments and secondary structure of the kringle
domain from urokinase.";
Biochemistry 31:9562-9571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR. MEDINE-89127526; PubMed=2536903; Oswald R.E., Bogusky M.J., Bamberger M., Smith R.A.G., Dobson C.M.; Ibynamics of the multidomain fibrinolytic protein urokinase from two-dimensional NMR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conne B., Berczy M., Belin D.;
"Detection of polymorphisms in the human urokinase-type plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96186279; PubMed-8652631;
Yoshimoto M., Ushiyama Y., Sakai M., Tamaki S., Hara H., Takahashi
Sawasaki Y., Hanada K.;
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MEDLINE-94149701, PubMed-8107091,
Li X., Bokman A.M., Llinas M., Smith R.A.G., Dobson C.M.;
"Solution structure of the kringle domain from urokinase-type blasminoden activator.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of single chain urokinase-type plasminogen activator with a novel amino-acid substitution in the kringle
                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDINE=$6000888; PubMed=$8591045;
Spraggon G.P., Phillips C., Nowak U.K., Ponting C.P., Saunders
Dobson C.M., Stuart D.I., Jones E.Y.;
The crystal structure of the catalytic domain of human
urokinase-type plasminogen activator:";
Structure 3:681-691(1995).
                        from human urine.";
Hoppe-Seyler's Z. Physiol. Chem. 363:1043-1058(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1293:83-89(1996).
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Thromb. Haemost. 78:973-973(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activator gene",;
Thromb. Haemost. 77:434-435(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Biol. 235:1548-1559(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 67-155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 337:579-582(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasminogen activator.
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THE MAY 43 13:03:07 4004

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of two chains, A and B. The high molecular mass form contains a long chain A. Cleavage occurs after residue 155 in the low molecular mass form to yield a short Al chain.

-!- PHARMACEUTICAL: Available under the name Abbokinase (Abbott). Used in Pulmonary Embolism (PE) to initiates fibrinolysis.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 BGF-like domain.

18-02-880-202-4:FBD

21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG SNEIHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG Gaps .; 0 Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-70;
Matches 135; Conservative 0; Mismatches 0; Indels EMBL; X02419; CAA26268.1; EMBL; M15476; AAA61253.1; EMBL; M0244; BAA61253.1; EMBL; D11143; BAA01919.1; EMBL; X02760; CAAA6535.1; EMBL; X02760; CAAA6535.1; EMBL; X02760; CAA86382.1; EMBL; K02286; AAH5755.1; EMBL; K02286; AAA61252.1; EMBL; X02286; AAA61252.1; EMBL; A18397; CAA01390.1; PIR; A00931; UKHU. PLVQECMVHDCADGK 135 141 PLVQECMVHDCADGK 155 121 ò 셤 à d ò g

9 80

> RESULT 2
> UROK PAPCY
> UROK PAPCY
> ID UROK PAPCY
> AC 216227;
> DT 01-APR-1990 (Rel. 14, Last sequence update)
> DT 01-APR-1990 (Rel. 41, Last sequence update)
> DT 28-FEB-2003 (Rel. 41, Last annotation update)
> DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (UFA)
> N PLAU.

Papio cynocephalus (Yellow baboon).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.

TISSUBETOR PROM N.A.

TISSUE=Thoracic aorta;

MEDILE=90287734; PubMed=2113276;

MEDILE=90287734; PubMed=2113276;

MULINE=90287734; PubMed=2113276;

"Nucleotide and deduced amino acid sequences of baboon urokinase-type plasminogen activator.";

Nucleotide activator.";

Nucleotide Actids Ree. 18:3411-3411 (1990).

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

DB 1; Length 433; IndelB

Query Match
90.0%; Score 713.5; DB 1,
Best Local Similarity 91.9%; Pred. No. 9.2e-63;
Matches 124; Conservative 4; Mismatches 6;

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SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 kringle domain.

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DR PROSITE; PS01186; EGF_2; FALSE_NEG.

DR PROSITE; PS50026; EGF_3; 1.

DR PROSITE; PS50021; KRINGLE_1; 1.

DR PROSITE; PS50040; TRYBSIN_LE_1; 1.

DR PROSITE; PS50040; TRYPSIN_LE_2; 1.

DR PROSITE; PS00135; TRYPSIN_ERS; 1.

DR PROSITE; PS00135; TRYPSIN_ERS; 1.

KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; KW Kringle; EGF-like domain; Zymogen; Signal.

FT SIGNAL 1 442 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.

TANN 21 188 CHAIN A (BY SIMILARITY).

TANN 21 188 CHAIN B (BY SIMILARITY).
                                                                                                                                                             CHAIN
CHAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
DISULFID
DISULFID
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                                                                                                     KASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                   SREL-QVPSDCGCLNGGTCMSNKYFSSIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 79
                                                                                                                                                                                                                                                                                                                                                                                                          TIŜSUE=Kidney;
MEDLINE=85087954; PubMed=6096832;
Magamine Y., Pearson D., Altus M.S., Reich E.;
"cDNA and gene nuclectide sequence of porcine plasminogen activator.";
Nucleic Acids Res. 12:9525-9541(1984).
                                       SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                               20-MAR-1987 (Rel. 04, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagamine Y.,
Submitted (DEC-1986) to the PIR data bank.
-- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in plasminogen to form plasmin.
-- SIMILARITY: Belongs to peptidase family S1.
-- SIMILARITY: Contains 1 EGF-like domain.
-- SIMILARITY: Contains 1 kringle domain.
-- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X01648; CAA25606.1; --
EMBL, X0324; CAA26511.1; --
PIR, A00322; UKPG.
HSSP; P00749; IKDU.
MEROPS; S01.231; --
InterPro; IPR006003; Cys Ser trypsin.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; Kringle.
InterPro; IPR001254; PeptIdase_S1.
InterPro; IPR001254; PeptIdase_S1.
Pfam; PF00051; Kringle; 1.
Pfam; PF00051; Kringle; 1.
Pfam; PF00051; Kringle; 1.
PRNFS; PRRF001144; UK plasm_act; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRODMINS; PR00128; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00130; KR; 1.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS00022; EGF 1; 1.
                                                                                                                                       121 PLVQECMVHDCADGK 135
                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  scrofa (Pig).
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UROK PIG
ID UROK PIG
P04185;
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59 RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                           21 SHELLQESGASNCGCLNGGKCVSYKYFSNIQRCSCPKKRQGEHCEIDTSQTCFEGNGHSY
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UROK BOVIN STANDARD; PRT; 433 AA.

UROK BOVIN STANDARD;

O1.62894 (Rel. 28, Created)

O1.FEB-1994 (Rel. 28, Last sequence update)

28-FEB-203 (Rel. 41, Last annotation update)

Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)

PLAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria; Cetartiodactyla, Ruminantia, Pecora, Bovoldea;
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                          76.7%; Score 608; DB 1; Length 442; 78.1%; Pred. No. 2.1e-52; ive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                               241 Q -> H (IN REF. 1; CAA25806).
242 Q -> H (IN REF. 1; CAA25511).
288 A -> GS (IN REF. 1; CAA55806).
49116 MW, EB32FCEF501321EE CRC64;
SEQUENCE FROM N.A.
TISSUE-Acrtic endethelium;
MEDLINE-93216119; PubMed-8385052;
Kraetzschmar J., Haendler B., Kojima S., Rifkin D.)
Schleuning W.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 78.1% Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                 442 AA;
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DISULFID
DISULFID
ACT SITE
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CONFLICT
CONFLICT
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                                                                                                                                                            DISULFID
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BOVIN
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"Bovine urokinase-type plasminogen activator and its receptor: cloning and induction by retinoic acid.", Gene 125:177-183(1993).

SEQUENCE OF 12-433 FROM N.A. TISSUE=Kidney;

Ravn P., Bergjund L., Petersen T.E.;
"Cloning and characterization of the bovine plasminogen activators upA
and tpA.";
Int. Dairy J. 5:605-617(1995).
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.
-!- INDUCTION: By retinoic acid.
-!- SIMILARITY: Delongs to peptidase family S1.
-!- SIMILARITY: Contains 1 Extrigle domain.
-!- SIMILARITY: Contains 1 kringle domain.

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EMBL; 103546; AAA51419.1; -
BR EMBL; 103546; AAA51419.1; -
BR EMBL; 103546; AAA51419.1; -
BR EMBL; 103546; AAA51419.1; -
BR EMBL; 103546; AAA51419.1; -
BR EMBL; 103546; AAA51419.1; -
BR EMBL; 103546; AAA51419.1; -
BR EMBL; 103546; ABA51419.1; -
BR EMBL; 10314.9 PO0749; ILWW.

BR InterPro; IPR000203; EGF_1ike.

BR InterPro; IPR000323; Pept_51A.uPA.

BR InterPro; IPR00323; Pept_61ase_51.

BR InterPro; IPR00323; Peptidase_51.

BR Fam; PP00039; Kringle; 1.

BR Fam; PR000139; Kringle; 1.

BR FRSF; SW00722; CHYMOTRYPSIN.

BR FRSF; SW00720; TRYPSIN.

BR SWART; SW00030; Kringle; 1.

BR PROSITE; PS00021; KRINGLE 1; 1.

BR PROSITE; PS00021; KRINGLE 1; 1.

BR PROSITE; PS00021; KRINGLE 1; 1.

BR PROSITE; PS00039; TRYPSIN HIS; 1.

BR PROSITE; PS00139; TRYPSIN HIS; 1.

BR PROSITE

UROKINASE-TYPE PLASMINOGEN ACTIVATOR. CHAIN A (BY SIMILARITY). CHAIN B (BY SIMILARITY). EGF-LIKE. KRINGIDE. SCINGIDE. SERINE PROTEASE. CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
DOMAIN
DISULPID

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY.) DISULFID ACT_SITE ACT_SITE

81 RGKANRDLSGRPCLAWDSPTVLLKMYHAHRSDAIQLGLGKHNYCRNPDNQRRPWCYVQIG 140 59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 21 SNEVHKESGESNCGCLNGGKCVTYKYFSNIQRCSCPKKFQGEHCEIDTSKTCYQGNGHSY 1 SNELHQV--PSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY Query Match
Pest Local Similarity 73.0%; Pred. No. 1.4e-49;
Matches 100; Conservative 13; Mismatches 22; Indels 2; Gaps CHARGE RELAY SYSTEM (BY SIMILARITY)
A -> T (IN REF. 2) 189 A -> T (IN REF. 2). 48730 MW; 4DE1B8D4DA47027A CRC64; 119 LKPLVQECMVHDCADGK 135 433 AA; ACT SITE CONFLICT SEQUENCE FT g ò 셤 ठे

118

28

Rattus norvegicus (Rat). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus. NCBI_TaxID=10116; 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
(U-phasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU. STANDARD; UROK RAT P29598;

STRAIN=Fischer 344; MEDLINES-2233409; PubMed=1568219; Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A., Kefford R.F.; Transcriptional and posttranscriptional activation of urokinase plasminogen activator gene expression in metastatic tumor cells."; Cancer Res. 52:2489-2496(1992). SEQUENCE FROM N.A.

SEQUENCE FROM N.A. TISSUE=Kidney;

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EMBL; X63434; CAA45028.1; -.
EMBL; X65651; CAA46601.1; -.
PIR; S24664; S18932.
HSSP, P00749; INDU.
MEROPS; S01.231; -.
InterPro; IPR009003; Cys_Ser_trypsin.

SIMILARITY). SIMILARITY).

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01-JAN-1988 (Rel. 06, Last sequence update)
By ERB-2003 (Rel. 41, Last annotation update)
Urckinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                           SEQUENCE FROM N.A. WITHOUSE STATE STATE SET SEQUENCE FROM N.A. WEDLINE=8117944; PubMed=2985383; WEDLINE=8117944; PubMed=2985383; Edin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y., Reich E., Kocher H.P., Duvoisin R.M.; M.; Cocher H.P., Duvoisin R.M.; Second Sequencing and expression of cDNAs encoding mouse urokinase-type plasminogen activator."; Eur. J. Biochem. 148:225-232(1985).
                                Mus musculus (Mouse)
                                                NCBI_TaxID=10090;
     89 RPCLAMNSPAVLQQTYNAHRSDALSLGLGKHNYCRNPDNQRRPWCYVQIGLKQFVQECMV 148
                                                                                                                                                                                                                                                                                                                        68
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RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV
                                                                                                                                                                                                                                                                                                                      SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
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UROK_MOUSE
ID UROK_MOUSE
AC P06869;
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Best Local
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01-JAN-1988 (Rel. 06, Created)

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EGF-LIKE.
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SERINE PROTEASE.
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AC D15638;

AC D15638;

DT O1.APR-1990 (Rel. 14, Created)

DT O1-APR-1990 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Salivary plaaminogen activator alpha 2 precursor (RC 3.4.21.68) (DSPA DE Sharoyca; Werazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Bukaryca; Werazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;

OC Desmodontinae; Desmodus.

NOB! TaxID=9430;
POTENTIAL.
UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A GPS SIMILARITY).
SHORT A CHAIN (A1).
CHAIN B (BY SIMILARITY).
EGF-LIKE.
KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Salivary gland;
MEDLINE-92039036, PubMed=1937019;
MEDLINE-92039036, PubMed=1937019;
MEDLINE-92039036, PubMed=1937019;
MEDLINE-92039036, PubMed=1937019;
MEDLINE-92039030, PubMed=1937019;
MEDLINE-92030 N., Bachaler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Deemodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
"WITH SEQUENCE.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

MEDLINE=90036867; PubMed=2509450;
Gardell S.J., Duong L.T., Dahell R.E., York J.D., Hare T.R.,
Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
"Isolation, characterization, and cDNA cloning of a vampire ]
salivary plasminogen activator.";
[3]
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.1%; Score 548; DB 1; Length 433; Best Local Similarity 71.7%; Pred. No. 1.6e-46; Matches 91; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                    48268 MW;
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CHARACTERIZATION.
MEDILINE-93393059; PubMed=1309059;
MEDILINE-93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
Donner P.;
Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity.";
Ann. N.Y. Acd. Sci. 667;395-403(1992).
Ann. N.Y. Acd. Sci. 667;395-403(1992).
-i. FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Probable potent thrombolytic
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us-09-880-503-4.rsp

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431
      send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 OCHTVPVKSCSELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTY 136
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01-APR-1990 (Rel. 14, Last sequence update)
28-FBB-2003 (Rel. 14). Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
Gallus gallus (Chicken).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
NCBI_TaxID=9031;
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11.7 Y -> H (IN REF. 2).
13.5 M -> K (IN REF. 2).
13.5 M -> K (IN REF. 2).
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197 SKFILEFCSVPVCS 210
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11 CDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRGKASTDTMGRP 70
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Query March
Best Local Similarity 54.2%; Pred. No. 1.4e-25;
Matches 58; Conservative 14; Mismatches 30; Indels 5
                                                                                                                                                                                                                                                     71 CLPWNSATVLQ-QTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQ 116
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BGF-LIKE.

KRINGLE.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
        Hydrolase, Serine protease, Glycoprotein;
                                                         POTENTIAL. SALIVARY PLASMINOGEN ACTIVATOR BETA
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Nature 301:214-221(1983)
             activation;
        Plasminogen activat
Kringle, EGP-like o
SIGNAL 1
CHAIN 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-407(11992).
---- FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Probable potent thrombolytic
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
88-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA beta).
                                                                                                                            Desmodus rotundus (Vampire bat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

TISSUB=2811vary gland;

MEDLINE=9203036, PubMed=1937019;

Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.; The plasminogen activator family from the salivary gland of the vampire bat Deemodus rotundus: cloning and expression.";

Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE=93393059; PubMed=1309059; Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T., Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W., Donner P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Monomer.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
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PIR, JS0599; JS0599.
HSSP, P98119; JA51.
MENCPS; SOI1.239; -...
InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR00124; Peptidase_S1.
InterPro; IPR00134; Peptidase_S1.
InterPro; IPR00134; Peptidase_S1.
Pfam; PF00008; EGF; 1.
Pfam; PF00008; EGF; 1.
Pfam; PR00051; Kringle; 1.
PRINTS; PR00121; CHYMOTRYPSIN.
PRINTS; PR00121; EGF_1: 1.
PROSITE; PS00022; EGF_1: 1.
PROSITE; PS00021; EGF_1: 1.
PROSITE; PS00021; EGF_1: 1.
PROSITE; PS00021; EGF_1: 1.
PROSITE; PS00021; EGF_1: 1.
PROSITE; PS00146; TRYPSIN_DRD; 1.
PROSITE; PS00146; TRYPSIN_HIS; 1.
PROSITE; PS00146; TRYPSIN_HIS; 1.
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42 SELRCFNGGTCWQAASFSDF-VCQCPKGYTGKQCEVDTHATCYKDQGVTYRGTWSTSESG 100
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TISSUE=Melanoma;
MEDLINE=81315262; PubWed=6337343;
Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A.,
Ward C.A., Bennett W.F., Yelverton B., Seeburg P.H., Heyneker H.L.,
Goeddel D.V., Collen D.;
"Cloning and expression of human tissue-type plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Fetal lung;
TISSUE=Fetal lung;
SISSUE=88262579; PubMed=3133640;
SASAKI H., SAITO Y., HAYAShi M., Otsuka K., Niwa M.;
"Nucleotide sequence of the tissue-type plasminogen activator cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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P00750; 015103; 015101, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
11-SHAR-2004 (Rel. 43, Last annotation update)
(1-PA) (t-plasminogen activator) (Alteplase) (Reteplase).
PLAT.
                                                                                                                                                                                                                        1;
                                                                                                            Query Match
41.4%; Score 328.5; DB 1; Length 431;
Best Local Similarity 47.6%; Pred. No. 5.3e-25;
Matches 59; Conservative 16; Mismatches 48; Indels 1;
699B5E675B162CBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCOUNT REPORT OF THE PROPERTY ```

us-09-880-503-4.rsp

SEQUENCE OF 31-562 FROM N.A.
MEDLINE-91291340; PubMed=1366681;
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
"Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
Agric. Biol. Chem. 55:1225-1232(1991). TISSUE=Melanoma;
MEDLINE=8500466; PubMed=6431976;
Poll G. Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.;
Poll G., Kaellstroem activator: peptide analyses confirm an indirectly derived amino acid sequence, identify the active site serine residue, establish glycosylation sites, and localize variant differences."; SEQUENCE OF 1-36 FROM N.A. MEDLINE-85289338, PubMed-3161893; Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R., Schleuning W.-D.; "Isoletinon and characterization of the human tissue-type plasminogen activator atructural gene including its 5' flanking region."; [11] "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray crystal structure of single-chain human tPA."; EMBO J. 16:4797-4805(1997). X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
MEDLINE=96200985; PubMed=8613982;
Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
The 2.3 A crystal structure of the catalytic domain of recombinant
two-chain human tissue-type plasminogen activator.";
J. Mol. Biol. 258:117-135(1996). Ä X.FAY CRYSTALLOGRAEHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN. MEDLINE=97449126; PubMed=9305622; Relatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert TISSUE=Melanoma; MEDLINE=83209620; MEDLINE=83209620; PubMed=6682760; Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.; "Purification and characterization of a melanoma cell plasminogen DISULFIDE BONDS IN KRINGLE 2.
MEDLINE-91244765; PubMed=1645336;
Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.;
"Disulfide pairing of the recombinant kringle-2 domain of tissue plasminogen activator produced in Escherichia coli.";
J. Biol. Chem. 266:10070-10072(1991). t 0 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
MEDLINES-29118803; PubMed-1310033;
MEDLINES-29118603; PubMed-1310033;
MEDLINES-29118603; PubMed-1310033;
MEDLINES-2918604 N.I., Kossiakof A.A.; CARBOHYDRATE-LINKAGE SITE THR-96.
MEDLINE=91159408; PubMed=1900431;
Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
Harris R.D., Leonard C.K., Guzzetta A.W., Spellman M.W.;
Hissue plasminogen activator has an O-linked fucose attached threonine-61 in the epidermal growth factor domain.";
Biochemistry 30:2311-2314(1991). STRUCTURE OF CAREOHYDRATES.
MEDLINE=90092112; PubMed=2513186;
Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
"Carbohydrate structure of recombinant human uterine tissue plasminogen activator expressed in mouse epithelial cells.";
Eur. J. Blochem. 186:273-286(1989). Eur. J. Biochem. 132:681-686(1983). [13] SEQUENCE OF 33-52 AND 311-330. SEQUENCE OF 36-562. activator." Bode W.; 

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EMBL, MA18697, AAA41812.1,

EMBL, MA18697, AAA42812.1,

EMBL, MA1185, AAA42261.1, JOINED.

EMBL, MA1186, AAA42261.1, JOINED.

EMBL, MA1186, AAA42261.1, JOINED.

EMBL, MA1189, AAA42261.1, JOINED.

EMBL, MA1189, AAA42261.1, JOINED.

EMBL, MA1191, AAA42261.1, JOINED.

EMBL, MA1194, AAA42261.1, JOINED.

EMBL, MA1194, AAA42261.1, JOINED.

EMBL, MA1194, AAA42261.1, JOINED.

EMBL, MA1195, AAA42261.1, JOINED.

EMBL, MA1196, AAA42261.1, JOINED.

EMBL, EMBL, MA1196, JOINED.

EMBL, PROOTIS, EMF, JOINED.

EMART, SMOODS, EMPL, JOINED.

EMBL, PROSITE, PSOOLS, EMF, JOINED.

EMBL, JO
 58
 3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
 SEQUENCE FROM N.A.

MEDLINE=9013048; PubMed=2105315;

MEDLINE=9013048; PubMed=2105315;

"The Structure of the TATA-less rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.";

J. Biol. Chem. 265:2022-2027(1990)
 Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxiD=10116;
 MEDLINE BY NMR OF KRINGLE 2.
MEDLINE=90122799; PubMed=2558718;
Byeon I.-J.L., Kelley R.F., Illnas M.;
Byeon I.-d.L., Kelley R.P., Illnas M.;
I'H NMR structural characterization of a recombinant kringle 2 domain from human tissue-type plasminogen activator.";
Biochemistry 28:9350-9360(1989).
 STRUCTURE BY NMR OF KRINGLE 2.
MEDLINE-22106329; PubMed=1762144;
Byeon I.-J.L., Llinas M.;
"Solution structure of the tissue-type plasminogen activator kringle
2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
 Gaps
 Tatlorum By NMR OF KRINGLE 2.

MEDLINE=91200042; PubMed=1901789;
Byeon I.-J.L., Kelley R.F., Lilinas M.;
"Kringle-2 domain of the tissue-type plasminogen activator. IH-NMR sasignments and secondary structure.";
Eur. J. Biochem. 197:155-165(1991).
"Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4-A resolution.";
Biochemistry 31:270-279(1992).
 TPA RAT STANDARD; PRT; 559 AA.

199637; Created)
01-FPB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (RC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator).
 5
 / Match 41.4%; Score 328.5; DB 1; Length 562; Local Similarity 46.3%; Pred. No. 6.9e-25; nes 63; Conservative 14; Mismatches 54; Indels 5;
 drug.";
J. Mol. Biol. 222:1035-1051(1991),
 196 GKYSSEFCSTPACSEG 211
 119 LKPLVQECMVHDCADG 134
 Query Match
 Best Loca
Matches
 RESULT 1
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FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events. CATALYTIC Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

SUBJUIT: Heterodimer of chain A and chain B held by a disulfide

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-1- SUBCELLULAR LOCATION: Secreted, extracellular.

-1- SUBCELLULAR LOCATION: Secreted, extracellular.

-1- FTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUB KALLIKREIN OR FACTOR XA.

-1- SIMILARITY: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.

-1- SIMILARITY: Contains I Egg-like domain.

-1- SIMILARITY: Contains I fibronectin type I domain.

-1- SIMILARITY: Contains 2 kringle domains.

us-09-880-503-4.rsp

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RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
 Gaps
 Mus musculus (Mouse),
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
 FIRRONECTIN TYPE-I.
EGF-LIKE.
KRINGLE 1.
KRINGROWELAY SYSTEM.
KRINGLARITY.
BY SIMILARITY.
BY SIMILARITY
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Plasma; Kringle; EGF-like domain; Repeat; Signal.
1 17 PROBABLE.
PROBEP 18 29 TISSUE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN 30 308 TISSUE-TYPE PLASMINOGEN ACTIVATOR.
 TISSUE-TYPE PLASMINOGEN ACTIVATOR, TISSUE-TYPE PLASMINOGEN ACTIVATOR A CHAIN.

TISSUE-TYPE PLASMINOGEN ACTIVATOR B
 TPA MOUSE STANDARD, PRT, 559 AA.
P11214; Q91VP2;
01-JUL-1989 (Rt. 11, Created)
10-OCT-2003 (Rt. 14, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation
115-MAR-2004 (Rel. 43, Last annotation)
 5.
 th ... 40.5%; Score 321.5; DB 1; Length 559; Similarity 45.6%; Pred. No. 3.3e-24; 62; Conservative 14; Mismatches 55; Indels 5;
 7DBD3809C1D1C921 CRC64;
 SEQUENCE FROM N.A.
MEDLINE=88087303; PubMed=2826484;
 62903 MW;
 119 LKPLVQECMVHDCADG 134
 GKYTTEFCSTPACPKG 208
 309
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RESUBENCE FROW N.A.

TISSUB-Mammary gland;

RA Strausberg R.L., Faingold E.A., Grouse L.H., Derge J.G.,

RETAUSPERS R.L., Faingold E.A., Grouse L.H., Schauler G.D.,

RA Altsuberg R.D., Collins F.S., Wagner L. Schaefer C.F., Bhat N.K.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Halma L.,

RA Richards S., Worley N.C., Wokernan K.J., Abramson R.D., Mullahy S.J.,

RA Rodards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human man mouse CDNA sequences."

RA Generation and initial analysis of more than 15,000 full-length human man mouse CDNA sequences."

R. Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).

C. -- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin-mediated protecolysis, it plays an important controlling plasmin-mediated protecolysis, it plays an important plasminogen to form plasmin.

C. C. CAPALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in bond in bond.
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EMBL; MO3520; AAA40470.1; --
EMBL; A29941; A29941.256.1; --
FIR; A29941; A29941.
 bond.

-!- SUBCELLULAR LOCATION: Secreted; extracellular.
-!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKARINO OR FACTOR XA.
-|- MISCELLANDOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
-|- SIMILARITY: Belongs to peptidase family S1.
-|- SIMILARITY: Contains 1 EGF-like domain.
-|- SIMILARITY: Contains 2 Kringle domains.
Rickles R.J., Darrow A.L., Strickland S.;
"Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA and its expression during F9 teratocarcinoma cell differentiation.";

Biol. Chem. 263:1563-1569(1988).
 MEROFS; S01.232; -.
MEROFS; S01.232; -.
MOJ; MOI:97610; Plat.
InterPro; IPR009003; Cys_Er_trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; ISGF.
InterPro; IPR000001; Kringle.
InterPro; IPR00134; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
Fram; PP00008; EGF; 1.
Pfam; PP00003; fn1; 1.
Pfam; PP00051; kringle; 2.
 SEQUENCE FROM N.A.
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R PFIMIS; PRO0089; trypsin; 1.

R PRIMIS; PRO0722; CHYMOTRYPSIN.

PRIMIS; PRO0722; CHYMOTEN.

R PRON018; Kringle; 2.

R SWART; SM00181; EGF; 1.

SWART; SM00181; EGF; 1.

SWART; SM00120; KR; 2.

R PROSITE; PS01166; EGF_2; 1.

R PROSITE; PS01166; EGF_2; 1.

R PROSITE; PS01021; KRINGLE_1; 2.

R PROSITE; PS00021; KRINGLE_2; 2.

R PROSITE; PS00014; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

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R PROSITE; PS00135; TRYPSIN SER; 1.

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PROFITE; PS00135; TRYPSIN SER; 1.
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 8CCEE2BDB94514D9 CRC64;
 KRINGLE 1.
KRINGLE 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
 FIBRONECTIN TYPE-I. EGF-LIKE.
 63122 MW;
 61; Conservative
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RESULT 13

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GlycoSuiteDB, P98119, -.
Interpro, IPR009003; Cys Ser trypsin.
Interpro, IPR006209; BGF_like.
 EMBL; M63987; AAA31591.1; -. EMBL; M63986; AAA31592.1; -.
 PIR; JS0597; JS0597.
PDB; 1A51; 23-MAR-99.
MEROPS; S01.232; -.
 74 OCHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEEQGITY 132
 RGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
 28
 3 ELHOVP ---- SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
 Gaps
 ..
ت
39.8%; Score 315.5; DB 1; Length 559; 44.5%; Pred. No. 1.3e-23; ive 15; Mismatches 56; Indels 5;
 119 LKPLVQECMVHDCADGK 135
 GKYTTEFCSTPACPKGK 209
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133

193

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TISSUB-Salivary gland;

WEDLINE-98022741; PubMed-9354616;

MEDLINE-98022741; PubMed-9354616;

Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,

Renatus M.D., Bode W.;

Rohleuning W.D., Bode W.;

"Catalytic domain structure of vampire bat plasminogen activator: a
molecular paradigm for proteolygis without activation cleavage.";

molecular paradigm for proteolygis without activation cleavage.";

Elochemistry 36:1343-1343(1991).

"Le HUNCTION: Probably essential to support the feeding habits of this exclusively hematophagous animal. Potent thrombolytic agent.

"CATALYIZ ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

"ENZYMEN REGULATION: Activity toward plasminogen is stimulated in the presence of fibrin I.

"ENZYMEN The fibronectin type-I domain mediates binding to fibrin, and the kringle domain apparently mediates fibrin-induced stimulation of activity.

"SIMILARITY: Contains I EGF-like domain.

"SIMILARITY: Contains I fibronectin type I domain.

"SIMILARITY: Contains I fibronectin type I domain.

"SIMILARITY: Contains I kringle domain. This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on it was by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch). ol-red-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity."; Ann. N.Y. Acad. Sci. 667:395-403(1992). TISSUB-Salivary gland;
MEDLINE-92039036; PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991). Desmodus rotundus (Vampire bat). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi, Mammalia; Eutheria; Chiroptera, Microchiroptera; Phyllostomidae; Desmodontinae; Desmodus. CHARACTERIZATION. MEDLINE=93393059; PubMed=1309059; Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T., Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W., 477 AA X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS). 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last seq 15-MAR-2004 (Rel. 43, Last ann STANDARD; SEQUENCE FROM N.A. NCBI\_TaxID=9430; URTI DESRO P98119; 

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Query Match 39.2%; Score 310.5; DB 1; Length 477; Best Local Similarity 45.5%; Pred. No. 3.4e-23; Matches 60; Conservative 14; Mismatches 53; Indels 5.
 HELIX
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InterPro; IPR000083; Fibrnctn1.

R InterPro; IPR000201; IEGF.

InterPro; IPR001301; Kringle.

R InterPro; IPR001314; Peptidase_S1A.

R InterPro; IPR001314; Peptidase_S1A.

R Pfam; PF00009; EGF; 1.

Pfam; PF00009; EGF; 1.

R Pfam; PF00009; EGF; 1.

R Pfam; PF00009; Kringle; 1.

R PRINTS; PR00722; CHYMOTRYPSIN.

R PRINTS; PR00729; Kringle; 1.

R RNART; SM0018; KRINGLE.

R SMART; SM0018; KRINGLE.

R SMART; SM0018; KRINGLE.

R SMART; SM0018; EGF 1.

R SMART; SM0018; EGF 1.

R SMART; SM0018; EGF 2; 1.

R SMART; SM0018; EGF 2; 1.

R PROSITE; PS01025; EGF 2; 1.

R R SSITE; PS01025; REIRONECTIN 1; 1.

R R SSITE; PS01034; KRINGLE 2; 1.

R R SSITE; PS01034; TRYPSIN H.HS; 1.

R R SSITE; PS01035; MAINGLE 2; 1.

R R SSITE; PS01035; MAINGLE 3; SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1. FIBRONECTIN TYPE-I. EGF-LIKE.
 N-LINKED (GLCNAC. ..).
/FTId=CAR_000027.
N-LINKED (GLCNAC. ..).
/FTId=CAR_000028.
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121 PLVQECMVHDCA 132

5 HOVPSN-CD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG

53616 MW; AA06FD1739C10E5E CRC64;

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 O'10-1097 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
Tissue-type plasminogen activator).
PLAT.
Bos taurus (Bovine).
Bos taurus (Rovine).
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovines Bos.

NCEL_TAXID=9913;
 566 AA.
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199 FTSESCSVPVCS 210
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-:- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-314 CAPALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-:- MISCELLANEOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
-:- SIMILARITY: Belongs to peptidase family \$1.
-:- SIMILARITY: Contains 1 EGF-like domain.
-:- SIMILARITY: Contains 2 kringle domains. 

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SERINGLE 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
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BY SIMILARITY.

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282 BY SIMILARITY.
295 BY SIMILARITY.
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343 BY SIMILARITY.
342 BY SIMILARITY.
423 BY SIMILARITY.
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46 BY SIMILARITY.
47 BY SIMILARITY.
48 N'LINKED (GLCKAC. .) (POTENTIAL).
487 N'LINKED (GLCKAC. .) (POTENTIAL).
487 N'LINKED (GLCKAC. .) (POTENTIAL). S66 AA; 180 2219 2219 2240 3340 4448 488 488 488 488 488 488 488 488 DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID CARBOHYD CARBOHYD SEQUENCE 

3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58 Gaps 5 Query Match 37.9%; Score 300.5; DB 1; Length 566; Best Local Similarity 44.0%; Pred. No. 3.9e-22; Matches 59; Conservative 16; Mismatches 54; Indels 5;

59 RGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118 

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119 LKPLVQECMVHDCA 132 

HGFA HUMAN STANDARD; PRT; 655 AA.

Q04736; Q14726;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF activator) (HGFA).

Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalía; Buthería; Primates; Catarrhini; Hominidae; Homo.

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUE-Liver, and Serum;

MEDLINE-93228818; PubMed=7683665;

Miyazawa K., Shimomura T., Kitamura A., Kondo J., Morimoto Y.,

Kitamura N.;

"Molecular cloning and sequence analysis of the cDNA for a human
earine protease reponsible for activation of hepatocyte growth
factor. Structural similarity of the protease precursor to blood
coagulation factor XII...;

J. Biol. Chem. 268:10024-10028(1993).

P SEQUENCE OF 40-655 FROM N.A.

SEQUENCE OF 40-655 FROM N.A.

Zhao S., Odell C.;

Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.

Converting it from a single chain to a heterodimeric form.

C -1- FUNCTION: Activates hepatocyte growth factor (HGF) by converting it from a single chain to a heterodimeric form.

C -1- SUBMIT: Dimer of a short chain and a long chain linked by a disulfide bond.

C -1- SUBCELLULAR LOCATION: Secreted as an inactive single-chain precursor and is then activated to a heterodimeric form.

C -1- SIMILARITY: Contains 1 fibronectin type I domain.

C -1- SIMILARITY: Contains 1 fibronectin type II domain.

C -1- SIMILARITY: Contains 1 kibronectin type II domain.

C -1- SIMILARITY: Contains 1 kibronectin type II domain.

C -1- SIMILARITY: Contains 1 kibronectin type II domain.

C -1- SIMILARITY: Contains 1 kindle domain.

C -1- CAUTION: It is uncertain whether Met-1 is the initiator.

18-07-880-505-4.rep

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242 HTACLSSPCLNGGTC-----HILVATGTTVCACPPGFAGRLCNIBPDERCFLGNGT 292
 5 HOVPSNCDCLNGGTCVSNKYFSNIHW-----CNCPKKFGGQHCBIDKSKTCYEGNGH 56
 57 FYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
 293 GYRGVASTSASGLSCLAMNSDLLYQELHVDSVGAAALLGLGPHAYCRNPDNDERPWCYV 351
 32.8%; Score 260.5; DB 1; Length 655;
43.7%; Pred. No. 3.8e-18;
tive 8; Mismatches 42; Indels 17; Gaps
BY SIMILARITY.
BY SIM
 P12.

Gavia porcellus (Guinea pig).

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enkaryota; Metazoa; Chordata; Hystricognathi; Caviidae; Cavia.

NCBI_TaxID=10141;
 70681 MW;
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Best Local Similarity 43...
Best Local Similarity 63...
Solution 52, Conservative
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 73 PWNSATVLQQTYHAHRSD-ALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
 239 RWAS----BATYRNMTAEQALRRGLGHHTFCRNPDNDTRPWCFVWMGNRLSWEYCDLAQC 294
 72
 13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
 Gaps
BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Q9R099; Q9UKV4;

16-0CT-2001 (Rel. 40, Created)

16-0CT-2001 (Rel. 40, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Hépatcoyte growth factor activator precursor (EC 3.4.21.-) (HGF activator) (HGFA).
 SEQUENCE FROM N.A.
MEDLINE=21226753; PubMed=11032833;
van Adelsberg J.S., Sehgal S., Kukes A., Brady C., Barasch J.,
Yang J., Huan Y.;
"Activation of hepatocyte growth factor (HGF) by endogenous HGF
activator is required for metanephric kidney morphogenesis in
 32.4%; Score 257; DB 1; Length 603; 40.8%; Pred. No. 7.6e-18; indels ive 17; Mismatches 46; Indels
 STRAIN=BALB/C;
ltoh H., Kataoka H., Koono H.;
"Mouse hepatocyte growth factor activator.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

similarity).
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kringle domain.

 66795 MW;
 Similarity 40.8 49; Conservative
 STANDARD;
 Mus musculus (Mouse).
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 NCBI_TaxID=10090;
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SIMILARITY).
 ALPHA-FACTOR XIIA HEAVY CHAIN. ALPHA-FACTOR XIIA LIGHT CHAIN. FIBRONECTIN TYPE-II.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kringle domain.
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BMBL, BMBL, BMBL.2; BMBL.2; BMBL.2; --

BMBL, BMBL.2; BR00089; BMBL.2; --

BMBL, BMBL.2; BR00081, Kringle. --

BMBL, BR00081, BMBL.2; --

BMBL.2; BR00081, BMBL.2; --

BMBL.2; BR00081, FMB.1; --

BMBL.2; BR00081, FMB.1; --

BMBL.2; BR00081, FMB.2; --

BMBL.2; BR00081, FMB.1; --

BMBL.2; BR00081, FMB.2; --

BMBL.2; BR00081
the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EGF-LIKE 2.
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SERINE PROTEASE.
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SECUENCE OF 561-615 FROM N.A.
TISSUE=Blood;
MEDLINE=9613302; PubMed=852815;
Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Engel W.;
"The novel acceptor splice site mutation 11396(G-->A) in the factor
XII gene causes a truncated transcript in cross-reacting material
negative patients.";
Hum. Mol. Genet. 4:1235-1237(1995). SECURNCE OF 20-379.
MEDLINE-85182674, McMullen B.A., Fubikawa K.; "Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated Hageman factor)."; (activated Hageman factor)."; J. Biol. Chem. 260:5328-5341(1985). SEQUENCE OF 146-615 FROM N.A. MEDILINE-86216049, PubMed=3011063; Que B.G., Davie E.W. "Characterization of a cDNA coding for human factor XII (Hageman J. Biol. Chem. 260:5328-5341(1305).

[7]

REQUENCE OF 354-362 AND 373-615.

MEDLINE-83291041; PubMed=6604055;

Fujikawa K., McMullen B.A.;

"Amino acid sequence of human beta-factor XIIa.";

L. Biol. Chem. 258:10924-10933(1983). Biochemistry 25:1525-1528(1986) factor)." 

18-08-08-1801 18-08-880

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CARBOHYDRATE-LINKAGE SITE THR-109.
MEDLINE-29184750; PubMed-1544894.
MEDLINE-29184750; PubMed-1544894.
Med fuces is present in the first epidermal growth factor domain of factor XII but not protein C.";
J. Biol. Chem. 267:5102-5107(1992).

VARIANT WASHINGTON D.C. SER-590.
Whibline=90046788; PubMed=2510163;
Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B., Saito H.;
Coagulation factor XII (Hageman factor) Washington D.C.: inactive factor XIIa results from Cys-771-->Ser substitution.";
Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).

VARIANT LOCARNO PRO-372. MBDLINE-94325559; Pubmed=8049433; HOvinga J.K., Schaller J., Stricker H., Wuillemin W.A., Furlan M., Laemmle B.;

"Coagulation factor XII Locarno: the functional defect is caused by the amino acid substitution Arg-353-->Pro leading to loss of a kallikrein closs of select as a plood 84:1173-1181(1991.";

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-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kringle domain. 

us-09-880-503-4.rsp

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 183 CLHGGRCLE---VEGHRLCHCPVGYTGPFCDVDTKASCYDGRCLSYRGLARTTLSGAPCQ 239
 72
 "Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-4031992).
-:- FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Probable potent thrombolytic
 13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
 URIG_DESRO STANDARD; PRT; 394 AA.
P49150;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator gamma precursor (BC 3.4.21.68) (DSPA
 Desmodus rotundus (Vampire bat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
 SEQUENCE FROM N.A.
TISSUB-Salivary gland;
MEDLINE=92039036. PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the
vampire bat Descodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
 CHARACTERIZATION.
MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 agent.
--- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SUBUNIT: Monomer.
 .;
8
 29.4%; Score 233; DB 1; Length 615; 42.3%; Pred. No. 1.8e-15; ive 12; Mismatches 40; Indels
 240 PWAS----EATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFV 279
 73 PWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
 PRO-ECH.

SERINE PROTEASE.

O-LINKED (FUC).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).
 -!- SIMILARITY: Belongs to peptidase family S1. -!- SIMILARITY: Contains 1 kringle domain.
FIBRONECTIN TYPE-I
 EGF-LIKE
KRINGLE.
 44; Conservative
 Local Similarity
 1133
1244
1274
1309
1308
1308
1308
1308
1308
 Donner P.;
DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
CARBOHYD
 CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
 Query Match
 RESULT 19
URTG_DESRO
 Matches
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45 DKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRN 104
 40 DPHATCYKDQGVTYRGTWSTSESGAQCINWNSNLLIRRTYNGRMPEAVKLGLGNHNYCRN 99
 R MERCE'S; SOL-259; -----
R InterPro; IPR000001; Kringle.
R InterPro; IPR00124; Peptidase_S1.
R InterPro; IPR00124; Peptidase_S1.
R InterPro; IPR001214; Peptidase_S1.
R Pfam; PF00009; Kringle; 1.
R Pfam; PF00009; Kringle; 1.
R PRINTS; PR000125; KRINGLE.
R PRINTS; PR000126; KRINGLE.
R PRODOM; PR000139; KRINGLE.
R PRODOM; PR000139; KRINGLE.
R SMART; SW00020; KRINGLE.
R SMART; SW00020; TRFINGLE.
R PROSITE; PS00010; KRINGLE.
R PROSITE; PS000114; TRYPSIN DM; 1.
R PROSITE; PS00134; TRYPSIN DM; 1.
R PROSITE; PS00135; TRYPSIN JSR; 1.
R PROSITE; PS00135; TRYPSIN JSR; 1.
R PROSITE; PS00135; TRYPSIN JSR; 1.
R PROSITE; PS00136; TRYPSIN JSR; 1.
R PROSITE; PS00136; TRYPSIN JSR; 1.
R PROSITE; PS00137; TRYPSIN JSR; 1.
R
 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.
KRINGLE.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
115-MRA-2004 (Rel. 43, Last annotation update)
Coaqulation factor XII precursor (BC 3.4.21.38) (Hageman factor)
(HAF) (Fragment).
 N-LINKED (GLCNAC. . .) (POTENTIAL)
9CCD6F52F3D81FCD CRC64;
 28.1%; Score 223; DB 1; Length 394; 44.3%; Pred. No. 1.1e-14; ive 13; Mismatches 36; Indels
 593 AA.
 105 PDNRRRPWCYVQVGLKPLVQECMVHDCA 132
 100 PDGASKPWCYVIKARKFTSESCSVPVCS 127
send an email to license@isb-sib.ch)
 PRT;
 44105 MW;
 EMBL; M63990; AAA31595.1; -. PIR; JS0600; JS0600.
 Best Local Similarity 44.33
Matches 39; Conservative
 STANDARD;
 HSSP; P98119; 1A5I.
MEROPS; S01.239; -.
 RESULT 20
FA12_BOVIN
ID FA12_BOVIN
AC P98140;
 CHAIN
DOMAIN
DOMAIN
ACT SITE
ACT SITE
ACT SITE
DISULFID
DISULFID
 DISULFID
DISULFID
DISULFID
DISULFID
 DISULFID
DISULFID
CARBOHYD
SEQUENCE
 Query Match
```

Bos taurus (Bovine). Bukaryota: Metazoos; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos

NCBI\_TaxID=9913; [1] SEQUENCE FROM N.A. 'n

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64 IDIMGRPCLPMNSAIVLQQIY-HAHRSDALQLGLGKGHNYCRNPDNRRRPWCVVQVGLKPL 122
 223 TILSGAPCQSWAS----BATYWNVTAEQVLNWGLGDHAFCRNFDNDTRPWCFINKGDRLS 278
 PROSITE; PS50070; KRINGLE 2; 1.

PROSITE; PS50104; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

ROMINGLOISE; PS00134; TRYPSIN SER; 1.

A Clycoprocein; Blood coagulation; Plasma; Kringle; Serine protease; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.

A STORMAL (1) 349 POTENTIAL.

TOWAIN 150 593 ALPHA-FACTOR XIIA HEAVY CHAIN.

FT DOMAIN 123 163 BAPPA-FACTOR XIIA LIGHT CHAIN.

FT DOMAIN 123 163 BAPPA-FACTOR XIIA LIGHT CHAIN.

FT DOMAIN 207 287 ALPHA-FACTOR XIIA LARITY.

FT DOMAIN 207 287 ALPHA-FACTOR XIIA LARITY.

FT DISULPID 111 120 BY SIMILARITY.

FT DISULPID 125 153 BY SIMILARITY.

FT DISULPID 207 287 BY SIMILARITY.

FT DISULPID 207 287 BY SIMILARITY.

FT DISULPID 208 BY SIMILARITY.

FT DISULPID 334 453 BY SIMILARITY.

FT DISULPID 334 BY SIMILARITY.

FT DISULPID 341 BY SIMILARITY.

FT DISULPID 341 BY SIMILARITY.

FT DISULPID 344 BY SIMILARITY.

FT DISULPID 345 BY SIMILARITY.

FT DISULPID 346 BY SIMILARITY.

FT DISULPID 347 BY SIMILARITY.

FT DISULPID 348 BY SIMILARITY.

FT DISULPID 348 BY SIMILARITY.

FT DISULPID 349 BY SIMILARITY.

FT DISULPID 341 BY SIMILARITY.

FT DISULPID
 6 QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYE--GNGHFYRGKAS
 Gaps
 EGF-LIKE 1.

FIRRONECTIN TYPE-1.

EGF-LIKE 2.

KRINGLE

KRINGLE

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

BY SIMILARITY.

BY
 58; Indels 10;
 RESULT 21

RORI DROME

1D RORI DROME

AC 024488;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 42, Last sequence update)

DT 10-CT-2003 (Rel. 42, Last sancheation update)

DT 10-CT-2003 (Rel. 42, Last sancheation update)

DE Tyrosine-protein kinase transmembrane receptor Ror precursor

DE (EC 2.7.1.112) (dRor).

DE (EC 2.7.1.112) (dRor).

OS Drosophila melanogaster (Fruit fly).

OS Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 27.4%; Score 217; DB 1; Length 593;
llarity 35.7%; Pred. No. 6.3e-14;
Conservative 15; Mismatches 58; Indels 1
 721592BA792BD61F CRC64;
 21 DEPT PROPERTY OF THE PROPER
 123 VOECMVHDC 131
 279 WNYCRLAPC 287
 Query Match
Best Local Similarity
Matches 46; Conservat
 DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Canton-S; TISSUE=larval brain;
MEDLINE=93348222; PubMed=8394009;
Wilson C., Goberdhan D.C.I., Steller H.;
"Dror, a potential neurotrophic receptor gene, encodes a Drosophila homolog of the vertebrate Ror family of Trk-related receptor tyrosine kinases."; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993). SEQUENCE FROM N.A. NCBI\_TaxID=7227; 

RC STRAIN=Berkeley.

KNETNIN=2-0196006; PubMed=10731132;

RADININ=2-0196006; PubMed=10731132;

RADININ=10716 C., Radinin A., An H.-J., Andraws-Franchon C.R., Miklos G.L.G., RADININ Basu A., An H.-J., Andraws-Franchon C.R., Miklos G.L.G., RADININ R., Bouck J., Baryakararoglu L., Basley E.M., Ballew R.M., Baruk J., Bayawakararoglu L., Basley E.M., Ballew R.M., Bauck J., Ballew R.M., Bauck J., Ballew R.M., Bauck J., Ballew R.M., Camlew B.P., Bhandari D., Botshaxov E.M., Radinin M.R., Bouck J., Gadreu E., Center A., Chandra I., Radinin R., Camlew B., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M., Durbin K.J., Banger R.M., Dugan-Rocha S., Dunkov B.C., Dunn P., Boller C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Aloster D., Langer B., Levitsky A.B., Harris M., Harris N.L., Harver D.A., Heiman T.J., Hernandez J.R., Houck W., Gong F., Garrell G.H., Glasser M. Duder M. Morph R.M., Houston M., Matuleh B., McIntoen G.H., May M., Matuleh B., McIntoen G.H., Marin D., Marker D., Matuleh B., McIntoen M., Murphy B., Murphy L., Muzny D.M., Nelsen D.L., Alber D. Lai Y., Levitsky A.A., Li J.H., Marzy D.M., Nelsen D.L., Alber D. L., Marker D.M., Mathan M.V., Mobarry C., Morris J., Moorle C., Shen H., Mang K.H., 
MEDLINE=98401146; PubMed=9731193;

MEDLINE=98401146; PubMed=9731193;

MEDLINE=98401146; PubMed=9731193;

MEDLINE=98401146; PubMed=9731193;

MEDLINE=98401146; PubMed=9731193;

Sampling the genomic pool of protein tyrosine kinase genes using the polymerase chain reaction with genomic DNA.";

Blochem. Blobhys. Res. Commun. 249:660-667(1998).

-!- FUNCTION: Tyrosine-protein kinase receptor that functions during early stages of neuronal development.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

-!- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous

SIMILARITY: Belongs to the Tyr family of protein kinases. ROR

-!- SIMILARITY: Contains 1 frizzled (FZ) domain.

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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
S26162D27D5FD7C7 CRC64; Query Match
21.3%; Score 169; DB 1; Length 685;
Best Local Similarity 28.8%; Pred. No. 3.7e-09;
Matches 38; Conservative 27; Mismatches 35; Indels 3 FZ.
KRINGLE.
PROTEIN KINASE.
ATP (BY SIMILARITY).
SY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY RECEPTOR ROR. EXTRACELLULAR (POTENTIAL). SIMILARITY). PHOSPHORYLATION (AUTO-) (BY PHOSPHORYLATION (AUTO-) (BY SIMILARITY). POTENTIAL. CYTOPLASMIC (POTENTIAL). SIMILARITY) 45 63 N-L 129 N-L 144 N-L 250 N-L 550 N-L 269 45 63 129 144 250 685 AA; 569 570 25 DOMAIN TRANSMEM DOMAIN DOMAIN DOMAIN NP BIND NP BIND BINDING ACT SITE MOD\_RES CARBOHYD CARBOHYD SEQUENCE CARBOHYD CARBOHYD MOD\_RES MOD\_RES SIGNAL CHAIN 

3 ELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKA

35; Indels 32;

```
212 DCQKLPQHKDCLSLGITI -------EVDKTENCYWEDGSTYRGVA
 63 STDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN-RRRPWCYVQVGLKP
 CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
MEDLINE=21303595; PubMed=11294842;
Garner B., Merry A.H., Royle L., Harty D.J., Rudd P.M., Thillet J.;
Garner B., Merry A.H., Royle L., Hardor D.J., Rudd P.M., Thillet J.;
Structural elucidation of the N- and O-glycans of human apolipoprotein(a): role of o-glycans in conferring protease resistance.";
J. Biol. Chem. 276:22200-22208(2001).
 MEDLINE=95002201; PubMed=7918682; Minman J.; Scann A.M., Pfaffinger D., Lee J.C., Hinman J.; Scann A.M., Pfaffinger D., Lee J.C., Hinman J.; scann A.M., Pfaffinger D., Lee J.C., Hinman J.; associated with a lysine binding defect in Lp(a)."; Biochim. Biophys. Acta 1227;41-45(1994).

-i. FUNCTION: Apod a is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinase activity and is able of autoproceolysis. Inhibits tissue-type plasminogen activator 1. Lp(a) may be a ligand for megalin/Gp 330.

-i. SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
 MEDLINE=96217891; PubMed=8642595;
Mikol V., Lograsso P.V., Boettcher B.R.;
Mikol V., Lograsso P.V., Boettcher B.R.;
"Crystal structures of apolipoprotein(a) kringle IV37 free and complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic acid: existence of novel and expected binding modes.";
J. Mol. Biol. 256:751-761(1996).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 SEQUENCE FROM N.A.

MEDLINE=88039109; PubMed=3670400;

MCLean J.W., Tonlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,

Fless G.M., Scanu A.M., Lawn R.M.;

"cDNA sequence of human apolipoprotein(a) is homologous to

plasminogen.";

Nature 330:132-137(1987).
 MEDLINE=90076123; PubMed=2531657;
Salonen E.-M., Jauhiainen M., Zardi L., Vaheri A., Ehnholm C.;
"Lipoprotein(a) binds to fibronectin and has serine proteinase activity capable of cleaving it.";
EMBO J. 8:4035-4040(1989).
 01-AUG-1988 (Rel. 08, Created)
1-AUG-1988 (Rel. 08, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Apolipoprotein(a) precursor (EC 3.4.21.) (Apo(a)) (Lp(a)).
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
 MEDLINE=90049223; PubMed=2530631;
Utermann G.;
"The mysteries of lipoprotein(a).";
Science 246:904-910(1989).
 301 IIELCDIPKCAD 312
 122 LVQECMVHDCAD 133
 STANDARD;
 SERINE PROTEASE ACTIVITY
 Homo sapiens (Human)
 APOA HUMAN
P08519;
 250
 REVIEW.
 APOA_HUMAN
 RESULT
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- PTM: N- and O-glycosylated. The N-glycans are complex biantennary structures present in either a mono- or disialylated state. The O-glycans are mostly (80%) represented by the monosialylated core type I structure, Neuklacalpha2-3Galbeta1-3GalNAc, with smaller amounts of disialylated and non-sialylated O-glycans also
- detected.
  --- DISRAE: Elevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with anternally occurring proteolytic fragments are correlated with atherosclerosis. Homology with plasminogen kringles IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin (ogen) binding.
  --- MISCELLANBOUS: Apo(a) is known to be proteolytically claeved, leading to the formation of the so called mini.Lp(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thromogenesis. O-glycosylation may limit the extent of proteolytic fragmentation.
  --- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily. <u>-</u>-

This Sylvandry: Contains 38 Kingle domains.

This sylvandry: Contains 38 Kingle domains.

This sylvandry: Contains 38 Kingle to the Sylvandry of the Sylvandry 

APOLIPOPROTEIN(A).
KRINGLE TYPE IV, 1.
KRINGLE TYPE IV, 3.
KRINGLE TYPE IV, 4.
KRINGLE TYPE IV, 4.
KRINGLE TYPE IV, 6.
KRINGLE TYPE IV, 6.
KRINGLE TYPE IV, 6.
KRINGLE TYPE IV, 9.
KRINGLE TYPE IV, 9.
KRINGLE TYPE IV, 9.
KRINGLE TYPE IV, 10.
KRINGLE TYPE IV, 11.
KRINGLE TYPE IV, 11.

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 104
 96
 47 SKTCYEGNGHPYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRN
 ch
1. Similarity 45.1%; Pred. No. 1.6e-08;
32; Conservative 7; Mismatches 28; Indels 4; Gaps
 10 WSC.

121 CUB.

122 CUB.

132 CUB.

133 N-LINKED (GLCNAC. .) (POTENTIAL).

133 N-LINKED (GLCNAC. .) (POTENTIAL).

133 N-LINKED (GLCNAC. .) (POTENTIAL).

134 N-LINKED (GLCNAC. .) (POTENTIAL).

135 N-LINKED (GLCNAC. .) (POTENTIAL).

136 N-LINKED (GLCNAC. .) (POTENTIAL).

137 N-LINKED (GLCNAC. .) (POTENTIAL).

138 N-LINKED (GLCNAC. .) (POTENTIAL).

139 N-LINKED (GLCNAC. .) (POTENTIAL).
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Macaca.
 | R | Reference |
 RESULT 24
APOA MACMU STANDARD; PRT; 1420 AA.

AC P14417;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein(a) (BC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment)
GN LPA.

ON Macaca mulatta (Rhesus macaque)
 -!- SIMILARITY: Contains 1 CUB domain.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 WSC domain.
 105 PDNRRRPWCYV 115
 87 PDGDVSPWCYV 97
 [1] =
SEQUENCE FROM N.A
 Query Match
Best Local &
 셤
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 RESULT 23

KRM1 RAT

LD KRM1 RAT

AC 092454;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 42, Last sequence update)

DT 28-FEB-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE And the nose) (Dickkopf receptor).

EXEMENIOR KREMEN

OS Rattus norvegicus (Rat).

OC BUKARYOTA, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC BUKARYOTA, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC BUKARYOTA, Metazoa; Chordata; Craniata; Waridae; Murinae; Rattus.

NOSI TAXID-10116;

RN 11]

RA Nakamura T., Nakamura T.;

RA Nakamura T., Nakamura T.;

RA Nakamura T., Nakamura T.;

RA Nakamura T. PUCATION: Type I membrane protein (Potential).

C -: SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 3802 TCQSWSSMT---PHWHQRTTEYYPNGGLTRNYCRNPDABIRPWCYT---MDPSVRWEYCN 3855
 70 PCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKFUV--QECM 127
 69
 27 NIHW--CN---CP-----KKFGGQHCEIDKSKT---CYEGNGHFYRGKASTDTMGR
1385 1498 KRINGLE TYPE IV, 13.
1613 1612 KRINGLE TYPE IV, 14.
1613 1726 KRINGLE TYPE IV, 14.
1721 1840 KRINGLE TYPE IV, 15.
1841 1954 KRINGLE TYPE IV, 16.
2068 KRINGLE TYPE IV, 19.
2062 2183 2296 KRINGLE TYPE IV, 20.
2183 2296 KRINGLE TYPE IV, 20.
2297 2410 KRINGLE TYPE IV, 21.
2411 2524 KRINGLE TYPE IV, 21.
2525 2638 KRINGLE TYPE IV, 23.
2639 2752 KRINGLE TYPE IV, 23.
2640 KRINGLE TYPE IV, 24.
2753 2866 KRINGLE TYPE IV, 26.
2867 2980 KRINGLE TYPE IV, 31.
3895 3322 KRINGLE TYPE IV, 31.
3896 3721 XRINGLE TYPE IV, 31.
3894 KRINGLE TYPE IV, 31.
3894 KRINGLE TYPE IV, 31.
3894 412 KRINGLE TYPE IV, 35.
3895 3998 KRINGLE TYPE IV, 35.
3896 3998 KRINGLE TYPE IV, 35.
3896 3998 KRINGLE TYPE IV, 37.
3897 3998 KRINGLE TYPE IV, 37.
3897 3998 KRINGLE TYPE IV, 37.
3896 3998 KRINGLE TYPE IV, 36.
3999 412 KRINGLE TYPE IV, 37.
3897 3998 KRINGLE TYPE IV, 37.
3898 3998 KRINGLE TYPE IV, 37.
3898 3998 KRINGLE TYPE IV, 37.
3898 3998 KRINGLE TYPE IV, 37.
3899 3998 KRINGLE
 25;
 Query Match 20.5%; Score 162.5; DB 1; Length 4548; Best Local Similarity 33.1%; Pred. No. 1e-07; Matches 41; Conservative 12; Mismatches 46; Indels 25;
 3856 LTQC 3859
 128 VHDC 131
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CYEGNGHEYRGKASTDTWGRPCLPWNSATVLQ--QTYHAHRSDALQLGLGKHNYCRNPDN 107
 KRMI_XENLA

ID KRMI_XENLA

FRMI_XENLA

FRMI_XENLA

O90950;

DT 10-0CT-2003 (Rel. 42, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DE Kremen protein 1 precursor (Kringle-containing protein marking the eye

DE And the nose) (Dickkopf receptor).
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 KREMEN PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
 CYTOPLASMIC (POTENTIAL)
KRINGLE.
 (GLCNAC.
(GLCNAC.
(GLCNAC.
 PROSITE; PS01180; CUB; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00070; KRINGLE 2; 1.
TRAISEMAING pathway; Glycoprotein; Kringle;
Transmembrane; Signal;
 1123 DIGPWCFT---MDPSVRREYCNLTRCSD 1147
 108 RRRPWCYVQVGLKPLVQE - CMVHDCAD 133
 N-LINKED (N-LINKED (N-LINK
 KREMENI.
Xenopus laevis (African clawed frog)
 EMBL; AB070851; BAB64294.1; -...
InterPro; IPR000859; CUB.
InterPro; IPR000801; Kringle.
InterPro; IPR002889; WSC.
Pfam; PF00431; CUB; 1.
Pfam; PF00431; Kringle; 1.
Pfam; PF001822; WSC; 1.
Pfam; PF00018; Kringle; 1.
ProDom; PD000395; Kringle; 1.
SMART; SM00042; CUB; 1.
SWART; SM00130; KR; 1.
 SEQUENCE FROM N.A.
 NCBI_TaxID=8355;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 The surface another application of the surface of t
 DR InterPro; S01.226; -.

DR InterPro; IPR000001; Kringle.

EnterPro; IPR001254; Peptidase_S1.

EnterPro; IPR001314; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR Fdam; PF000089; Kringle; 11.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00130; Kringle; 10.

R PROMITS; PR000130; Kringle; 10.

R PROMITS; PR000130; Kringle; 10.

R PROSITE; PS00001; KRINGLE_2; 10.

R PROSITE; PS00101; KRINGLE_2; 10.

R PROSITE; PS00114; TRYPSIN DOM; 11.

R PROSITE; PS00114; TRYPSIN DOM; 11.

R PROSITE; PS00114; TRYPSIN ER; FALSE_NEG.

R PROSITE; PS001135; TRYPSIN ER; FALSE_NEG.

R Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein; T NON TER.

T DOMAIN 49 127 KRINGLE 1.
MEDLINE-89174660; PubMed=2925643;
Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 20.3%; Score 161; DB 1; Length 1420; 40.9%; Pred. No. 4.6e-08; ive 9; Mismatches 31; Indels 1;
 127 KRINGLE 1.
241 KRINGLE 2.
469 KRINGLE 3.
583 KRINGLE 5.
670 KRINGLE 5.
803 KRINGLE 6.
803 KRINGLE 7.
917 KRINGLE 9.
1031 KRINGLE 9.
145 KRINGLE 10.
145 KRINGLE 10.
1420 SERINE PROTEASE.
7 158367 MM; BE102949E03G5B0E CRC64;
 EMBL; J04635; AA316833.1; -. PIR; A32869; A32869. PISSP; PO0744; 2PX4. MEROPS; S01.226; -.
 1420 AA;
 Similarity
 SEQUENCE
 Query Match
 Best Local
Matches 3
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Gaps

12;

Conservative

36;

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 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 **Molecular cloning and characterization of Kremen, a novel
Kringle-containing transmembrane protein.";
Biochim. Biophys. Acta 1518:63-72(2001).

Li FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
C-1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
C-1- SUBCELLUAR LOCATION: Type I membrane protein (Potential).

--- TISSUE SPECIFCITY: In the adult, widely expression is first detected
C-1- TISSUE SPECIFCITY: In the embrane protein is first detected
C-1- DEVELOPMENTAL STAGE: In the embryo, expression is first detected
C-1- DEVELOPMENTAL STAGE: In the embryo, expression is first detected
C-1- TISSUE SPECIFCITY: In the embryo, expression is first detected
C-1- DEVELOPMENTAL STAGE: In the embryo, expression is first detected
C-1- DEVELOPMENTAL STAGE: In the developing fore- and hindlinb buds,
C-1- SIMILARITY: Contains 1 CUB domain.
C-1- SIMILARITY: Contains 1 CUB domain.
C-1- SIMILARITY: Contains 1 kingle domain.
C-1- SIMILARITY: Contains 1 kingle domain.
 7
 42 CEIDKSKICYEGNGHFYRGKASIDIM--GRPCLPWNSAIVLQQTYHAHRSDALQLGLGKH 99
 22 CSDSFHSECYTVNGADYRGTQNQTSLDGGKPCLFWNE--TFQHPYNTLKYPNGEGGLGEH 79
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 SECUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY. ITSSUE=Brain, and Kidney;
MEDLINE=21167372; PubMed=11267660;
Nakamina T., Aoki S., Kitajima K., Takahashi T., Matsumoto K., Nakamira T.,
(GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
 4,
 Length 452;
 32; Indels
128 N-LINKED (GLCNAC. . .) (PC 44 N-LINKED (GLCNAC. . .) (PC 50188 MW; ED24BCD1AF4564E2 CRC64;
 Score 159; DB 1;
Pred. No. 2.3e-08;
9; Mismatches 32
 MGD; MGI:1933988; Kremen.
GO; GO:0016021; C:integral to membrane; NAS.
InterPro; IPR000859; CUB.
InterPro; IPR002001; Kringle.
InterPro; IPR02289; WSC.
Pfem; PF00431; CUB; 1.
Pfem; PF00051; kringle; 1.
 EMBL; AB059617; BAB40968.1; -.
HSSP; P00747; 1CEA.
 100 NYCRNPDNRRRPWCYV 115
 80 NYCRNPDGDVSPWCYI 95
 20.1%;
ilarity 40.8%;
Conservative
 STANDARD;
 Mus musculus (Mouse)
328
344
352 AA;
 Similarity
 and the nose) (Dic
KREMEN1 OR KREMEN.
 NCBI_TaxID=10090;
 31;
 KRM1 MOUSE
099N43;
CARBOHYD
CARBOHYD
SEQUENCE
 Query Match
Best Local S:
Matches 31
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50 CYBGNGHFYRGKASTDTM--GRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN 107
 32 CPTANGADYRGTQSWTALQGGKPCLFWNE--TFOHPYNTLKYPNGEGGLGEHNYCRNPDG 89
 SEQUENCE FROM N.A. (ISOFORM SHORT).

MEDILINE=9703043; PubMed=887295;

Reddy U.R., Phatak S., Pleasure D.;

"Human neural tissues express a truncated Rorl receptor tyrosine kinase, lacking both extracellular and transmembrane domains.";

Oncogene 13:1555-1559(1996).

-i. FUNCTION: Tyrosine-protein kinase receptor whose role is not yet
 Gaps
 SEQUENCE FROM N.A. (ISOFORM LONG).
MEDIINE-93100347; Pubmed=1334494;
MEDIINE-9310047; Carroll R.D.;
"A movel family of cell surface receptors with tyrosine kinase-like
"A novel family of cell surface
 RORI HUMAN STANDARD; PRT; 937 AA.

RORI HUMAN STANDARD; PRT; 937 AA.

ROL172001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 43, Last annotation update)

15-MAR-2004 (Rel. 43, Last annotation update)

Tyrosine-protein kinase transmembrane receptor RORI precursor

Tyrosine-protein kinase transmembrane receptor RORI precursor

(RC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1).

RORI OR NIPKRI.

Homo saplens (Human)

Eukaryota, Metazoa; Ohordata, Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 4.
 (POTENTIAL)
 (POTENTIAL)
 Score 159; DB 1; Length 473; Pred. No. 2.5e-08; 7; Mismatches 26; Indels
 CRC64;
 EXTRACELLULAR (POTENTIAL)
 Transmembrane; Kringle
 CYTOPLASMIC (POTENTIAL).
 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 586827788BE3FDD1
 (GLCNAC.
(GLCNAC.
(GLCNAC.
 KREMEN PROTEIN 1.
 (GLCNAC
 (GLCNAC
 POTENTIAL.
 N-LINKED
N-LINKED
N-LINKED
N-LINKED
 N-LINKED
N-LINKED
 domain.";
J. Biol. Chem. 267:26181-26190(1992)
 KRINGLE
PRINTS; PRO0018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SWART; SN00042; CUB; 1.
SWART; SN00130; KR; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
 8
 Wnt signaling pathway; Signal; SIGNAL
 51716 MW;
 20.1%;
 45.6%;
 l Similarity 45.6
31; Conservative
 108 RRRPWCYV 115
 90 DVSPWCYV 97
 345
473 AA;
 NCBI_TaxID=9606;
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 236 DÉTSSVPKPRDLCRDECETLENVLCOTEYTFARSNPMILMRLKLPNCEDLPOPESPEAAN 295
 MEDLINE=9948426; PubWed=10231382; MEDLINE=9948426; PubWed=10231382; MEDLINE=9948426; PubWed=10231382; Medaukuro A., Ueda T., Liu Z.J., Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J., Hatta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y., Spatio-temporally regulated expression of receptor tyrosine kinases, mRorl, mRorl, mRorl, anouse development: implications in development and function of the nervous system."; Genes Cells 4:41-56 (1999).

-1- FUNCTION: Tyrosine-protein kinase receptor whose role is not yet
 2 NELHOVP-----SNCDCLNGGTCVSNKYFS-----NIHWCNC-----PKKFGGQH
 C------EIDKSKTCYEGNGHPYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL
 D RORI MOUSE STANDARD, PRT, 937 AA.

C 92239;
T 16-OCT-2001 (Rel. 40, Created)
T 16-OCT-2003 (Rel. 42, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E Tyrosine-protein kinase transmembrane receptor RORI precursor
E (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1)
E (MCORI).
N RORI OR NTRKRI.
S Mus musculus (Mouse).
C Mammalia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Mus.
N NCBI TaxID=10090;
 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
 clear.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

subfamily.
SIMILARITY: Contains 1 frizzled (FZ) domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 kringle domain.

 20.0%; Score 158.5; DB 1; Length 937; 29.7%; Pred. No. 5.4e-08;
 51; Indels
PROTEIN KINASE.
SER/THR-RICH.
PRO-RICH.
SER/THR-RICH.
 14; Mismatches
 93 QLG--LGKHNYCRNPDNRRR-PWCY 114
 ACT_SITE
MOD_RES
DISULFID
 42
 CARBOHYD
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 Isold=Q01973-1; Sequence=Displayed;

Name=Short; Synonyms=T-ROR1;

Isold=Q01973-2; Sequence=VSP_005008;

Isold=Q01973-2; Sequence=VSP_005008;

IISSUE SPECIFICITY: Expressed strongly in human heart, lung, and kidney, but weakly in the CNS. The short isoform is strongly cancers including those originating from CNS or PNS neuroectoderm.

DEVELOPMENTAL STACE: Expressed at high levels during early embryonic development. The expression levels drop strongly around day 16 and there are only very low levels in adult tissues. SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
 subfamily.
-!- SIMILARITY: Contains 1 frizzled (FZ) domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- SIMILARITY: Contains 1 kringle domain.
 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 IG-LIKE C2-TYPE.
FZ.
KRINGLE.
 DOMAIN
TRANSMEM
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us-09-880-503-4.rsp
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). | 194 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 EMEL, ABOLO383; BAA75480.1; EMEL, ABOLO383; BAA75480.1; EMEL, ABOLO347; LCEA.

MGD; MGI.1347520; Ror1.

DR InterPro; IPR000014; Fz domain.

EnterPro; IPR000014; Fz domain.

EnterPro; IPR000015; Kringle.

DR InterPro; IPR00001; Kringle.

DR InterPro; IPR00051; Fyr\_Dkinase.

EnterPro; IPR00051; Fyr\_Dkinase.

DR Ffam; PF00061; Prinage; 1.

DR Pfam; PF00061; Prinage; 1.

DR Pfam; PF00061; Prinage; 1.

DR PRINTS; PR00109; Prinage; 1.

DR PRINTS; PR00109; Prinage; 1.

DR PRINTS; PR00109; FrXRINASE.

DR PRINTS; PR00109; FXRINGLE

DR PRONTS; PR00109; FXRINGLE

DR PRONTS; PR00109; PROTEIN KINASE DOM; 1.

DR PROSTIE; PS00010; PROTEIN KINASE DOM; 1.

PROSTIE; PS00107; PROTEIN KINASE ATP; FALSE NEG.

PROSTIE; PS00107; PROTEIN KINASE TRY; 1.

PROSTIE; PS00107; PROTEIN KINASE TRANSMEMBRANE TRANSMEMB POTENTIAL. TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR ROR1, EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE. FZ. KRINGLE. PROTEIN KINASE. SER/THR-RICH. DOMAIN
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DISÜLFID
CARBOHYD CARBOHYD CARBOHYD SEQUENCE 

2 NELHQVP-----SNCDCLNGGTCVSNKYFS-----NIHWCNC-----PKKFGGQH 1. Similarity 29.7%; Pred. No. 5.4e-08; Similarity 29.7%; Pred. No. 5.4e-08; Indels 37; Gaps 13; Conservative 14; Mismatches 51; Indels 37; Gaps 43; Query Match Best Local S: Matches 43;

C------EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOOTYHAHRSDAL 42

g ò 8 8

93 QLG--LGKHNYCRNPDNRRR-PWCY 114

295

KENILT 29
KRM1 HUMAN STANDARD; BRT; 475 AA.

AC Q96MUB; Q99V70; Q9UG85; Q9UGU1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor). SEQUENCE FROM N.A. (ISOFORM 2).

Tachiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,

Tachiro H., Yamazaki M., Romiyama M., Sugiyama T., Irie R.,

Otsuki T., Sato H., Wakametu A., Ishii S., Yamamoto J., Isono Y.,

Kawai-Hio Y., Saito K., Nichikawa T., Kimura K., Yamashita H.,

Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,

Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama M.,

Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,

Isogai T.,

"NEDO human cDNA sequencing project.",

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. SEQUENCE FROM N.A. (ISOFORM 1).
Nakamura T., Nakamura T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. NCBI\_TaxID=9606; 

RP 95 RP 1817 RP 18

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DR SWISL, 205116, CABASOSCII;

DR SWISL, 205116, CABSOSCII;

DR SWISL, 205116, CABSOSCII;

DR SWISL, 205116, CABSOSCII;

DR Genew, HGNG:1756, CREMENTA.

DR GO: GO:0005624; C:nembrane fraction; TAS.

DR GO: GO:0005624; C:nembrane fraction; TAS.

DR HIGHER PROSIDES (C:nembrane) in the captor of the commentation; TAS.

DR HIGHER PROSIDES (C:nembrane) in the captor of the commentation; TAS.

DR Ffam; PROO154; C:nembrane fraction; TAS.

DR Ffam; PROO155; CUB; I.

DR Ffam; PROO155; KINGLE.

DR PROSIDES (C:nembrane) in the captor of the capt
Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
Khan A.S., Lane L., Tilahun Y., Wright H.;
"The DNA sequence of human chromosome 22.";
 -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Mat/beta-catenin signaling (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
 2).
MISTIG=VSP 003900.
MISSING (IN REF. 1).
I -> V (IN REF. 2).
HPE86FD80F96A0A4 CRC64;
 Name=1;
Isold=Q96MU8-1; Sequence=Displayed;
Name=2; Isold=Q96MU8-2; Sequence=VSP_003900;
Note=No experimental confirmation available;
-!- SIMILARITY: Contains 1 Kringle domain.
-!- SIMILARITY: Contains 1 kringle domain.
 Event=Alternative splicing; Named isoforms=2;
 51898 MW;
 30
 29
206
275 AA;
 CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
 CONFLICT
CONFLICT
SEQUENCE
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Score 156; DB 1; Length 475;

19.7%;

Query Match

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Rest Local Similarity 4.1% Pred. N. 4.3e-06; Indals 4; daps 2

Matches 30; Conservative 8; Mismatches 26; Indals 4; daps 2

Of Crecomerracine 8; Mismatches 26; Indals 4; daps 2

Of Crecomerracine 8; Mismatches 26; Indals 4; daps 2

Of Crecomerracine 8; Mismatches 26; Indals 4; daps 2

Of 108 REMARKY 115

DEAM BOUNT 8; TANDARD) RRT; 812 AA.

DEAM BOUNT 8; TANDARD) RRT; 812 AA.

DEAM BOUNT 8; TANDARD) RRT; 812 AA.

DEAM BOUNT 8; TANDARD 115, MISMATCH 9; MISMAT
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 This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-i- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
-i-SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-i- SIMILARITY: Contains 5 kringle domains.
 TRYPSIN_DOM; 1.
TRYPSIN_HIS; 1.
TRYPSIN_HIS; 1.
TRYPSIN_FER; 1.
TRYPSIN_FER; 1.
Fibrinolysis; Plasma; Glycoprotein; Fibrinolysis; Plood coagulation; Kringle; Zymogen; Repeat;
 /FTId=CAR_000015.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N -> D (IN REF. 2).
Q -> H (IN REF. 2).
P -> L (IN REF. 2).
T -> R (IN REF. 3).
T -> R (IN REF. 3).
 N-LINKED (GLCNAC. ..).
/FTIG=CAR 000014.
O-LINKED (GALNAC. ..),
 4 H
 PLASMIN HEAVY CHAIN
PLASMIN LIGHT CHAIN
 19.7%; Score 156; DB 1; 28.3%; Pred. No. 8.2e-08;
 KRINGLE 5.
SERINE PROTEASE.
N-LINKED (GLCNAC
 PLASMINOGEN
 InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR001569; Pan_app.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001366; Peptidase_SIA.
InterPro; IPR003966; Peptidase_SIA.
 KRINGLE 3.
 Pfam; PF00021; Kringle; Pfam; PF00021; Kringle; Pfam; PF00024; Trypsin; 1. Pfam; PF00089; Trypsin; 1. PRINTS; PR00089; KRINGLE; PRINTS; PR00089; KRINGLE; PRODOM; PF0000399; KRINGLE; SMART; SM00403; KR, S. SMART; SM00403; Tryp_SPC; 1. PROSITE; PS00021; KRINGLE_1; S. PROSITE; PS00021; KRINGLE_1; S. PROSITE; PS000021; KRINGLE_2; S.
 91216 MW;
 EMBL; X79402; CAA55939.1; -. EMBL; K02035; AAA30714.1; -. PIR; S45046; PLBO.
HSSP; P00747; 2284.
MEROPS; S01.233; -.
 365
 GlycoSuiteDB; P06868;
 335
516
555
744
812 AA;
 PROSITE; PS50240; T
PROSITE; PS00134; T
PROSITE; PS00135; T
Hydrolase; Serine D
 Query Match
Best Local Similarity
 issue remodeling;
 365
 ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
 CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 DOMAIN
CARBOHYD
 CARBOHYD
 Signal.
SIGNAL
 CHAIN
DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 CHAIN
 SOLUTION TO THE TENEFITY TO THE SECOND TO TH
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54; Gaps

12; Mismatches

Conservative HOVPSNCDCLN----

47;

Matches

ò

Length 812; 53; Indels ----GGTCVSNKYPSNIHW--CNCPKKFGGQHCEIDKSKT

..

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367 ERMDVPVPPEQTPVPQDCYHGNGQSYRGTSSTIIIGRKCQSWSS-----MTPHRHLKTPE 421
 ENZYME REGULATION: Converted into plasmin by plasminogen cartivators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.

PTM: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINE, SIALIC ACID AND IS CORE TOCSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENRITY).
 SEQUENCE OF 1-560.
Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli B.B.;
"Amino acid sequence of the heavy chain of porcine plasmin. Comparison
of the carbohydrate attachment sites with the human and bovine
 immediately after dissociation from the clot.
- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
- SIMILARITY: Contains 5 kringle domains.
 CARBOHYDRATE-LINKAGE SITES.
MEDLINE-88185229; PubMed=3356193;
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Marti G.J., van Halbee H., Vliegenthart J.F.,
"The N- and O-linked carbohydrate chains of human, bovine and porcine
plasminogen. Species specificity in relation to sialylation and
 Pur. J. Biochem. 193:57-63 (1988).

Pur. J. Biochem. 193:57-63 (1988).

Pur. J. Biochem. 193:57-63 (1988).

Pur. J. Biochem. Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as CI and CS. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

Public Schartzic Activity: preferential cleavage: Lys-|-Xaa > Arg-|-Xaa, higher selectivity than trypsin. Converts fibrin into soluble
315 NRTPENFPCKNLEENYCRNPNGEKAPWCYTTN--SEVRWEYCTIPS-----CESSPLST
 -------CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAH---RS
 Euteleostomi;
 MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 MEDINE=85203907; PubMed=3846533;
Marti T., Schaller J., Rickli E.E.;
"Determination of the complete amino-acid sequence of porcine.
 133
 90 DALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD
 422 NYPNAGL-TMNYCRNPDADKSPWCYT---TDPRVRWEFCNLKKCSE
 Sus scrofa (Fig).
Makaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
 Last sequence update)
Last annotation update)
 Ā
 miniplasminogen.";
Eur. J. Biochem. 149:279-285(1985).
 Created)
 .brinolysis 1:91-102(1987).
 01-JAN-1988 (Rel. 06, Crea
01-FEB-1991 (Rel. 17, Last
28-FEB-2003 (Rel. 41, Last
Plasminogen (EC 3.4.21.7).
 STANDARD;
 HSSP; P00747; SHPG.
MEROPS; S01.233; -.
GlycoSuiteDB; P06867;
 fucosylation patterns.
 SEQUENCE OF 450-790.
 RESULT 31
PLMN PIG
ID FLMN PIG
AC P06867;
 20
 species.
```

```
SEQUENCE OF 95-580, 581-626, 657-700 AND 732-810, AND VARIANT ASN-472. Softrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.; (In) Bavidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.); Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209, Raven Press, New York (1978).
 MEDLINE=73149248; PubMed=4694729; Robbins K.C., Bernabe P., Arzadon L., Summaria L.; Robbins K.C., Bernabe P., Arzadon L., Summaria L.; The histidine loop "The primary structure of human plasminogen. II. The histidine sequence."; of human plasmin: light (B) chain active center histidine sequence."; J. Biol. Chem. 248:1631-1633(1973).
 MEDINE-8502311, PubMed-6148961,
Malinowski D.P., Sadler J.E., Davie E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for
human and bovine plasminogen.",
Biochemistry 23:4243-4250(1994).
Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.; "Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system."; Biol. Chem. 265:6104-6111(1990).
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 SEQUENCE FROM N.A., AND VARIANTS LYS-57, GLN-133; HIS-261; TRP-408; ASN-472; VAL-494 AND TRP-523
Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N., Toch E.J., Yi Q., Nickerson D.A.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
MEDLINE=87162400; PubMed=3030813;
FORESTOR M., Raden B., Israelsson M., Larsson K., Heden L.-O.;
"Molecular cloning and characterization of a full-length cDNA clone for human plasminogen.";
For human plasminogen.";
FEBS Lett. 213:254-260(1987).
 SEQUENCE OF 483-604.
MEDLINE=76043692; PubMed=126863;
Wiman B., Wallen P.;
"Amino-acid sequence of the cyanogen-bromide fragment from human plasminoqen that forms the linkage between the plasmin chains.";
Eur. J. Biochem. 58:539-547(1975).
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 "Primary structure of the B-chain of human plasmin.";
Eur. J. Biochem. 76:129-137(1977).
 SEQUENCE OF 20-810, AND VARIANT ASN-472.
Sottrup-Jensen L., Petersen T.E., Magnusson S.;
Submitted (JUL-1977) to the PIR data bank.
 [12]
OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
MEDLINE-82213905, PubMed=6919539;
 SEQUENCE OF 20-100.
MEDLINE=75093329; PubMed=122932;
Wiman B., Wallen P.;
 MEDLINE=77225245; PubMed=142009;
 SEQUENCE OF 292-810 FROM N.A.
 SEQUENCE OF 581-810.
 ACTIVE SITE.
 ACTIVE SITE
 Wiman B.;
 8
 345 APVPPEQTPVAQDCYRGNGESYRGTSSTTITGRKCQSW-----VSMTPHRHEKTPGNFPN 399
 46
 93
 -----SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHR---SDALQ
 5 HOVPSNCDCLNGGTCVSNKYFSN----IHWC-NCPKKFGGQHCEIDK------
 Gaps
 R InterPro; IPR009003; Cys Ser_trypsin.

R InterPro; IPR000001; Kringle.

R InterPro; IPR001014; PAN.

R InterPro; IPR001014; PAN; I.

R Pfam; PF00009; Lrypsin; I.

R Pfam; PF00009; Lrypsin; I.

R PRINTS; PR001014; PAN; I.

R PRINTS; PR001018; RXINGLE.

R PRNTS; PR001019; RXINGLE.

R SMART; SM00019; Kringle; S.

R SMART; SM000103; Kringle; S.

R SMART; SM00010; KR; S.

R PROSITE; PS000101; RRINGLE 1; S.

R PROSITE; PS000101; RRINGLE 2; S.

R PROSITE; PS001014; TRYPSIN LHS; PALSE NEG.

R PROSITE; PS001010; RRINGLE 2; S.

R PROSITE; PS001010; RRINGLE 3;
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 46;
 19.5%; Score 155; DB 1; Length 790; 27.2%; Pred. No. 1e-07; tive 16; Mismatches 56; Indels 4
 21.JUL-1986 (Rel. 01, Created)
1-JUR-1989 (Rel. 10, Last sequence update)
15.MAR-2004 (Rel. 43, Last annotation update)
Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin]
 400 AGL-TWNYCRNPDADKSPWCYT---TDPRVRWEYCNLKKCSE 437
 LGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
 KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 3.
KRINGLE 5.
CHARGE RELAY SYSTEM.
O-LINKED (GLCNAC. . .).
/FTIA-CAR_00019.
 F04EA06E74BCD58E CRC64;
 SERINE PROTEASE
 810 AA.
 [1]
SEQUENCE FROM N.A., AND VARIANT ASN-472.
 790 AA; 88592 MW;
 44; Conservative
 STANDARD;
 340
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 Query Match
Best Local Similarity
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 340
 PLMN HUMAN
ID PLMN HUMAN
AC P00747;
 DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
CARBOHYD
 47
 94
 CARBOHYD
 SEQUENCE
 DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 Matches
 RESULT
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Biochemistry 30:10576-10588(1991).
 human plasminogen kringle 4.";
Biochemistry 30:10589-10594(1991),
 numan plasminogen 2.";
J. Biol. Chem. 272:7408-7411(1997)
 CARBOHYDRATE-LINKAGE SITE SER-268.
 Eur. J. Biochem. 173:57-63(1988).
 plasminogen.";
Biochemistry 36:8100-8106(1997).
 PHOSPHORYLATION SITE SER-597
 [15]
CARBOHYDRATE-LINKAGE SITES
 18]
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```
308 NRTPENFPCKN----LDENYCRNPDGKRAPWCHTINSQVRWEYCKIPSCDSSPVSTEQLA 363
 364 PTAPPELTPVVQDCYHGDGQSYRGTSSTTTTGKKCQSWSS----MTPHRHQXTPENYPN 415
 5 HOVPSNCDCLNGGTCVSNKYFSN----IHWCNCP-KKFGGQHCBI---DKS------ 47
 -----KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHR---SDALQ 93
 X.-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
MEDLINE=98198034; PubMed=9521645;
Chang X., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
Castellino F.J.;
Structure and ligand binding determinants of the recombinant kringle
5 domain of human plasminogen.";
Biochemistry 37:3258-3271 (1998).
 Erinaceus europaeus (Western Buropean hedgehog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
[1]
 RickII E.E.;
"Recombinant gene expression and 1H NWR characteristics of the "Recombinant gene expression and 1H NWR characteristics of the Aringle (2 + 3) supermodule: spectroscopic/functional individuality of plasminogen kringle domains.";
Biochemistry 35:2357-2364(1996).
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
MEDLINE=96180681, PubMed=8611560;
Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
"Crystal structures of the recombinant kringle 1 domain of human plasminogen in complexes with the ligands epsilon-aminocaproic acid and trans 4-(aminomechyl) cyclohexane-1-carboxylic Acid.";
Biochemistry 35:2567-2576(1996).
 STRUCTURE BY NMR OF 183-354.
MEDLINE=96194156; PubMed=8652577;
Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas
 STRUCTURE BY NMR OF 96-184.
MEDLINE=94237157; PubMed=8181475;
Rejante M.R., Llinas M.;
"1H-NMR assignments and secondary structure of human plasminogen kringle 1.";
 MEDIJNE=94237158; PubMed=8181476; Rejante M.R., Llinas M.; "Solution structure of the epsilon-aminohexanoic acid complex of
 46;
 Length 810;
 50; Indels
 419 AGL-TMNYCRNPDADKGPWCFT---TDPSVRWEYCNLKKCS 455
 94 LGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCA 132
 19.4%; Score 154; DB 1; 28.0%; Pred. No. 1.3e-07;
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasminogen precursor (BC 3.4.21.7).
 810 AA.
 20; Mismatches
 J. Biochem. 221:927-937(1994)
 human plasminogen kringle 1.";
Eur. J. Biochem. 221:939-949(1994)
 STRUCTURE BY NMR OF 374-461.
MEDLINE=90219023; PubMed=2157850;
 STRUCTURE BY NMR OF 96-184
 Conservative
 STANDARD;
 Query Match
Query Match
Best Local Similarity
Local 45; Conserva'
 ERIEU
 48
 PLMN ER
Q29485;
 RXCOORDIGATION
 ద
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 a
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 셤
 CHARACTERIZATION OF ANGIOSTATIN.
MEDLLIBE 97238710; PubMed=9102221;
MEDLLIBE 97238710; PubMed=9102221;
Sim B.K., O'Really M.S., Lidang H., Fortier A.H., He W., Madsen J.W.,
Lapcevich R., Nacy C.A.;
"A recombinant human angiostatin protein inhibits experimental primary
and metastatic cancer ", 19997).
Cancer Res. 57:1329-1334 (1997).
 ĸ.
 porcine
 Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
 Trexler M., Vali Z., Patthy L., "Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen. Arginine 70 and aspartic acid 56 are essential for binding of ligand by kringle 4.";
 X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
Stec B., Yamano A., Whitlow M., Teeter M.M.;
"Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277
A possible structural role of disordered residues.";
Acta Crystallogr. D 53:169-178(1997).
 MEDLINE-92031503, PubMed-1657149, Wulichak A.M.; Wulichak A.M.; Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.; The refined structure of the epsilon-aminocaproic acid complex of
 and 34
 MEDLINE=88185329; PubMed=3356193;
Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
"The N- and O-linked carbohydrate chains of human, bovine and pc
plasminogen. Species specificity in relation to sialylation and
Eucosylation patterns.";
 CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
MEDLINE=59042728; PubMed=7520077;

O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;

"Angiostatin: a novel angiogenesis inhibitor that mediates the
suppression of metastases by a Lewis lung carcinoma.";

Cell 79:315-328(1994).
 MEDLINE-92031502; PubMed-1657148;
Mulfoak A.M., Tulinsky A., Ravichandran K.G.;
Mcrystal and molecular structure of human plasminogen kringle
refined at 1.9-A resolution.";
 FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
MEDLINE-85054794; PubMed=6094526;
Vali Z., Parthy L.;
"The fibrin-binding site of human plasminogen. Arginines 32 a are essential for fibrin affinity of the kringle 1 domain.";
J. Biol. Chem. 259:13690-13694(1984).
 MEDLINE=97345939; PubMed=9201958;
Wang H., Prorok M., Bretthauer R.K., Castellino F.J.;
"Serine-578 is a major phosphorylation locus in human plasma
 MEDLINE=97207306; PubMed=9054441;
Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
 X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
 K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
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 TISSUE-Liver;

MEDLINE=96025778; PubMed=7592597;

MEDLINE=96025778; PubMed=7592597;

Lam R.M., Boomark N.W., Meer K., Lindahl G.E., Wade D.P.,

Byrne C.D., Pong K.J., Meer K., Eatthy L.;

Lam R.M., Meer K., Eatthy L.;

Line recurring evolution of lipoprotein(a). Insights from cloning of hedgehog apolipoprotein(a).";

Line recurring evolution of lipoprotein(a). Insights from cloning of hedgehog apolipoprotein(a).";

Line recurring evolution of lipoprotein(a). Insights from cloning of heart of them. 270:24004-24009(1995).

REVISIONS.

Lam R.M.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

Line R.M.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

Line R.M.;

Submitted (PEB-1997) to the EMBL/GenBank/DDBJ databases.

Line R.M.;

Line R.M.;

Line R.M.;

Li
 -!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activators being bound to fibrin. Cannot be activated with streptokinase.
-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
-!- SIMILARITY: Belongs to opptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Contains 5 kringle domains.
 BMBL; U33171; AAC48717.1; -.

R HSR; 146260; 146260.

R HSR; 146260; 146260.

R HSRP; 900747; 14026.

R HSRP; 900747; 14026.

R HRCPPC; 150000001; Cya_Ser_trypsin.

R InterPro; 150000001; Faligle.

R InterPro; 150000001; Pan app.

R InterPro; 150001254; Peptidase_S1.

R InterPro; 150001254; Peptidase_S1.

R InterPro; 15000134; Peptidase_S1.

R InterPro; 15000134; Peptidase_S1.

R InterPro; 15000134; Peptidase_S1.

R Pfam; PF000024; PAN; 1.

R Pfam; PF000024; PAN; 1.

R Pfam; PF000039; trypsin; 1.

R RINTS; PR00103; KRINGLE.

R SMART; SM000130; KR; 5.

R SMART; SM00100; KR; 5.

R SMART; SM00010; KR; 5.

R RART; SM00010; KR; 5.

R RART; MN0010; KR; 5.

R PROSITE; PS00101; TRYPSIN INS; 1.

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SIMILARITY)
 PLASMINOGEN.
PLASMIN HEAVY CHAIN A (BY
PLASMIN LIGHT CHAIN B (BY
SERINE PROTEASE.
 BY SIMILARITY.
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboratio
 361 HSDAPVIVPPEQTPVVQECYQGNGQTYRGTSSTTITGKKCQPWTSMRPHRHSKTPENYPD 420
 Synthesis...

J. Biol. Chem. 264:5957-5965(1989).

J. Biol. Chem. 264:5957-5965(1989).

J. Biol. Chem. 264:5957-5965(1989).

J. PUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the uroxinase-type plasminogen activation follicle. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

J. CAPALYTIC ACTIVITY: Preferential cleavage: Lys- - Xaa > Arg- - Xaa, higher selectivity than trypsin. Converts fibrin into soluble
 ------CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQIYHAHRSDA
 QVPSNCDCLN-------GGTCVSNKYFSNIHW--CNCPKKFGGQHCEIDKSKT-
 Gaps
 MEDLINE-89174660; PubMed=2925643;
Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 PIG.

Macaca mulatta (Rhesus macaque).

Macaca mulatta (Rhesus macaque).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
 45;
 (POTENTIAL)
 19.4%; Score 153.5; DB 1; Length 810; 27.3%; Pred. No. 1.4e-07; rive 12; Mismatches 47; Indels 45.
KRINGLE 1.
KRINGLE 3.
KRINGLE 4.
KRINGLE 4.
KRINGLE 4.
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . .) (POTF
 01-007-1989 (Rel. 12, Created)
01-007-1989 (Rel. 12, Last sequence update)
08-ERB-2003 (Rel. 41, Last annotation update)
Plasminogen precursor (EC 3.4.21.7).
 92 LOLGLGKHNYCRNPDNRRRPWCY 114
 421 ADLTM---NYCRNPDGDKGPWCY 440
 90902
 Query Match
Best Local Similarity 2/...
Best Local Similarity 2/...
 STANDARD;
 103
185
275
275
379
622
622
662
760
760
7810 AA;
 SEQUENCE FROM N.A.
 RESULT 34
PLMN MACMU
ID PLMN MACMU
 DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
CARBOHYD
SEQUENCE
 20
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MEDLINE-91250378; PubMed=1645711;

MEDLINE-91250378; PubMed=1645711;

Ranalas J.J., Maxker S.P.;

Teceptor site for plasminogen.",

J. FinCTION: Plasminogen.",

D. Biol. (Chem. 266:10825-10829)

T. Following dector in a variety of other processes including a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as Cl and C5.

It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

Millebrand factor.

CATALYTIC ACTIVITY: Preferential cleavage: Iys-|-Xaa > Arg-|-Xaa > Ar
 57 FYRGKASTDIMGRPCLPWNSAIVLQQIYHAHR----SDALQLGLGKHNYCRNPD-NRRRP 111
BY SIMILARITY.
O-LINKED (GALNAC. . .) (BY SIMILARITY).
MY, A75EICSIAIA0F24A CRC64;
 10 NCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQ-------HCEIDKSKTCYEGNGH
 488 GYRGKKATTVTGTPEQEWAA-----QEPHSHRIFTPETNPRAGLEK-NYCRNPDGDVGGP
 Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
 19.2%; Score 152.5; DB 1; Length 810; 31.9%; Pred; No. 1.8e-07; ive 10; Mismatches 61; Indale No.
 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fragment).
 112 WCYVQVGLKPLVQECMVHDCA 132
 542 WCYT-INPRKLFDYCDVPQCA 561
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 550
543
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555
668
662
662
745
965
90255 1
 Local Similarity — hes 45; Conservative
 STANDARD;
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552
5531
567
607
729
756
365
810 AA;
 SEQUENCE FROM N.A.
 PLMN RAT
Q01177;
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
 | REAL | 194697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204697 | 204
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Name=1; Synonyma=kremen2a;

IsoId=Q8NCW0-1; Sequence=Displayed;
Name=2; Synonyma=kremen2a;

IsoId=Q8NCW0-2; Sequence=VSP_050509, VSP_050510;

Name=3; Synonyma=kremen2b;

IsoId=Q8NCW0-3; Sequence=VSP_050511, VSP_050512;

Name=3; Synonyma=kremen2b;

IsoId=Q8NCW0-4; Sequence=VSP_050513, VSP_050512;

Name=4; Synonyma=kremen2b;

IsoId=Q8NCW0-4; Sequence=VSP_050513, VSP_050514;

IsoId=Q8NCW0-4; Sequence=VSP_050511, VSP_050514;

IsoId=Q8NCW0-4; Sequence=VSP_050513, VSP_050514;

IsoId=Q8NCW0-4; Sequence=VSP_050511, VSP_050514;

IsoId=Q8NCW0-4; Sequence=VSP_050514;

IsoId=Q8NCW0-4; Sequence=VSP_050
 REAUTONING FROM N.A. (ISOFORMS 3 AND 4).

TISSUE=Brain, and Uterus;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. B., Boetow K.H., Schaefer C.F., Bhat N.K.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Sories M.B., Bonaldo M.F., Casarvant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan R.J., Mallek J.A., Gunarathe P.H.,

RA Brownstein M.J., McKernan R.J., Mallek J.A., Gunarathe P.H.,

RA Richards S., McWan P.J., McKernan R.J., Mallek J.A., Gunarathe P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hatting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.

RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Snailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RODELLUAR seceptor for Dickkopf protein. Cooperates with Dickkopf

C. I-FUNCIION: Receptor for Dickkopf protein. Cooperates with Dickkopf

C. Tecceptor LRP6 from the plasma membrane (By similarity).

PROFILE ALLEA LULAR LOCATION: Type I membrane protein (Potential).

REAURENTIANITUS RODORTION: Type I membrane protein (Potential).

RANDELLULAR LOCATION: Type I membrane protein.
 Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human cDNA sequencing project.", Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 Event=Alternative splicing; Named isoforms=4;
 EMBL, A8084605 BAC00823.1;
EMBL, A8086356; BAC00823.1;
EMBL, A8086356; BAC00823.1;
EMBL, A8086356; BAC00824.1;
EMBL, AK07659; BAB55281.1;
EMBL, AK076033; BAC1365.1;
EMBL, BC003533; AA403383.1;
EMBL, BC003533; AA403383.1;
EMBL, BC003503; AA403383.1;
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 3 EYCEIPSCGSSVSPDQSDSSVLPEQTPVVQECYQGNGKSYRGTSSTTNTGKKCQSW---- 58
 40 QHCEI------DKS-----KTCYEGNGHFYRGKASTDTMGRPCLPWNSAT 78
 TREMEZ HUMAN STANDARD; PRT; 462 AA.

QBNCWO; QBNZJ4; QBNCW1; Q9GGL8; Q9BTP9;
10-OCT-2003 (Rel. 42, Leated)
10-OCT-2003 (Rel. 42, Leat sequence update)
10-OCT-2003 (Rel. 42, Leat annotation update)
10-OCT-2003 (Rel. 42, Leateded)
10-OCT-2003 (
 Query Match
19.2%; Score 152; DB 1; Length 169;
Best Local Similarity 32.2%; Pred. No. 4.3e-08;
Matches 39; Conservative 16; Mismatches 30; Indels 36; Gaps
 [2]
SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
TISSUE=Ovarian carcinoma;
ISOGai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 | RMEL; M62832; A40522 | A4052 | A40522 :
114 E 114
 133 D 133
 KRM2 HUMAN
 RESULT 36
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VAINANTS RRS CYS-184; TRP-189; TRP-366 AND LYS-620.
MEDLINE=20392394; PubMed=10932186;
Afzal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,
Ternes-Pereira E., Tueysuez B., Murday V.A., Patton M.A.,
Wilkie A.O.M., Jeffery S.;
Wilkie A.O.M., Jaffery S.;
Nacestive Robinow syndrome, allelic to dominant brachydactyly type B,
is caused by mutation of ROPS.";
Nat. Genet. 25:419-422(2000).
 ERRATUM.

Van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.,
Nat. Ganet. 26:383-383(2000)

-! FUNCTION: Tyrosine-protein kinase receptor which may be involved
in the early formation of the chondrocyves. It seems to be
required for cartilage and growth plate development.
-! CATALTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 SEQUENCE FROM N.A.
MEDLINE=93100347; PubMed=1334494;
Masiakowski P., Carroll R.D.;
"A novel family of cell surface receptors with tyrosine kinase-like domain."; Chem. 267:26181-26190(1992).
 SEQUENCE OF 34-574 FROM N.A., AND VARIANT THR-245.
MEDLINE=20442029; PubMed=10986040;
Schwabe G.C., Tinschert S., Buschow C., Meinecke P., Wolff G.,
Gillessen-Kaesbach G., Oldridge M., Wilkie A.O.M., Koemec R.,
Mundlos S.,
"Distrinct mutations in the receptor tyrosine kinase gene ROR2 cause
brachydactyly type B.",
Am. J. Hum. Genet. 67:822-831(2000).
 [2]
SEQUENCE OF 34-943 FROM N.A., AND VARIANT ILE-819.
MEDLINE=20164326, Pubmed=10700182; MEDLINE=20164326, Pubmed=10700182; MEDLINE=20164326, Pubmed=10700182; Maringa M., Propping P., Mansour S., Pollitt C., DeChiara T.M., Kimble R.B., Valenzuela D.M., Parnorpoulos G.D., Wilkie A.O.M.; "Dominant mutations in RORZ, encoding an orphan receptor tyrosine kinase, cause brachydactyly type B."; Net. Genet. 24:275-278(2000).
 VEX.TANT RRS TYR-182.
MEDLINE-20392395; PubMed=10932187;
MEDLINE-20392395; PubMed=10932187;
MEDLINE-20392395; PubMed=10932187;
Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.:
Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.:
"Mutation of the gene encoding the ROR2 tyrosine kinase causes autosomal recessive Robinow syndrome.";
Nat. Genet. 25:423-426(2000).

 CYEGNGHFYRG---KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
93
 N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
SCLLAPCKGPPALGASKGPRRSWAWYQOPR -> CGALGQ.
GLRADRWWGAGAPEGNRARKELLGS (in isoform
 ARVESTYTAVSVILLILLGILRPIRRRSCILAPGKQPPALG
ASRGPRRSWAVWY -> GAVCWLREKGPRRWGLPGAPGEAG
LCGTWSPEGWPCPAPPGTPRLRVLPRATGL (in
 /FIId=WSP 050511.
Missing (in isoform 3).
Missing 050512.
ARVESTYANGWLLLLLIGILRPLRRRSCLLAP -> GEAGARDGSESGSRPIAPILITAAVCPQPGSSRR (in isoform
 Gaps
 ر.
در
 /Frid=vSP_050513.
Missing (In isoform 4).
Prid=vSP_050514.
Missing (In Ref. 2; BAC11365).
A -> D (in Ref. 2; BAC11365).
W; CE33015917A9AA68 CRC64;
 ch 18.7%; Score 148.5; DB 1; Length 462; Similarity 42.0%; Pred. No. 2.6e-07; 29; Conservative 9; Mismatches 26; Indels 5;
 ///
/Prid=VSP_050509.
Missing (in isoform 2),
 soform 3)
 202 Mi
285 A
48849 MW;
 420
 462
 399
 107 NRRRPWCYV 115
 :|||||
94 GDVQPWCYV 102
 164 2
285 2
462 AA;
 Local Similarity
 367
 421
 367
 400
 CONFLICT
CONFLICT
SEQUENCE
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 Query Match
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 VARSPLIC
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tyrosine phosphate.

1. SUBCELLULAR LOCATION: Type I membrane protein.

1. SUBCELLULAR LOCATION: Type I membrane protein.

1. DEVELOPMENTAL STAGE: Expressed at high levels during early embryonic development. The expression levels during strongly around day 16 and there are only very low levels in adult tissues.

1. DISEASE: Défecté in ROR2 are a cause of brachydactyly type B1 disorder characterized by hypoplasia/aplasia of distal phalanges and and mails. In BDB1 the middle phalanges are short but in addition the terminal phalanges are rudimentary or absent. Both fingers and toes are affected. The thumbs and big toes are usually deformed.

1. DISEASE: Défecte in ROR2 are a cause of recessive Robinow syndrome (RRS) (MIN:26810). RRS is an autosomal disorder characterized by skeletal dysplasia with generalized limb bone shortening, segmental defects of the spine, brachydactyly and a dysmorphic
 This SWISS-FROT entry is copyright. It is produced through a collaboratio
 SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
 subfamily.
-!-SIMILARITY: Contains 1 frizzled (FZ) domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- SIMILARITY: Contains 1 kringle domain.
 facial appearance.
```

D \_ROAZ\_HUMAN STANDARD; PRT; 943 AA.

C 001074, 09HbA1;

T 16-OCT-2001 (Rel. 40, Created)

T 15-OKT-2004 (Rel. 43, Last annotation update)

T 15-OKT-2004 (Rel. 43, Last annotation update)

E C 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).

R CRC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).

R CRC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).

S Homo sapiens (Human).

C Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;

C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(1)

RESULT 37 ROR2 HUMAN

m

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 TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR ROR2.
 EXTRACELLULAR (POTENTIAL)
 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
 FZ.
KRINGLE.
PROTEIN KINASE.
 POTENTIAL
 440
440
4440
4440
4440
4440
4440
 Disease mutation.
SIGNAL 1
CHAIN 34
 DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
```

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349
 CHARACTERIZATION.
MEDIJNBE-20164355; PubMed=10700181;
MEDIJNBE-20164355; PubMed=10700181;
DeChiara T.M., Kimble R.B., Poueymirou W.T., Rojas J., Masiakowski P., Valenzuela D.M., Yancopoulos G.D.;
"Ror2, encoding a receptor-like tyrosine kinase, is required for cartilage and growth plate development.";
Nat. Genet. 24:271-274(200).
Nat. Genet. 24:271-274(200).
 SECURICE FROM N.A.
MEDLINE=99248456; PubMed=10231392;
MEDLINE=99248466; PubMed=10231392;
MEDLINE=99248466; PubMed=10231392;
MEDLINE=99248466; PubMed=10231392;
MEDLINE=99248456; PubMed=10231392;
MEDLINE=99248410 Minami Y.;
"Spatio-temporally regulated expression of receptor tyrosine kinases, mRorl, mRorl, during mouse development: implications in development and function of the nervous system.";
Genes Cells 4:41-56(1999).
 299 NCMRIGIPAERLGRYH-----QCYNGSGMDYRGTASTTKSGHQCQPW--ALQHPHSHH
 32 NC-----PKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYH
 SER/THR-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NOBI_TaxID=10090;
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase transmembrane receptor ROR2 precursor
(BC 2.7.1.112) (Meurotrophic tyrosine kinase, receptor-related 2)
(mROR2).
 18;
 86 AHRSDALQLGLGKHNYCRNPDNRRR-PWCYVQVGLKPLVQECMVHDCA 132
 350 LSSTDFPELG-GGHAYCRNPGGQMEGPWCFTQ-NKNVRMELCDVPSCS 395
 Query Match 18.7%; Score 148; DB 1; Length 943; Best Local Similarity 34.3%; Pred. No. 5.8e-07; Matches 37; Conservative 12; Mismatches 41; Indels
 943 AA; 104726 MW; DBAC1E4622B5ECA0 CRC64;
 BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
C-> Y (in RRS).
FTIG=VAR. 0.10911.
R-> C (in RRS).
FTIG=VAR. 0.10769.
FTIG=VAR. 0.10769.
 R -> W (in RRS).
/FIId=VAR 010770.
N -> K (in RRS).
/FIId=VAR_010771.
 FTId=VAR_010912.
 FTIG=VAR 010913
 STANDARD;
 184
 189
 819
 819
 753
859
859
850
646
646
646
833
1188
1188
 184
 189
 245
 366
 620
 ROR2 MOUSE
ID ROR2 MOUSE
AC Q92138;
DOMAIN
DOMAIN
DOMAIN
NP BIND
BINDING
BACT SITE
MOD_RES
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
 SEQUENCE
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
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24;

us-09-880-503-4.rsp

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TISSUB-LIVE-2138B27; PubMed=12477932;

A KIAUSHDE-2138B27; PubMed=12477932;

A KIAUSHDER R.D., Feligold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Bacpleton M., Soares M.B., Bonaldo M.F., Carannor P.K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Doshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Robark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raber J., Helton B.K. Retreman M., Madan A., Rodrigues S., Sanchez A.,

Raber J., Helton B.K., Krayminski M.J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Schläka U., Smailus D.E.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

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B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones S.J.M., Marra M.A.,

B. Abrianch A., Schein J.E., Jones B., W. S., Marra M.A.,

B. Abrianch A., Schein J.E., Jones B., W. S., Marra M.A.,

B. Abrianch A., Schein J.E., Jones B., W. S., Marra M.A.,

B. Abrianch A., Schein J.E., Jones B., W., Marra M.B., S., Schein J., B., Jones B.,
 32 NC-----PKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYH
 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
 SEQUENCE OF 1-16 FROM N.A.
STRAIN-1292/SVJ, TISSUE-Liver;
PubMed=12149246;
Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
Parmer R.J., Miles L.A.,
"Localization of regulatory elements mediating constitutive and
cytokine-stimulated plasminogen gene expression.";
 86 AHR---SDALQLGLGKHNYCRNPDNRRR-PWCYVQVGLKPLVQECMVHDCA 132
 347 SHRLSSTEFPELG-GGHAYCRNPGGQMEGPWCFTQ-NRUVRVELCDVPPCS 395
 STRAIN=129/Sv, Maeltz P., Qian Y., Dudekula D., Schlessinger D. Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D. Nagaraja R., "Genomic sequence analysis in the mouse t-complex region."; "Genomic sequence analysis in the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
MEDLINE-91184812; PubMed-2081600;
Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
Characterization of the cDNA coding for mouse plasminogen and localization of the gene to mouse chromosome 17.";
Genomics 8:49-61(1990).
 P20918 (BCLS2; QSINUS; Created)
01-FEB-1991 (Rel. 17, Created)
11-CCT-2003 (Rel. 42, Last sequence update)
11-MAR-2004 (Rel. 43, Last annotation update)
Plasminogen precursor (EC 3.4.21.7) [Contains: Anglostatin].
 18.7%; Score 148; DB 1; Length 944; Conservative 11; Mismatches 36; Indels 2
 and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 812 AA
 STANDARD;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
TISSUE-Liver;
 Query Match
Best Local Similarity
Matches 40; Conserv
 PLMN MOUSE
 d
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 SER/THE-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
 EMBL; ABD10384; BAA75481.1; -.

R HSSP; PO0747; SHPG.

R MGD; MGI:1447521; Ror2.

R GO; GO:0001501; P:Reletal development; IMP.

InterPro; IPR001024; Fz_domain.

R InterPro; IPR001024; Fz_domain.

R InterPro; IPR001039; Fz_domain.

R InterPro; IPR001039; Fz_domain.

R InterPro; IPR00139; Fz_1.

R InterPro; IPR001245; Tyr_Dkinase.

R PF00047; Mgi 1.

PR PF00047; Mgi 1.

PR PF00049; KRINGLE; I.

PROSITE; PS00019; Fz; I.

PROSITE; PS00019; Fz; I.

PROSITE; PS00019; RKRINGLE 1; I.

PROSITE; PS00107; PROTEIN_KINASE_DOM; I.

PROSITE; PS00107; PROTEIN_KINASE_TOM; I.

PROTEIN PROSITE; PS00107; PROTEIN_KINASE_TOM; I.

PROSITE; PROSITE; PS00107; PROTEIN_FOM; I.

PROTEIN PROSITE; PROSITE I.

PROSITE; PROSITE; PROSITE I.

PR
 TYROSINE-PROTEIN KINASE TRANSMEMBRANE
RECEPTOR ROR2.
EXTRACELLULAR (FOTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 SÚBCELLULÂR LÔCATION: Type I membrane protein.
SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
in the early formation of the chondrocytes. It seems to be required for cartilage and growth plate development. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 subfamily.
--- SMILARITY: Contains 1 frizzled (FZ) domain.
--- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
---- SIMILARITY: Contains 1 kringle domain.
 CD2EEBC710387A56 CRC64;
 FZ.
KRINGLE.
PROTEIN KINASE.
SER/THR-RICH.
PRO-RICH.
 POTENTIAL.
 105050
 188
318
944 AA;
 DOMAIN
TRANSMEM ·
DOMAIN
 ACT_SITE
MOD_RES
DISULFID
CARBOHYD
 CARBOHYD
CARBOHYD
SEQUENCE
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP BIND
BIND
 SIGNAL
 CHAIN
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RIL 3. BIOL. Chem. 277:18579-18586[2002].

RIL 4. BIOL. Chem. 277:18579-18586[2002].

RIL 5. BIOL Chem. 277:18579-18586[2002].

RIL 5. BIOLOGICAL CHEM. C. BOUNDSTAIN, AND PARTIAL SEQUENCE.

RIL 5. BIOLOGICAL CHEM. C. BOUNDSTAIN, AND PARTIAL SEQUENCE.

RIL 5. BIOLOGICAL CHEM. C. C. C. C. S. S. SEG. E. H., Folkman J., C. C. C. Resenthal R. A., Messe N., Association of constants of the Constant of
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```
308 NRTPENFPCKN----LEENYCRNPDGETAPWCYTTDSQLKWEYCEIPSCESSASPDGSDS 363
 364 SVPPEEQTPVVQECYQSDGQSYRGTSSTTITGKKCQSW--AAMFPHRHSKTPENFPDAGL 421
 5 HOVPSNCDCLNGGTCVSNKYFSy----IHWC-NCPKKFGGQHCEI------DKS-- 47
 96
 48 ------KICYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGL
 Gaps
 SIMILARITY).
SIMILARITY).
SIMILARITY).
PROSITE; PSC0240; TRYPSIN_DOM; 1.
PROSITE; PSC0134; TRYPSIN_HIS; 1.
PROSITE; PSC0135; TRYPSIN_SER; 1.
HYDGTOLASE; Serine procease; Plasma; Glycoprotein; Fibrinolysis; Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 40;
 Length 812;
 ď
 56; Indels
 INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C -> H (IN REF. 1).
C -> D (IN REF. 1).

 PLASMIN SHORT FORM OF CHAIN ANGIOSTATIN.
 97 GKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
 PLASMINOGEN.
PLASMIN HEAVY CHAIN A.
ACTIVATION PEPTIDE.
 PLASMIN LIGHT CHAIN B.
KRINGLE 1.
 CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (STATIANITY)

BY SIMILARITY.

 Query Match
18.5%; Score 147; DB 1;
Best Local Similarity 26.4%; Pred. No. 6.3e-07;
Matches 42; Conservative 21; Mismatches 56;
 Ą
 461
 KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
 KRM2 MOUSE

ID KRM2 MOUSE STANDARD;

AC QRK.57;

DT 10-OCT-2003 (Rel. 42, Created)
 90781 MW;
 525
649
612 AA;
 ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
 DISULFID
DISULFID
DISULFID
DISULFID
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DISULFID
DISULFID
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 CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 DISULFID
 Signal.
CHAIN
CHAIN
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CHAIN
CHAIN
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DOMAIN
DOMAIN
DOMAIN
 SULFID
 DISULFID
 DOMAIN
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107 NRRRPWCYV 115

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CTHIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way conditied and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/announce/corsend an email to license@isb-sib.ch).

EMBL: AJ457192; CAD29805.1; -

DR EMBL: AJ457192; CAD29805.1; -

EMBL: AJ457192; CAD29805.1; -

EMBL: AJ457192; CAD29805.1; -

EMBL: AJ457192; CAD29805.1; -

EMBL: AJ457192; CAD29805.1; -

DR FEAR; PRO0001; Kringle: BR InterPro; IPRO0001; Kringle: BR InterPro; IPRO0001; Kringle: IRR InterPro; IPRO0001; Kringle: IRR INTERPROSO01; KRINGLE: IRR INTERPROSO001; KRINGLE: IRR INTERPROSO0001; KRINGLE: IRR INTERPROSO00001; KRINGLE: IRR INTERPROSO00001; KRINGLE: IRR INTERPROSO00001;
 10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Kremen protein 2 precursor (Kringle-Containing protein marking the eye and the nose) (Dickkopf receptor 2).
KREMEN2.
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 SEQUENCE FROM N.A., AND FUNCTION.
 NCBI_TaxID=10090;
 DOMAIN
DOMAIN
CARBOHYD
 CARBOHYD
 CARBOHYD
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N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
6D58C4A2858E09DA CRC64;
 49170 MW;
 48
221
243
350
350
461 AA;
 SEQUENCE
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50 CYEGNGHFYRGK---ASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPD 106

Query Match
18.5%; Score 146.5; DB 1; Length 461;
Best Local Similarity 42.0%; Pred. No. 4e-07;
Matches 29; Conservative 8; Mismatches 27; Indels 5;

Gaps

5,

35

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 TISSUE-Liver;
MEDLINE-9340141; PubMed-8393443;
MEDLINE-9340141; PubMed-8393443;
MEDLINE-93540141; PubMed-8393443;
MEDLINE-93540141; PubMed-872483;
Cloning, sequencing, and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of Kringle protein and locates the MSP gene on chromosome 3.";
J. Biol. Chem. 268:15461-15488 (1933).
-: FUNCTION: Probably has no proteolytic activity, since crucial AA characteristic of serine proteases catalytic sites are not
 -!- PTM: MAY BE CLEAVED AFFER AA 484, TO YIELD A TWO-CHAIN MOLECULE HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.
-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Contains 4 kringle domains.
 HGFL HUMAN STANDARD, PRT; 711 AA.
P26927; 013350; 014870;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 24, Last sequence update)
18-PEB-2003 (Rel. 41, Last annotation update)
Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP) (Macrophage stimulating protein)
MST1 OR HGFL
Momo sapiens (Human)
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
 TISSUE=Liver;
MEDLINE=92002016; PubMed=1655021;
Han S., Stuart L.A., Friezner Degen S.J.;
"Characterization of the DNF1582 locus on human chromosome 3:
identification of a gene coding for four kringle domains with
homology to hepatocyte growth factor.";
Biochemistry 30:9768-9780(1991).
 MIM, 142408; -.
InterPro; IRR009003; Cys Ser_trypsin.
InterPro; IRR000001; Kringle.
InterPro; IRR003014; PAN.
InterPro; IRR003104; PAN.
InterPro; IRR0031034; PAN.
InterPro; IRR0031534; Peptidase_S1.
InterPro; IRR0013134; Peptidase_S1A.
InterPro; IRR003966; IRR003166; PRINTS; PR00039; IRR003166; PRINTS; PR00722; CHYMOTRYPSIN.
 EMBL; M74178; AAASO165.1; -.
EMBL; U37055; AACS0471.1; -.
EMBL; L11924; AAAS9872.1; -.
PIR; A40331; A47136.
HSSP; P00747; 2PK4.
MEROPS; S01.975; -.
 MEROPS; S01.975; -. Genew; HGNC:7380; MST1.
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 conserved.
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77 ATVLQQTYHAHRSDALQLGLG--KHNYCRNPDNRRRPWCYVQVGLKPLVQEC---MVHDC 131
 361
 92
 ----QIPHQHRFTPEKYACKDLRENFCRNPDGSBAPWCFT---LRPGMRAAFCYQIRRC
 30 WC-NCPKKFGGQHCEIDK-----SKTCYEGNGHFYRGKASTDTMGRPCLPWNS
 Gaps
 POTENTIAL.
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
 (POTENTIAL). (POTENTIAL). (POTENTIAL).
PRINTS; PRO0018; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN.
Prodomy pb000395; Kringle; 4.
SMART; SM00130; KR; PAN AP; 1.
SMART; SM00130; KR; PAN AP; 1.
SMART; SM00120; TXPG SP; 1.
PROSITE; PS50070; KRINGLE 1; 4.
PROSITE; PS50240; TRYPSIN DOM; 1.
KRINGLE 2; 4.
PROSITE; PS50240; TRYPSIN DOM; 1.
SKINGLE; 1. 4.
PROSITE; PS50240; TRYPSIN DOM; 1.
 26;
 BY SIMILARIT.

BY SIMILARIT.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

FY MILARITY.

THIRARITY.

 18.2%; Score 144; DB 1; Length 711; larity 27.0%; Pred. No. 1.1e-06; Conservative 19; Mismatches 44; Indels
 INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
 /Frid=vAR 006632.
E -> K (in dbSNP:7798).
L TIG=vAR 014569.
L -> F (IN REF. 2).
i, 596ED21F180290E4 CRC64;
 ???
 SERINE PROTEASE-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 (GLCNAC.
 FTId=VAR_006631.
 SIMILARITY
 SIMILARITY
 SIMILARITY
 KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
 BY SIMILAR
BY SIMILAR
BY SIMILAR
N-LINKED (
N-LINKED (
N-LINKED (
 80379 MW;
 9/9
 711 AA;
 Similarity
 676
 AD 133
 TĎ 363
 33;
 CHAIN
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 310
 CONFLICT
 132
 362
 DISULFID
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 Query Match
 CARBOHYD
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 VARIANT
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HGF_HUMAN
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PRT;

HGF HUMAN STANDARD; P14210; Q9BYL9; Q9UDU6; 01-JAN-1990 (Rel. 13, Created)

DA FD

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MEDLINE=90066676; PubMed=2531289;
Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
Sugimura A., Tashiro K., Shimizu S.;
"Molecular cloning and expression of human hepatocyte growth factor ";
Nature 342:440-443 (1989)
 TISSUB=Placenta;
MEDLINE=89392017; Pubmed=2528952;
MEDLINE=89392017; Pubmed=2528952;
Arakaxi K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
Arakaxi N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
Gohda E., Dahkuhara Y., Kitamura N.;
"Molecular cloning and sequence analysis of cDNA for human hepatocyte
growth factor.";
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 SEQUENCE FROM N.A.
MEDLINE-91340155; PubMed=1831432;
Seki T., Hagjya M., Shimonishi M., Nakamura T., Shimizu S.;
"Organization of the human hepatocyte growth factor-encoding gene.";
Gene 102:213-219(1991).
 SEQUENCE FROM N.A.
TISSUB-Leukocyte;
MEDLINE=91025062; PubMed=2145836;
Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T.,
Asami O., Hagiya M., Nakamura T., Shimizu S.;
"Isolation and expression of CDNA for different forms of hepatocyte
growth factor from human leukocyte.";
Biochem. Biophys. Res. Commun. 172:321-327(1990).
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 site
 Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
Miyamoto K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson
Schackwitz W.S., Shrowod J.K., Mitrak L.A., Nickerson D.A.;
Submitted (FEB-2003) to the BMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
TISSUE-Embryonic fibroblast;
MBDLINE-91334393; PubMed=1831266;
MBDLINE-91334393; PubMed=1831266;
MRidner K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weiffeler H., Fonatsch C., Tsubouchi H., Hishida T., Daikuhara Y Birchmeier W.;
Birchmeier W.;
"Evidence for the identity of human scatter factor and human hepatocyte growth factor.";
Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
 SEQUENCE OF 249-695 FROM N.A.
MEDLINE=91369928; PubMed=1832556;
Miyazawa K., Kitamura A., Kitamura N.;
Structural organization and the transcription initiation inum hepatocyte growth factor gene.";
Biochemistry 30:9170-9176(1991).
 SIGNAL SEQUENCE CLEAVAGE SITE.
MEDLINE=91207365; PubMed=1826837;
Yoshiyama Y., Arakakai N., Naka D., Takahashi K., Hirono
 Courtney L., Elliot G., Angell S.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
 SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
TISSUE-Liver;
 iochem. Biophys. Res. Commun. 163:967-973(1989)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

NCBI\_TaxID=9606;

01-AUG-1991 (Rel. 19, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hepatocyte growth factor precursor (Scatter factor) (SF) (Hepatopoeitin A)

STRUCTURE BY NMR OF 31-127.
MEDIATE-98154323; PubMed=9493722;
Zhou H., Mazzulla M.J., Staffan J.D., Stahl S.J., Wingfield P.T.,
Rubin J.S., Bottaro D.P., Byrd R.J.;
"The solution structure of the N-terminal domain of hepatocyte growth
factor reveals a potential heparin-binding site.";
Structure 6:109-116(1998). CARBOHYDRATE-LINKAGE SITE THR-476.
MEDLINE=93129192; PubMed=1482348;
Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
Nakamura T., Shimizu S.;
"Hepatcoyte grown factor is linked by 0-glycosylated oligosaccharide on the alpha chain.";
Blochem. Blophys. Res. Commun. 189:1329-1335(1992). Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T., Hishlda T., Dalkuhara Y.; "Identification of the N-terminal residue of the heavy chain of both native and recombinant human hepatocyte growth factor."; Blochem. Blophys. Res. Commun. 175:660-667(1991). MEDLINE=99036858; PubMed=9817840;
Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;
Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;
Crystal structure of the NK1 fragment of human hepatocyte growth factor at 2.0-A resolution.";
Structure 6:1383-1393(1998).
-!- FUNCTION: HGF is a potent mitogen for mature parenchymal hepatocyte cells, seems to be an hepatotrophic factor, and acts as growth factor for a broad spectrum of tissues and cell types. It has no detectable protease activity.
-!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a disulfide bond. WEDLINE=92331602; PubMed=1321034;
MEDLINE=92331602; PubMed=1321034;
Baker N.A., Mark M.R., Luis B.A., Bennett G.L., Robbins K.A.,
Baker J.B., Gedowski P.J.;
"Structure-function analysis of hepatocyte growth factor:
"Identification of variants that lack mitogenic activity yet retain high affinity receptor hindred and the particle of receptor mitographic activity in EMBO J. 11:2501(1992). MUTAGENESIS 

Y246560; AAO61091.1; -.

SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily. SIMILARITY: Contains 4 kringle domains.

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EMBL, D90334, BAA14348.1, EMBL, D90318, BAA14348.1, OINED. EMBL, D90319, BAA14348.1, JOINED. EMBL, D90320, BAA14348.1, JOINED. EMBL, D90322, BAA14348.1, JOINED. EMBL, D90324, BAA14348.1, JOINED. EMBL, D90324, BAA14348.1, JOINED. EMBL, D90325, BAA14348.1, JOINED. EMBL, D90326, BAA14348.1, JOINED. EMBL, D90326, BAA14348.1, JOINED. EMBL, D90329, BAA14348.1, JOINED. EMBL, D90330, BAA14348.1, JOINED. EMBL, D90331, BAA14348.1, JOINED. EMBL, D90332, BAA14348.1, JOINED. EMBL, D90333, BAA14348.1, JOINED. EMBL; EMBL; EMBL;

CAA34387.1

X16323;

Query Match
17.8%; Score 141.5; DB 1; Length 728;
Best Local Similarity 30.3%; Pred. No. 2e-06;
Matches 44; Conservative 12; Mismatches 64; Indels 25; Gaps 10 53 GNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAH---RSDALQLGLGKHNYCRNP-DNR 108 335 HEHDMIPENFKCKOLRENYC-RNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 393 394 GNGKNYMGNLSQTRSGLTCSMWDKN---WEDLHRHIFWEPDASKL---NENYCRNPDDDA protease homolog; Repeat; 2 NELHQVPSNCDC--LNGGTCVSNKYFSNIHWC-----NCPKKFGGQ--HCBIDKSKTCYE MIN; 142409; —

GO; GO:0008083; F:growth factor activity; NAS.

R GO; GO:0008083; F:growth factor activity; NAS.

R GO; GO:0008083; F:growth factor activity; NAS.

R GO; GO:0008003; Cys Ser\_trypsin.

InterPro; IPR000001; Kringle.

R InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Psptidase\_S1.

InterPro; IPR001254; Fxingle; 4.

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us-09-880-503-4.rsp

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Plasminogen
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 TISSUE=Plasma;
X MEDINE=Pol17323; PubMed=2626424;
X Schaller J. Straub C., Kaempfer U., Rickli B.E.;
Schaller J. Straub C., Kaempfer U., Rickli B.E.;
Complete amino acid sequence of canine miniplasminogen.";
"Complete amino acid sequence of canine miniplasminogen acid acid a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follacle. It activates the urckinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5.
It claaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

C.:-CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
C.:-CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
C.:-CATALYTIC ACTIVITY: Converts fibrin into soluble
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
 Canis familiaris (Dog).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
 40
 ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound tfibrin. Activated with urokinase and high concentrations of
 SERINE PROTEASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
(Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 40, Last annotation update)
(EC 3.4.21.7) (Fragment).
 01-NOV-1991
01-NOV-1991
16-OCT-2001
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 50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHR----SDALQLGLGKHNYCRNP 105
 4 CMFGNGKGYRGKKATTVMGIPCQEWAA-----QEPHRHSIFTPETNPQAGLEK-NYCRNP 57
 -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 adrenal.

-!- DEVENOPMENTAL STAGE: Is expressed at low levels during gestation.

Just before birth the level increases dramatically and remains stable afterwards.

-!- PTH: MX BE CLEAVED AFTER AA 488, TO VIELD A TWO-CHAIN MOLECULE HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPRATE POLYPEPTIDES.
 152 152 STREPTOKINAE-BINDING SITE (PROBABLE)
186 186 STREPTOKINASE-BINDING SITE (PROBABLE)
264 264 STREPTOKINASE-BINDING SITE (PROBABLE)
277 277 SITE OF SUBSTRATE SPECIFICITY
(BY SIMILARITY).
333 AA, 36678 MW, C8C0271B6C6AC8D4 CRC64;
 Mus musculus (Mouse),
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Buthazoa, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
 conserved.
-!- TISSUE SPECIFICITY: Liver. Lower levels in lung, placenta and
(BY SIMILARITY)
 34; Indels 12;
 ch 17.8%; Score 141; DB 1; Length 333; I Similarity 41.4%; Pred. No. 1e-06; 36; Conservative 5; Mismatches 34; Indels 1
 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
14-patocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP).
 EMBL; M74180; AAAS0166.1; -.
EMBL; M74181; AAAS0167.1; -.
EMBL; M440332; A40332.
HSSP; P00747; IKRN.
MEROPS; S01.975; -.
MGD; MGI-95690; MSL1.
GO; 0007566; P:embryo implantation; IC.
InterPro; IPR009003; Cye_Ser_trypsin.
 106 D-NRRRPWCYVQVGLKPLVQECMVHDC 131
 58 DGDVNGPWCYT-MNORKLFDYCDVPQC 83
 STANDARD;
 Local Similarity
 HGFL MOUSE
P26928;
ACT_SITE
SITE
SITE
SITE
 SEQUENCE
 Query Match
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MEDLINE=94060105; PubMed=8241272;

Liu Y., Michalopoulos G.K., Zarnegar R.;

Liu Y., Michalopoulos G.K., Zarnegar R.;

Liu Y., Michalopoulos G.K., Zarnegar R.;

In Molecular cloning and characterization of cDNA encoding mouse

"Molecular cloning and characterization of cDNA encoding mouse

"Molecular cloning and characterization of cDNA encoding mouse

"Molecular Control Hor and the control of control in the control is seems to be an hepatotrophic factor, and acts as growth factor for a broad spectrum of tissues and cell types. It

"Molecular Control Hor and a broad spectrum of tissues and cell types. It

"SubMIT: Dimer of an alpha chain and a beta chain linked by a disulfide bond.

"Isoufe-Enlernative splicing; Named isoforms=2;

"Mame=Long;

Isoufe-Q08048-1; Sequence-Displayed;
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 Name=Short;
Isold=008048-2; Sequence=VSP_005408;
- SIMILARITY: Belongs to peptidase family Sl. Plasminogen subfamily.
|- SIMILARITY: Contains 4 kringle domains.
 SECTION OF AND SHORT), AND SEQUENCE OF 496-504. TISSUE=Bammary fibroblast;
MEDLINE=94183257; PubMed=8135822;
Sasaki M., Nishio M., Sasaki T., Enami J.;
Identification of mouse mammary fibroblast-derived mammary growth factor as hepatocyte growth factor.";
Biochem. Biophys. Res. Commun. 199:772-779(1994).
 TISSUE-Liver;
MEDLINE=94363381; PubMed=8081873;
Lee C.C., Kozak C.A., Yamada K.M.;
Lee C.C., genetic mapping, and expression of the mouse Hgf/scatter factor gene.";
Cell Adhes. Commun. 1:101-111(1993).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
01-NOV-1995 (Rel. 32, Last sequence update)
28 FRB-2003 (Rel. 41, Last annotation update)
Hepatocyte growth factor precursor (Scatter factor) (SF)
(Hepatopoeitin A).
 Cys_Ser_trypsin
Kringle.
 Pan_app.
Peptidase_S1.
Peptidase_S1A.
 EMBL; D10212; BAA01064.1; -.
EMBL; D10213; BAA01065.1; -.
EMBL; S71816; AAB31855.1; -.
EMBL; X72307; CAA51054.1; ALT_INIT.
PIR; JC2117; A60185.
 Fram, PF00051; Kringle, 4.
Pfam, PF00024; PAN, 1.
Pfam, PF00089; trypsin, 1.
 MECOPS, SOL.982; ...
MGD, MGI:96079; Hgf.
InterPro; IPR000001; K;
InterPro; IPR000001; K;
InterPro; IPR000001; K;
 InterPro; IPR001254;
InterPro; IPR001314;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 nterPro; I
 168 WCYTTNRSVRF--QSCGI---KTCREAVCVLCNGEDYRGEVDVTESGRECQRWD----L 217
 30 WC---NCPKKFGGQHCEIDKSKTCYEG----NGHFYRGKASTDTMGRPCLPWNSATVLQ 81
 POTENTIAL. HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
 22;
 protease homolog; Repeat; Signal.
 BY S.

BY SIMIL.

BY SIMILARIA

34 BY SIMILARITY.

364 BY SIMILARITY.

452 BY SIMILARITY.

452 BY SIMILARITY.

9 SIMILARITY.

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9 SIMILARITY.

9 SIMILARITY.

7 TARITY.

7 TARITY.

7 TARITY.
 17.5%; Score 139; DB 1; Length 716; 39.6%; Pred. No. 3.4e-06; ive 4; Mismatches 32; Indels
 -> Q (IN GENOMIC SEQUENCE)
BBCE02EF85213ACC CRC64;
 KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 3.
KRINGLE 4.
SERINE PROTEASE-LIKE.
BY SIMILARITY.
INTERCHAIN (BY SIMILAR
 218 OHPHSHPFQPEKFLDKDL-KDNYCRNPDGSERPWCY 252
 N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
 82 QTYHAH --- RSDALQLGLGKHNYCRNPDNRRRPWCY
 InterPro; IPR003014; PAN.
InterPro; IPR0030014; PAN.
InterPro; IPR001304; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF000014; Fingle; 4.
Pfam; PF000014; FAN; 1.
PRINTS; PR001018; KRINGLE.
PRINTS; PR001018; KRINGLE.
PRINTS; PR0010395; Kringle; 4.
SMART; SM001019; KR; 4.
SMART; SM001019; KR; 4.
SMART; SM001019; KR; 4.
SMART; SM00101; KR; MG; 1.
PROSITE; PS00021; KR; MG; 2.
KR; PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 2.; 4.
PROSITE; PS00021; KR; MG; 3.; 4.
PROSITE; PS00021; MG; MG; 3.; 4.
PROSITE; PS00021; MG; MG; MG; 3.; 4.
PROSITE; PS
 HGF MOUSE STANDARD;
QO8048; Q61662; Q64007;
01-NOV-1995 (Rel. 32, Created)
 80588 MW;
 IPR000001; Kringle.
 Conservative
 637 6
662 6
72 173 13
305 3
620 6
 Similarity
38; Conserv
 DISULFID
DISULFID
DISULFID
 CONFLICT
 DISULFID
 CARBOHYD
CARBOHYD
 DOMAIN
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Best Local
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 DISULFID
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 RESULT 45
HGF_MOUSE
ID HGF_M
AC Q0804
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EMBL; D90102; BAA14131.1; -.

EMBL; D90102; BAA14131.1; -.

BIRI; A35644; A35644.

BIRSP; P14210; LBHT.

MENOPS; S01.978; -.

BIRCPED; IPR000303; Cys Ser trypsin.

InterPro; IPR001314; Peptidase S1.

INTERPO; IPR001314; Peptidase S1.

INTERPRO; INTERPR
 -!-SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!-SIMILARITY: Contains 4 kringle domains.
-!-SIMILARITY: Contains 4 kringle domains.

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 SEQUENCE FROM N.A.
STRAINS-Wistar; TISSUB-Liver;
STRAINS-Wistar; TISSUB-Liver;
STRAINS-Wistar; TISSUB-Liver;
MEDLINE-91031482; PubMed-2146117;
Okajima A., Miyazawa W., Kitamura N.;
Nerimary structure of rat hepatocyte growth factor and induction of its many attructure of rat hepatocyte growth factor injury.";
Bur. J. Blochem. 193:375-381(1990).
I- FUNCTION: HGF is a potent mitogen for mature parenchymal hepatocyte cells, seems to be an hepatotrophic factor, and acts as growth factor for a broad spectrum of tissues and cell types. It has no detectable protease activity.
I- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
 KRINGLE 1.
KRINGLE 2.
KRINGLE 4.
SERING 4.
SERING POTABLE 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
 "Deduced primary structure of rat hepatocyte growth factor and expression of the mRNA in rat tissues.";
Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
 82905 MW;
 71
488
295
403
569
728 AA;
 disulfide bond.
 DOMAIN
DISULFID
DISULFID
 CARBOHYD
CARBOHYD
SEQUENCE
 CARBOHYD
 DOMAIN
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 SO THE TETER TRANSPREAM OF THE PROPERTY AND THE PROPERTY OF THE PROPERTY AND THE PROPERTY A
PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00018; KRINGLE.

PRODOM; PD000395; Kringle; 4.

PRODOM; PD000395; Kringle; 4.

SMART; SM00473; PR.

PROSITE; PS00021; KRINGLE_1; 4.

PROSITE; PS50070; KRINGLE_2; 4.

PROSITE; PS50040; TRYPSIN DOM; 1.

PROSITE; PS50240;
 11;
 444
 338 HDITPENFKCKDLRENYC-RNPDGAESPWCFTTDPNIRVGYCSQIPK-----CDVSSGQ 390
 HQV-PSNCDC--LNGGTCVSNKYFSNIHWC------NCPKKFGGQHCEIDKSK 48
 391 DCYRGNGROYMGNLSKTRSGLTCSMMDKN---MEDLHRHIFWEPDASKL---NKOYYCRNP
 49 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH---RSDALQLGLGKHNYCRNP
 11; Mismatches 57; Indels 38; Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
 KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 3.
KRINGLE 4.
SERINE PROTEASE-LIKE.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
Missing (in isoform Short).
/FTIG=VSP 005408.
N -> K (IN REF. 2).
V -> L (IN REF. 2).
K -> H (IN REF. 2).
K -> H (IN REF. 2).
 Pyrrolidone carboxylic acid.
BY SIMILARITY.
HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
HEPATOCYTE GROWTH FACTOR BETA CHAIN.
BYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=Wistar; TISSUS=Liver;
MEDLINE=9022197; PubMed=2139229;
Toshiro K., Hagiya M., Nishizawa T., Seki T., Shimonishi M.,
Shimizu S., Nakamra T.,
 17.5%; Score 139; DB 1; Length 728; 28.9%; Pred. No. 3.4e-06;
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hepatocyte growth factor precursor (Scatter factor) (SF)
(Hepatopoeitin A).
 728 AA
 106 -DNRRRPWCYVQVGLKPLV--QECMVHDC 131
 445 DDDAHGPWCYTG---NPLIPWDYCPISRC 470
 82944 MW;
 STANDARD;
 Rattus norvegicus (Rat).
 344 3
479 4
564 5
728 AA;
 CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
 CONFLICT
CONFLICT
CONFLICT
 DOMAIN
DOMAIN
DOMAIN
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 HGF_RAT
P17945;
 RESULT 46
HGF_RAT
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RN [2]
RN SGOURNEE FROM N.A.

RN STRAINBEZ2388257; PubMed=12477932;
RAS Strausberg R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

RAS Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat, N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Habth. R.K.,

RA Diatchenko L., Marusina K., Farmer R.A., Rubin G.M., Hong II.,

RA Diatchenko L., Marusina K., Parmer R.A., Rubin G.M., Hong II.,

RA Scapleton M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., NocEwan B.J., Nokernan K.J., Malek J.A., Gunaratne P.H.,

R. Rchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Hilalon D.K., Munzy D.M., Madan A., Rodrigues S., Sanchez A.

R. Sheey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 11 POSFAG------LITACVKGTGEGYRGTAALTVSGKACQAWASQT-----PGDVXS 115
 34 PKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQ
 MEDLINE-92212913; PubMed=1557383;

Banfield D.K., Macgillivray R.T.;

"Partial characterization of vertebrate prothrombin cDNAs:

"amplification and sequence analysis of the B chain of thrombin from nine different species.";
 Mus musculus (Mouse).
Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthazoa, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
 STRAIN=CSTBL/6; TISSUBE-Liver;
STRAIN=CSTBL/6; TISSUBE-Liver;
MEDLINE=91025551; PubMed=222810;
Fritzglbbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
Fitzglbbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
Characterization of the CDN coding for mouse prothrombin and localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
 / Match 17.2%; Score 136; DB 1; Length 325; Local Similarity 30.7%; Pred. No. 3.1e-06; nes 31; Conservative 7; Mismatches 41; Indels
296
308
325
35194 MW; 1B5F0B539AC6ED3C CRC64;
 94 LGLGKHINYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCADG 134
 116 CQGLVSNYCRNPDGEKLPWCYT----TEYCNVPSCTGG 149
 P19271,
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
F2 OR CF2.
 618
 SEQUENCE OF 384-618 FROM N.A.
295
307
315
325
325
325 AA;
 RESULT 48
THRE MOUSE
ID THRE MOUSE
NON CONS
NON CONS
NON CONS
NON TER
 Query Match
 Best Local
Matches
 FFFFS
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 Products.

1. SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.

2. I. SIMILARITY: Contains at least 2 kringle domains.

2. SIMILARITY: Contains at least 2 kringle domains.

2. SIMILARITY: Contains at least 2 kringle domains.

2. SIMILARITY: Contains at least 2 kringle domains.

3. SIMILARITY: SIMILARITY: Contains at least 2 kringle domains.

3. SIMILARITY: SIMILARITY: Contains RESIDER.

3. SIMILARITY: SIM
 391 DCYRGNGKNYMGNLSKTRSGLTCSMWDKN---MEDLHRHIFWEPDASKL---TKNYCRNP 444
 5 HQV-PSNCDC--LNGGTCVSNKYFSNIHWC------NCPKKFGGQHCBIDKSK 48
 Affolter M., Schaller J., Rickli B.B.;

"Isolation, characterization and partial amino acid sequence of
lamprey plasminogen.";

Protein Seq. Data Anal. 5:207-211(1993).

-!- FONCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion,
and inflammation.

-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
 338 HDITPENFKCKDLRENYC-RNPDGAESPWCFTTDPNIRVGYCSQIPK-----CDVSSGQ
 TCYBGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAH---RSDALQLGLGKHNYCRNP
 PLMN PETMA STANDARD; PRT; 325 AA.

933574;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 1, Last annotation update)
Plasminogen (EC 3.4.21.7) (Fragments).
Putamyoon marinus (Sea lamprey).
Eukaryoota; Meazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
Length 728;
 57; Indels
Query Match
17.5%; Score 139; DB
Best Local Similarity 29.5%; Pred. No. 3.4e.
Matches 44; Conservative 10; Mismatches
 445 DĎDAHGPWCYTG---NPĽVPWDYCPISRC 470
 106 -DNRRRPWCYVQVGLKPLV--QECMVHDC 131
 49
 SEQUENCE
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THKUNGLE 1.

KRINGLE 2.

SERING PROTASE.

CLEAVAGE (BY FACTOR XA).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

GAMMA -CARBOXYGLUTAMIC ACID.

GAMMA -CARBOXYGLUTAM
 THROMBIN HEAVY CHAIN (B)
 109 RRPWCYVQVGLKPLVQBCWVHDCAD 133
272 EGAWCYV-AGQPGDFEYCNLNYCEE 295
 STANDARD;
 AA;
 RESULT 49
THRB HUMAN
AC P00734,
DT 21-4UL-1986
DT 01-5AN-1990
DT 15-MAR-2004
DE Prothrombin 1970
CS Homo sapiens
OC BUKARYOTA; MOC MAMMALIA; FULL
OX NCBI_TAXID=99
RN [1]
RP SEQUENCE FROM
RY MEDLINE=8807
RY SEQUENCE FROM
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215 CLIERGRLYQGNLAVTLGSPCLPWNSLPAKTLSKYQDFDPEVKL---VENFCRNPDWDE
 50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD-NR
 Gaps
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 К. L.,
 5;
Query Match
15.8%; Score 125.5; DB 1; Length 618;
Best Local Similarity 31.8%; Pred. No. 6.2e-05;
Matches 27; Conservative 13; Mismatches 40; Indels 5
 SEQUENCE FROM N.A., AND VARIANT MET-165.
Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee
 SEQUENCE FROM N.A.
MEDLINE=88077877; PubMed=2825773;
Degen S.J.F., Davie E.W.,
"Nucleotide sequence of the gene for human prothrombin.";
Biochemistry 26:6165-6177(1987).
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DYSPROTHROMBINEMIA ALA-509

[13] VARIANT I

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X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
MEDLINE=9916251; PubMed=10051558;
Guinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di Cera E.;
"Unexpected crucial role of residue 225 in serine proteases.";
Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
 SEQUENCE OF 8-622 FROM N.A.
MEDLINE-83231469; PubMed-6305407;
Degen S.J.F., McGillivray R.T.A., Davie E.W.;
"Characterization of the complementary deoxyribonucleic acid and gene coding for human prothromin.";
Biochemistry 22:2087-2097(1983).
 성
 VARIANT DYSPROTHROMBINEMIA CYS-314.
MEDLINE=87033739; PubMed=3771562;
Rabbet M.-J., Furie B.C., Furie B.;
"Molecular defect of prothrombin Barcelona. Substitution of cysteine for arginine at residue 2733.";
J. Biol. Chem. 261:15045-15048(1986).
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=94350942; PubMed=8071320;
Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
Correa P.E., Fenton J.W. II, Tulinsky A.;
"Crystallographic structure of human gamma-thrombin.";
J. Biol. Chem. 269:22000-22006(1994).
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE=90327074; PubMed=2374926;
Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
Rydel T.C., Fenton J.W. II;
"The structure of a complex of recombinant hirudin and human alpha-
thrombin.";
 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

WEDLINES-90059942; PubMeda-2583108;

MOBLINES-90059942; PubMeda-2583108;

Mobe W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;

"The refined 1.9 A crystal structure of human alpha-thrombin:

"Interaction with D-Phe-Pro-Arg chloromethylketone and significance the Tyr-Pro-Pro-Pro-Pro-Insertion segment.";

EMBO J. 8:3467-3475 (1):899).
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MDDLINES-3757286. PubMed-9214615.
van de Locht A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
Esmon C.T., Stubbs M.T.;
The thrombin B1920-BPTI complex reveals gross structural
rearxangements: implications for the interaction with antithrombin
and thrombomodulin.";
 [5]
SEQUENCE OF 315-622.
MEDLINE=77207112; PubMed=873923;
Butkowski R.J., Elion J., Downing M.R., Mann K.G.;
"Primary structure of human prethrombin 2 and alpha-thrombin.";
J. Biol. Chem. 252:4942-4957(1977).
 MEDLINE=87008532; PubMed=3759958;
Rabiet M.J., Blashill A., Furie B., Furie B.C.;
"Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
activation in human plasma.";
J. Biol. Chem. 261:13210-13215(1986).
 SEQUENCE OF 44-314.
MEDLINE=77193964; PubMed=266717;
Walz D.A., Hewett-Emmett D., Seegers W.H.;
"Amino acid sequence of human prothrombin fragments 1 and 2.";
Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
Toth E.J., Yi Q., Nickerson D.A., to the EMBL/GenBank/DDBJ databases
 EMBO J. 16:2977-2984 (1997).
 Science 249:277-280(1990)
 Ozuna M., Poel C.L.,
Submitted (JAN-2002)
 10]
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VARIANT DYSPROTHROWBINEMIA VAL-601.
MEDLINE-89247398; PubMed=2719946;
Henriksen R.A., Mann K.G.;
"Substitution of valine for glycine-558 in the congenital dysthrombin thrombin Quick II alters primary substrate specificity.";
Biochemistry 28:2078-2082(1989).
 "Prothrombin Salakta: substitution of glutamic acid-466 by alanine reduces the fibrinogen clotting activity and the esterase activity."; Biochemistry 31:7457-7462(1992).
 "Detection of a single base substitution of the gene for prothrombin Tokushima, The application of PCR-SSCP for the genetic and molecular analysis of dysprothrombinemia."; Int. J. Hematol. 55:93-100(1992).
 MEDIINE=55313001, PubMed=7792730,
Degen S.J.F., McDowell S.A., Sparks L.M., Scharrer I.;
Prothrombin Frankfurt: a dysfunctional prothrombin characterized by substitution of Glu-466 by Ala.",
Thromb. Haemost. 73:203-209(1995).
 VARIANT DYSPROTHROMBINEMIA CYS-425.
MEDLINE-89207504; PubMed=3242619;
Henriksen R.-A., Mann K.G.;
Hightification of the primary structural defect in the dyschrombin thrombin Quick I: substitution of cysteine for arginine-382.";
Biochemistry 27:9160-9165(1988).
 "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan that impairs the fibrinogen clotting activity of derived thrombin
 VARIANT DYSPROTHROMBINEMIA TRP-461.

WINDLINE=87101511; Pubmed=3801671;
INDDOOR T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,
Miyoshi K., Morita T., Iwanaga S.;
Miyoshi K., Morita T., Iwanaga S.;
Prothrombin Tokushima: characterization of dysfunctional thrombin derived from a variant of human prothrombin.";
Blood 69:565-569(1987).
 VARIANTS DYSPROTHROMBINEMIA THR-380 AND HIS-431.
MEDILIBE-93043342; PubMed=1421398;
MEDILIBE-93043342; PubMed=1421398;
Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T., Yamaguchi K.,
"Prothrombin Himi: a compound heterozygote for two dysfunctional prothrombin molecules (Met-337-->Thr and Arg-388-->His).";
Blood 80:2275-2280(1992).
 an amino acid
 MEDLINE-92256895; PubMed=1149838;
Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito
Itakura M.;
 VARIANT DYSPROTHROMBINEMIA ALA-509.
MEDLINE-92378975; PubMed=1354985;
Miyata T., Aruga R., Umeyama H., Bezeaud A., Guillin M.-C.,
 VARÍANT DYSPROTHROMBINEMIA TRP-461.
MBDILNES91185407; PubMed=3567158;
Miyata I., Morita T., Inomoto T., Kawauchi S., Shirakami
Iwanaga S.;
 MEDLINE-95169898; PubMed-7865694;
James H.L., Kim D.J., Zheng D.-Q., Gizolami A.;
James H.E., Rim D.J., Zheng D.-Q., Gizolami A.;
Prothrombin Padua I: incomplete activation due to
subscitution at a factor Xa cleavage site.";
Blood Coagul. Fibrinolysis 5:841-844(1994).
 VARIANT DYSPROTHROMBINEMIA TRP-461.
 VARIANT DYSPROTHROMBINEMIA HIS-314.
 VARÍANT DYSPROTHROMBINEMIA LYS-200.
MEDLINE-83204687; PubMed-6405779;
 Biochemistry 26:1117-1122(1987).
 Tokushima.";
 [wanaga S.;
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us-09-880-503-4.rsp

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Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;

Lander E.S.;

Nat. Genet. 23:373-373 (1999).

-!- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin and activates factors V, VII, VIII, And, in complex with thrombomodulin, protein C. XIII, and, in complex with thrombomodulin, protein C. CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates fibrinogen to fibrin and releases fibrinopeptide A and B. SIBCELLULAR LOCATION: Expressed by the liver and secreted in plasma.
-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
-!- FIRSUE FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICHOSOWAL C.!- PTM: THE GAMMA-CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICHOSOWAL C.!- PTM: THE UITAMIN CARBOXYLAGE: THE MODIFIED RESIDUES ARE NECESSARY FOR THE CAPACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD-NR 108
 Lander E.S.; Additional A., Warrington J., Lipshutz R., Daley G.Q., "Lander E.S.;" "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";
 213 CVPDRGQQYQCRLAVTHGLPCLAWASAQAKALSKHQDFNSAVQL---VENFCRNPDGDE
 VARIANTS MET-165 AND THR-386.
MEDLINE-99318093; PubMed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 4; Gabs
Board P.G., Shaw D.C., "Determination of the amino acid substitution in human prothrombin type 3 (157 Glu leads to Lys) and the localization of a third thrombin cleavage site.";
 MEDLINE=20196006, PubMed=10731132,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 ROR2_DROME

ROR2_DROME

TO GOVERS, OGSCO1, O96391, Q9TYH9;

TO GOVERS, OGSCO1, O96391, Q9TYH9;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 41, Last sequence update)
 Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Meoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
 ch 15.6%; Score 124; DB 1; Length 622; I Similarity 38.8%; Pred. No. 8.7e-05; 26; Conservative 8; Mismatches 29; Indels
 SEQUENCE FROM N.A.
Frith K.J., Scott M.J.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
 Br. J. Haematol, 54:245-254(1983)
[23]
 human genes.";
.. Genet. 22:231-238(1999),
 109 RRPWCYV 115
 270 EGVWCYV 276
 STRAIN=Berkeley;
 20
 SEQUENCE
 Query Match
 Best Local
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 Matches
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brandon R.G., Worthman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej, R.G., Champe M., Pfeiffer B.D., R. Abrill J.F., Agdrawl A., An H.-D., Andrews-Frankoch C., Baldwin D., Ballew R.M., Basu A., Baxandle J., Bayraktaroglu L., Basaley E.M., Baeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakov S., Blorkova D., Botchan M.R., Bouck J., Barcketein P., Bottier P., Cadley E., Cawley S., Dahlke C., Davenport L.B. Doutiers P., Chadra I., R. Charles T., Canter A., Chadra I., R. Charles T., Canter A., Chadra I., R. Dougon C., Cawley S., Dahlke C., Davenport L.B., Davies P., R. Dougon C., Garley S., Dahlke C., Davenport L.B., Davies P., R. Dougon R., Gorzell J.H., Guz J., Ferriac S., Fleischmann W., R. Dougon E., Gorzell J.H., Guz J., Ferriac S., Fleischmann W., R. A. Dougon F., Gorzell J.H., Guz J., Harrey D.A., Harnandez J.R., Houck J., Harrey D.A., Harnandez J.R., Houck J., Harrey D.A., Harnandez J.R., Houck J., Markey D.A., Harnandez J.R., Indox M. M., Alaush F., Karpen G.H., Re Z., Kennison J.A., Noshrefi A., Andrei B., McIntosh T.C., McIndon M.P., Indox J., Moshrefi A., Monland T.J., Wei M.-H., Ibegwam C., Alauko P., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McIndon M.P., Morsher D.R., Pallson D.E., Mount S.M., Myor M., Mulphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murshy B., Murshy B., Murshy B., Murshy B., Musskern D.R., Smith T., Shine B.C., Siden-Kiamos I., Sungeon M., Stupski M.P., Smith T., Shine B.C., Siden-Kiamos I., Weinsenbach J., Wang Z., Mang Z.-Y., Wang Z., Zhan M., Zhong W., Zhong W., Zhong W., Zhong W., Zhong X., Wang Z., MEDLINE=98401146; PubMed=9731193;

MEDLINE=98401146; PubMed=9731193;

Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;

Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;

Sampling the genomic pool of protein tyrosine kinase genes using the polymerase chain reaction with genomic DNA.";

Biochem. Biochem. Stophys. Res. Commun. 249:660-667(1998).

-!- FUNCTION: Tyrosine-protein kinase receptor that functions during early stages of neuronal development (By similarity).

--- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein ENGUENCE OF 17-724 FROM N.A., AND CHARACTERIZATION.
TISSUB=Imaginal disks;
MEDLINE=9727331; PubMed=9115253;
MEDLINE=9727331; PubMed=0115253;
MEDLINE=9727331; PubMed=0115253;
MEDLINE=97270331;
The nervous system of the nervous system of the structural features and implication in developmental signaling.";
J. Biol. Chem. 272:11916-11923(1997). tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
ISSUB ESCIFICITY: Expressed in neural cell lineage from embryonic stage 11 onwards, resulting in expression in the brain and ventral nerve cord at the end of embryogenesis. REVISIONS.

MEDLINE-22426069; PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,

Benth C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

Lewis S.E., A. Droconhila melanogaster euchromatic genome: a Systematic review."; Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002) [5] SEQUENCE OF

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C. 1- DENTLONREWING STATES Expressed at thich levels in end-yos and carried and pulse show maximal expression.

1- SINILARITY: Belongs to the Tyr family of protein kinases. RGR enterast. In the Tyr family of protein kinases. RGR enterasts. Sinilarity: Contains I fringle domain.

1- ```

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Db 212 ESBVSYDCRNGRRPYMGITMAVSKSGIPCQRWDI-----QYPHKHPQPPLVFHQL-LEGE 265
QY 100 NYCRNPDNRR-RPWCYVQVGLKPLVQECMVHDCAD 133
Db 266 NYCRNAGGEEPHPWCYT-VDESVRWQHCDIPMCPD 299
```

Search completed: May 25, 2004, 14:53:49 Job time : 6.20596 secs

43 EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL---QLGLGKH 99

Query Match
15.2%; Score 120.5; DB 1; Length 724;
Best Local Similarity 35.8%; Pred. No. 0.00022;
Matches 34; Conservative 5; Mismatches 45; Indels 11; Gaps

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ATF.
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Q8m10 cryctolagus
Q8mhy7 cryctolagus
Q9tva8 bos taurus
Q9c612 mus musculu
Q727n2 homo sapien
Q9bu99 homo sapien
Q9xc70 cryctolagus
Q8xq23 sus scrofa
Q8xq23 sus scrofa
Q8xd22 mus musculu
Q14520 homo sapien
Q9xq3 mus scrofa
Q8xq24 mus musculu
Q14520 homo sapien
Q9xq4 mus scrofa
                                                                May 25, 2004, 14:44:05 ; Search time 22.362 Seconds (without alignments) 1904.795 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                US-09-880-503-4
793
1 SNBLHQVPSNCDCLNGGTCV.....QVGLKPLVQECMVHDCADGK 135
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                  1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 75 summaries
                                             - protein search, using sw model
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08M1L0
08M1L0
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02C6L2
02C6L2
02EVR8
09BU99
09M170
08SQ23
09MKB1
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1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
7: sp_mhc:*
8: pp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
11: sp_rodent:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_unclassified:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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444000000000000000000000000000000000000	109.1 109.1 109.0 10	7.4 1455 7.2 2869 7.1 2869 6.7 213 6.7 264 6.5 264 6.5 263 6.5 263 6.5 263 6.5 263 7.2 263 7.2 263 7.2 263 7.2 263 7.3 263 7.4 263 7.4 263 7.5 263 7.5 263 7.5 263 6.5
24,24,24,24,24,24,24,24,24,24,24,24,24,2	440 150.5 150.5 150.5 149 149 149 149 149 149 149 149 149 149	13. 13. 13. 13. 13. 13. 13. 13. 13. 13.
444000000000000000000000000000000000000		RESULT 777777777777777777777777777777777777
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59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNPRRPWCYVQVG 118
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CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC BMBL, X712288; AAMS1307.1; -

CG GO:0004639; F:chymotrypein activity; IEA.

CG; GO:0006501; F:kinase activity; IEA.

CG; GO:0006202; F:rypsin activity; IEA.

CG; GO:0006203; F:rypsin activity; IEA.

CG; CG:0006203; F:rypsin; IEA.

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Query Match

75.9%; Score 602; DB 6; Length 433;

Best Local Similarity 76.6%; Pred. No. 2.5e-57;

Matches 105; Conservative 10; Mismatches 20; Indels 2; Gaps
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Yano W., Matanabe M.;

Yano W., Matanabe M.;

Yano W., Matanabe M.;

Yono W., Matanabe M.;

Younglete daus cuniculus urokinase-type plasminogen activator, mRNA, complete das.",

Submitted (JUL-2012) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Urokinase-type plasminogen activator.
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"Overexpression of the amino-terminal fragment of human urokinase-type plasminogen activator in breast cancer cells results in decreased tumor invasion, growth and anglogenesis.";

Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.

"I. SIMILARITY: CONTAINS! KRINGLE DOWAIN.

BMBL; AY029337; AAK38734.1;

"I. SIMILARITY: CONTAINS! KRINGLE DOWAIN.

ROS GO: GO: GO: 1 PRO06020; EGF 11ke.

BRD: AR00001; Fringle.

PRODOM; PD000035; Kringle.

PRINTS; PR00018; KRINGLE.

PRODOM; PD000035; KRINGLE.

PRODOM; PD000035; KRINGLE.

ROSITE; PS00021; KRINGLE.

ROSITE; PS00021; KRINGLE.

ROSITE; RS00021; KR
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     Homo sapiens (Human).
Vakaryotes, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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MEDLINE=22155945; PubMed=12149463;
MEDLINE=22155945; PubMed=12149463;
Dichek D.A.;
Dichek D.A.;
"Increased expression of urokinase during atherosclerotic lesion development causes arrearial constriction and lumen loss, and accelerates lesion growth.";
Proc. Natl. Acad. Sci. U.S.A. 99:10665-10670(2002).
                                                                                                                                                                                                                                                                                                                                                                                       human
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Query Match

Sest Local Similarity 99.3%; Pred. No. 5.1e-77;

Matches 133; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                    Fu_J, Bai X., Ruan C.;
"Cloning and expression of the amino-terminal fragment of
"rokinase-type plasminogen activator.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Urokinase-type plasminogen activator.
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SEQUENCE_FROM N.A.
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QBMILO;
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5 DP ò 엄 ò RESULT 2

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RN 11)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUB=Covary;

RX MEDINE=2554663; PubMed=12466851;

RA THE PANTOM CONSORTIUM,

THE PANTOM CONSORTIUM,

THE PANTOM CONSORTIUM,

RA THE PANTOM CONSORTIUM,

RA THE PANTOM CONSORTIUM,

RA THE RIKEN Genome Exploration Research Group Phase I & II Team;

RA TANALYSIS Of the mouse transcriptome based on functional annotation of 60,770 full.length CDNAs.";

RI MALINE 420:563-573(2002).

BR THE AKO5434; BRC35743.1; -.

DR EMBL; AKO5434; PRC354.

DR GO; GO:0004295; F:Crypsin activity; IEA.

DR GO; GO:0004295; F:Crypsin activity; IEA.

DR GO; GO:0004295; F:Crypsin activity; IEA.

DR GO; GO:0006508; P:Proteclysis and peptidolysis; IEA.

DR InterPro; IPR000630; CRF like.

DR InterPro; IPR000630; F:Crypsin.

DR InterPro; IPR001629; F:Crypsin.

DR Pfam; PF00089; trypsin; 1.

DR Pfam; PF00089; trypsin; 1.

DR PF000M; PD000395; KRINGLE.

DR SMATT; SM00130; KR; 1.

DR PROSITE; PS00021; KRINGLE.

DR PROSITE; PS00021; KRINGLE.

NON MED:

231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CLNGGKCVTYKYFSNIQRCSCPKKFQGEHCEIDISKTCYQGNGHSYRGKANRDLSGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 CLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Plasminogen activator (Fragment).
Mus musculus (Mouse)

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.4%; Score 550; DB 6; Length 157; Best Local Similarity 75.6%; Pred. No. 3.9e-52; Matches 93; Conservative 11; Mismatches 19; Indels
                  NON TER 231 231 - SEQUENCE 231 AA; 25510 MW; 25E8980A682737F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia, Eutheria
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 DGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 VGK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 RGKANTDIMDRPCLAWNSANVLTKTYHAHRPDALQLGLGGGGNYCRNPDHQRRPWCYVQVG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 SHBLHGVSDASNCGCLNGGTCVTYKYFSNIMRCNCPKKFQGEHCBIDTLKTCYHGDGHSY 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNELHQV -- PSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIRSF; PIRSF011144; Urk plasm act; 1.
Glycoprotein; Hydrolase; KinaBe; Kringle; Protease; Serine protease.
SEQUENCE 433 AA; 48444 MW; 6DD35A371010A6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Urokinase plasminogen activator (Fragment).
Bus taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Skeletal muscle;

TISSUE=Skeletal muscle;

TISSUE=Skeletal muscle;

BEDINE=21071388; PubMed=11204721;

Balcerzak D., Querenguesser L., Dixon W.T., Baracos V.E.;

"Coordinate expression of matrix-degrading proteinases and their
"Coordinate expression of matrix-degrading proteinases and their
"coordinate expression of matrix-degrading proteinases and their
J. Anim. Sci. 79:94-107(2001).
-!- SIMILARITY: CONTAINS I KRINGLE DOMAIN.
BENEL; AF144761; AAD30301.1;
-!- SIMILARITY: CONTAINS I KRINGLE DOMAIN.
HSSP; POO749; IURX.

GO; GO:0016301; F. Kinase activity; IEA.
InterPro; IPR066209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.9%; Score 602; DB 6; Length 433; 76.6%; Pred. No. 2.5e-57; ive 10; Mismatches 20; Indels
EMBL; AV029517; AAK40239.1; -.

EMBL; AB087224; BAC02685.1; -.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004231; F:chymotrypsin activity; IEA.

GO; GO:0004233; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin.

InterPro; IPR005005; Cys Ser_trypsin.

InterPro; IPR006001; Kringle.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001214; Peptidase_S1.

InterPro; IPR001214; Peptidase_S1.

REAM; PR00121; Kringle; 1.

REAM; PR00122; CRINGLE.

REAM; PR00120; KRINGLE.

REAM; PR01214; RRINGLE.

REAM; PR01240; TRYPSIN IN.

REAM; PR011E; PS00124; TRYPSIN IN.

REAM; PR05ITE; PS00124; TRYPSIN IN.

REAM; PR05ITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 LKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 LKOLIQECKVHDCSSGK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 76.6%
Matches 105, Conservative
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Q7Z7N2 Q7Z7N2;

RESULT 6

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59 RGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.4%; Score 328.5; DB 4; Length 562; Best Local Similarity 46.3%; Pred. No. 2.3e-27; Matches 63; Conservative 14; Mismatches 54; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEFTIDASE FAMILY S1.
-1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
RFML; BC002795; AAH02795.1; -1.
RSP; PC00720; 1A5H.
CG; GG:0004283; F:chymotrypsin activity; IEA.
CG; GG:0004233; F:chymotrypsin activity; IEA.
CG; GG:0004233; F:trypsin activity; IEA.
CG; GG:0006508; P:trypsin activity; IEA.
CG; GG:0006508; P:proteolysis and peptidolysis; IEA.
RIGEPPO; IPR006209; CGF-like.
InterPro; IPR006209; GGF-like.
                                  R THEETPO: IPRO06003; Fibrings: and peptidolysis; LEA.

RINGERPO: IPRO06003; Fibring.

RINGERPO: IPRO06001; Fibring.

RINGERPO: IPRO00001; Fibring.

RINGERPO: IPRO01254; Peptidase_S1.

RINGERPO: IPRO01254; Peptidase_S1.

R PÉam; PRO0003; Firit 1.

R PÉAM; PRO0003; Firit 1.

R PÉAM; PRO0003; Firit 1.

R PEANTHS; PRO0013; Firingle; 2.

R SMART; SM00039; Kringle; 2.

R SMART; SM00125; Trypsin; 1.

R PROSITE; PS01253; FIRRONECTIN 1; 1.
                          peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to plasminogen activator, tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 LKPLVQECMVHDCADG 134
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196 GKYSSEFCSTPACSEG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 RPCLAWNAPAVLQKPYNAHRPDAISLGLGKEHNYCRNPDNQKRPWCYVQIGLRQPVQECWY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 RGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                30 SNCGCQNGGVCVSYK7FSRIRRCSCPRKFQGEHCEIDASKICYHGNGDSYRGKANIDIYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ELHQVP-SNCD---CLNGGTCVSNKYPSNIHWCNCPXKFGGQHCEIDKSKTCYEGNGHFY
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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2
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Best Local Similarity 46.3%; Pred. No. 1.1e-27;
Matches 63; Conservative 14; Mismatches 54; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Aleder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A., Madanek S.A. Rajkumar N., Toth E.J., Yi Q.,
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY291060, AAP34246.1; -
SEQUENCE 291 AA, 32191 MW; 874E38C52F50EFID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu Y., Xu L., Zeng Y., He X.;
"cDNA of tissue plasminogen activator.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY22111, AA034406.1;
GO, GO:0005576; C:extracellular; IEA.
GO, GO:0004263; F:chymotrypsin activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Plasminogen activator, tissue type isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                 291 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 25, Created)
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                                                                                                                                                                                                                                                              150 HDCSLSK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLAT.
Homo sapiens (Human)
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01-OCT-2003 (
01-OCT-2003 (
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Q86YK8 Q86YK8;

RESULT 7

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R InterPro; IPR000001; Kringle.
R InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
Pfam; PF00008; EGF; 1.
R Pfam; PF00008; EGF; 1.
R Pfam; PR00089; Lrypsin; 2.
R PRINTS; PR00018; KRINGLE.
R PRINTS; PR00018; KRINGLE.
R PRINTS; PR00018; KRINGLE.
R SMART; SM00130; KR; 2.
SMART; SM00130; KR; 2.
R SMART; SM00130; KR; 2.
R PROSITE; PS00021; EGF; 1, 1.
R PROSITE; PS00021; KRINGLE.; 2.
R PROSITE; PS00021; KRINGLE.; 2.
R PROSITE; PS00013; KRINGLE.; 2.
R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN LS; 1.
                                                                                                                                                                                                                                                                                                       516 AA; 57370 MW; BAB31901FDC96800 CRC64;
                                                                                                                                                                                                                                                                                       Serine protease
SEQUENCE 516
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Query Match
40.7%; Score 322.5; DB 4; Length 516;
Best Local Similarity 44.4%; Pred. No. 9.5e-27;
Matches 64; Conservative 13; Mismatches 56; Indels 11;

23 SQEIHARFRGARSYQGCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATC 81 1 SNELM------QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTC 50 ò g

111 PWCYVQVGLKPLVQECMVHDCADG 134 142 PWCYVFKAGKYSSEFCSTPACSEG 165 ò

01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Urokinase-type plasminogen activator (Fragment)
Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus. PRELIMINARY; RESULT 9 Q9XT70

TISSUE=Lung;

YIN 1, IGEAL S.;

A Yin J., IGEAL S.;

A Yin J., IGEAL S.;

A Yin J., IGEAL S.;

I "Partial mRNA of rabbit uPA.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

C -: SIMILARITY: CONTAINS I KRINGLE DOWAIN.

R HSSP; POOT99; ILD.

R MSOPS; SOL 23 1.

R GO; GO:0004263; F: Chymotrypsin activity; IEA.

GO; GO:0004263; F: P: Peptidase activity; IEA.

GO; GO:0006233; F: P: Peptidase activity; IEA.

GO; GO:0006268; F: P: Peptidase activity; IEA.

R GO; GO:0006283; F: P: Peptidase activity; IEA.

R InterPro; IPR000001; Kringle.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRO0722; CHYMOTRYPSIN.

PR00712; SM00130; KR; 1.

SMART; SM00130; KR; 1.

PR0STIR; PS0021; Tryp_SPC; 1.

PR0STIR; PS50240; TRYPSIN_DOM; 1.

PR0STIR; PS50134; TRYPSIN_DOM; 1.

PR0STIR; PS00134; TRYPSIN_HIS; 1.

Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.

SDQÜENCE 214 AA; 24314 MW; 69975C41C32B0D7E CRC64; Query Match 39.5%; Score 313; DB 6; Length 214; Best Local Similarity 78.3%; Pred. No. 4e-26; Matches 54; Conservative 5; Mismatches 10; Indels

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127 MVHDCADGK 135 | | | : | 61 KVHDSSGKK 69

Q8SQ23 PRELIMINARY; PRT; 562 AA.
Q8SQ23;
Q8SQ23;
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
T-plasminogen activator.
T-plasminogen activator.
Enskaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CRELID=9623; RESULT 10 Q8SQ23

us-09-880-503-4.rspt

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5 HOVP-SNCD---CLINGGICVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRG
                                                                                                                                                                        61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                       ; Score 301.5; DB 6; Length 564;
; Pred. No. 2.1e-24;
13; Mismatches 41; Indels 5;
                       PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease
SECUENCE 564 AA; 62726 MW; 459D8BACGD4A937C CRC64;
                                                                                                                                                                                                                                                                                              517 AA
                                                                                                          38.0%;
48.7%;
                                                                                                         Query Match 38.0%;
Best Local Similarity 48.7%;
Matches 56; Conservative
                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                        77 CCHSVPVKSCSEPRCFNGGTCLQAIYFSDF-VCQCPVGFIGRQCEIDARATCYEDQGITY 135
                                                                                                                                                                                                                                                  59 RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                     3 BLHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYBGNGHFY 58
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
PROSITE; PS00021; KRINGLE 1; 2.
PROSITE; PS50240; TRYPSIN_2: 2.
PROSITE; PS50240; TRYPSIN_0; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
BGF-like domain; Glycoprofein; Hydrolase; Kringle; Protease; Serine protease 562 AA; 6260 M.
                                                                                                                                  39.2%; Score 310.5; DB 6; Length 562;
43.8%; Pred. No. 2.1e-25;
tive 14; Mismatches 58; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiki M. Yoshida E., Anai K., Maruyama M.;
Sugiki M. Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDDES FAMILY SI.
-!- SIMILARITY: ERLONGS TO PEPTIDDES FAMILY SI.
R GO; GO:0004263; F:CNYDAINS 2 KRINGLE DOWAINS.
R GO; GO:0004263; F:CNYDAINA activity; IEA.
GO; GO:0004263; F:CNYDAINA activity; IEA.
R GO; GO:0004263; F:CNYDAINA activity; IEA.
R GO; GO:0004263; F:CNYDAINA activity; IEA.
R GO; GO:0004263; F:CNYDAINA activity; IEA.
R GO; GO:0004263; F:CNYDAINA activity; IEA.
R GO; GO:0006269; F:CNYDAINA activity; IEA.
R InterPro; IPR000003; Cys_Ser_trypsin.
InterPro; IPR000003; Cys_Ser_trypsin.
R InterPro; IPR000003; Cys_Ser_trypsin.
INTERPRO; IPR000003; File.
INTERPRO; IPR000003; File.
R InterPro; IPR000003; File.
R InterPro; IPR000003; File.
R InterPro; IPR000003; File.
R InterPro; IPR000003; File.
R InterPro; IPR000003; File.
R InterPro; IPR00003; Kringle; 2.
R PRINTS; PR00013; Kringle; 2.
R SWART; SM00130; KRINGLE.
R SWART; SM00130; FILE.
R SWART; SM00130; FILE.
R SWART; SM00130; FILE.
R PROSITE; PS01130; FILEROMECTIN 1; 1.
R PROSITE; PS01131; FILEROMECTIN 1; 1.
R PROSITE; PS01121; KRINGLE 1; 2.
R PROSITE; PS00013; KRINGLE 1; 2.
                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Tissue-type plasminogen activator.
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                    119 LKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                            196 EKYSPDFCSTPACTKEK 212
                                                                                                                                                             60; Conservative
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                              Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                               RESULT 11
QBMKB1
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13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
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01-MX-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
FXII.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                         Query Match 32.5%; Score 257.5; DB 4; Length 560; Best Local Similarity 42.1%; Pred. No. 1.3e-19; Matches 51; Conservative 18; Mismatches 49; Indels 3
PROSITE; PS00135; TRYPSIN_SER; 1.
BGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
Serine protease.
SEQUENCE 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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775 S 775
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                                                                                                   174 YWNSHLLLQETYNMFWEDAETHGIAEHNFCRNPDGDHKPWCFVKVNSEKVKWEYCDVTVC 233
                                                                                                                                                     73 PWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQE-CMVHDC 131
                                                                          13 CLNGGICVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Purification and characterization of a novel hyaluronan-binding protein (PHBP) from human plasma: it has three EGF, a kringle and a serine protease domain, similar to hepatocyte growth factor activator.";
                                                                                                                                                                                                                                                                                                    O14520; 000663; 01. Created)
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
HOF activator like protein (Hyaluronan binding protein 2).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96425001; PubMed=8827452;
Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
33.4%; Score 264.5; DB 11; Length 517; 42.5%; Pred. No. 2e-20; tive 18; Mismatches 48; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POUR SEQUENCE FROM N.A.

TISSUB=Colon, and Kidney;

Stratsberg R.;

Stratsberg R.;

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

-!- SIMILARITY: CONTAINS I KRINGLE DOWAIN.

EMBL; D49742; BAA08876.1; -.

EMBL; S83182; AAB46909.1; -.

EMBL; S83182; AAB46909.1; -.

EMBL; BOO7412; AAB41412.1; -.

EMBL; JC4795; JC4795.

R GO: CO. CO. CO. CO. S.;

R HSSP; POO763; IDPO.

R HSSP; POO763; IDPO.

R GO: CO. CO. CO. S.;

R GO: CO. CO. CO. S.;

R GO: CO. CO. CO. S.;

R GO: CO. CO. S.;

R GO: CO. CO. S.;

R GO: CO. CO. S.;

R InterPro; IPRO0903; Cys. Ser_trypsin.

R InterPro; IPRO01314; Peptidase_SI.

R InterPro; IPRO01354; Peptidase_SI.

R InterPro; IPRO0136; Peptidase_SI.

R Pfam; PRO0008; EGF. 3.

R Pfam; PRO0008; KRINGLE.

R PRINTS; PRO0125; KRINGLE.

R PROSITE; PS01025; KRINGLE.

R PROSITE; PS01025; KRINGLE.

R PROSITE; PS01036; KRINGLE.

R PROSITE; PS0104; TRYPSIN_DOM; I.

R PROSITE; PS0104; TRYPSIN_DOM; I.

R PROSITE; PS0104; TRYPSIN_DOM; I.

R PROSITE; PS0104; TRYPSIN_HIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biochem. 119:1157-1165(1996).
                                       51; Conservative
                                                                                                                                                                                                                                                                                         PRELIMINARY;
              Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kitamura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomita M.,
  Query Match
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Q14520
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69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 CLNGGTC----VSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08VCS4;

01-MAR-2002 (TYENBLrel. 20, Created)

01-MAR-2002 (TYENBLrel. 20, Last sequence update)

01-OCT-2003 (TYENBLrel. 25, Last annotation update)

Hypothetical protein.

Mus musculus (Mouse)

Mus musculus (Mouse)

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelecetomi,

Musmmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                      31.8%; Score 252.5; DB 13; Length 540; 39.5%; Pred. No. 4.3e-19; ive 15; Mismatches 51; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMOO181; EGP; 2.

SMART; SMOO181; ER1; 1.

SMART; SMOO182; ER1; 1.

SMART; SMOO182; ER2; 1.

R SMART; SMOO182; ER2; 1.

R PROSITE; PSOO182; EGF=1; 2.

R PROSITE; PSOO182; RIBROMELL; 1.

R PROSITE; PSOO191; KRINGLE 1; 1.

R PROSITE; PSOO191; KRINGLE 1; 1.

R PROSITE; PSOO191; KRINGLE 1; 1.

R PROSITE; PSOO193; TRYPSIN HS; 1.

R PROSITE; PSOO135; TRYPSIN HS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     653 A.A.
  Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 39.5%
hes 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 TSCA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00008;
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Matches
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Q8VCS4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 ÓVCSTNPCLNGGSCLQTE---GHRLCRCPTGYAGRLCDVDLKERCÝSDRGLSÝRGMAQTT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 IMGRPCLPWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 LSGAPCQPWAS----EATYWWMTAEQALNWGLGDHAFCRNPDNDTRPWCFVWRGDQLSWQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                            6 QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=22122796; PubMed=12128063;
Holbberger D.R., Becker A.E., Thurston R.J., Rice C.D.;
Holbberger D.R., Becker A.E., Thurston R.J., Rice C.D.;
"Expression of a hepatcoryte growth-factor activator protein in turkey (Meleagris gallopavo) deferent duct epithelial cells.";
Comp. Biochem. Physiol. 132:769-777 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0900Y7,
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocyte growth factor activator (Fragment).
Hepatocyte growth factor activator (Fragment).
Hepatocyte gallowed (Common turkey).
Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
11
                                                                  PROSITE; PS01253; FIBRONECTIN 1; 1.
PROSITE; PS0023; FIBRONECTIN 2; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS500240; KRINGLE 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A SEQUENCE FROM N.A.

A Holsberger D.R., Becker A.E., Thurston R.J., Rice C.D.;
L Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AV216598, AAQ46038.1, --
GO, GO:0004263, F:Chymotrypsin activity; IEA.
GO, GO:0004263; F:Chymotrypsin activity; IEA.
GO, GO:0004263; F:Chymotrypsin activity; IEA.
GO, GO:0004263; F:Chymotrypsin activity; IEA.
R GO, GO:0004263; F:Chymotrypsin activity; IEA.
R GO, GO:0004263; F:Chymotrypsin activity; IEA.
R GO; GO:0004263; F:Chymotrypsin activity; IEA.
R InterPro; IPR000043; CGF 2.
R InterPro; IPR000620; EGF 2.
R InterPro; IPR000621; IEGF 2.
R InterPro; IPR000621; IEGF 2.
R InterPro; IPR000124; Psptidase_S1.
R InterPro; IPR001254; Psptidase_S1.
R InterPro; IPR001254; Psptidase_S1.
R InterPro; IPR001254; Psptidase_S1.
R InterPro; IPR001254; Psptidase_S1.
                                                                                                                                                                                                                                                                                                                                          Query Match
32.4%; Score 257; DB 6; Length 616;
Best Local Similarity 40.9%; Pred. No. 1.6e-19;
Matches 52; Conservative 14; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                               616 AA; 68012 MW; 4C5FE3D71EBBD1A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 ECMVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 YCRLARC 295
                                                                                                                                                                                                                                                                Serine protease
SEQUENCE 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q800Y7
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Q800Y7
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73 PWNSAIVLQQIY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                        | Processor | Proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to coagulation factor XII (Hageman factor) (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P SEQUENCE FROM N.A.

C STRAIN-FVB/N; TISSUE=Liver;
Strausberg R.;
L Submitted (NAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC049867; AAH49867.1; ---
GO; GO:0005576; C:extracellular; IEA.

GO; GO:0004263; F:calium ion binding; IEA.

GO; GO:0004285; F:carium ion binding; IEA.

GO; GO:0004285; F:carium ion binding; IEA.

GO; GO:000608; F:carium ion binding; IEA.

RO; GO:000608; F:carium ion binding; IEA.

RO; GO:000608; F:carium ion binding; IEA.

RO; GO:0006509; F:carium ion binding; IEA.

InterPro; IPR006083; Cyg_Ser_trypsin.

RITERPRO; IPR000083; Fibrnctn1.

RITERPRO; IPR000083; Fibrnctn1.

RITERPRO; IPR000081; Fibrnctn1.

RITERPRO; IPR000081; Fibrnctn1.

RITERPRO; IPR000001; Kingle.

RITERPRO; IPR000001; Kringle.

RITERPRO; IPR001284; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
31.4%; Score 249; DB 11; Length 59'
Best Local Similarity 40.8%; Pred. No. 1.2e-18;
Matches 49; Conservative 14; Mismatches 49; Indels
                                         InterPro; IPR001314; Peptidase S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q80YCS

1D Q80YCS

D80YCS

D1-JUN-(1)

D1-JUN-(1)

D1-JUN-(1)

D2 01-JUN-(1)

D2 01-JUN-(1)

D3 01-JUN-(1)

D4 01-JUN-(1)

D5 01-JUN-(1)

D6 01-JUN-(1)

D7 01-JUN-(1)

D8 INTERPY

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                                              d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 HTACLSSPCLNGGTC-----HIVGTGTSVCTCPLGYAGRECNIVPTEHCPLGNGT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 HQVPSNCDCLNGGTCVSNKYFSNIHW------CNCPKKFGGQHCEIDKSKTCYEGNGH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 FYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 BYRGVASTAASGLSCLAMNSDLLYQELHVDSVAAAVLLGLGPHAYCRNPDKDERPWCYV 348
Pfam; PF00051; kringle; 1.

R Ffam; PR001099; trypsin; 1.

R RRINTS; PR00122; CHYMOTRYPSIN.

R RRINTS; PR00121; CHYMOTRYPSIN.

R PRO013; FNYPPE II;

R PCDOM; PD000995; Kringle; 1.

R PCDOM; PR00181; KRINGLE.

R PCDOM; PR00181; KRINGLE.

R SWART; SM00181; EGF; 2.

R SWART; SM00181; EGF; 2.

R SWART; SM00181; EGF; 2.

R SWART; SM00181; EGF 2; 1.

R SWART; SM00182; EGF 1; 2.

R PROSITE; PS001022; EGF 2; 1.

R PROSITE; PS001023; FIBRONECTIN 1; 1.

R PROSITE; PS001023; FIBRONECTIN 2; 1.

R PROSITE; PS00103; FIRRONECTIN 2; 1.

R PROSITE; PS00103; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R RAINGLE; PS00134; TRYPSIN DOM; 1.

R RAINGLE; PS00135; TRYPSIN DOM; 1.

R RAINGLE; PS00135; TRYPSIN DOM; 1.

R RAINGLE; PS00134; TRYPSIN DOM; 1.

R RAINGLE; PS00134; TRYPSIN DOM; 1.

R RAINGLE; PS00134; TRYPSIN DOM; 1.

R RAINGLE; PS00135; TRYPSIN DOM; 1.

R RAINGLE; PS00134; TRYPSIN DOM; 1.

R RAINGLE; PS00135; TRYPSIN DOM; 1.

R 
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%; Score 250.5; DB 11; Length 653; 42.0%; Pred. No. 8.8e-19; ative 11; Mismatches 41; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Schloesser M., Schwager S., Engel W., Schloesser M., Schwager S., Engel W., Schloesser M., Schwager S., Engel W., Schloesser M., Schloesser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-07N-1998 (TrEMBLrel. 05, Created)
01-07AN-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.09
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Factor XII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035727
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                    DRAW WWW SON BRANCH STREET STR
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Peptidase_S1A

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13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 29.4%; Score 233; DB 4; Length 615; Local Similarity 42.3%; Pred. No. 6.7e-17; nes 44; Conservative 12; Mismatches 40; Indels .8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BZW1;

Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Neonatal thrombolytic agent alpha-form (Fragment).

Homo sapiens (Human).

Bukaryota, Metazoa; Cordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 R PÉEMI; PO00089; EGG; 2.

R PÉEMI; PF000089; EGG; 2.

R PÉEMI; PF000089; EGG; 2.

R PÉEMI; PF000089; EGG; 2.

R PELINTS; PR000122; CHYMOTRYPEIN.

R PRINTS; PR00013; FNITYPEII.

R PRINTS; PR00018; FNITYPEII.

R PRODOM; PD000995; FNITYPEII.

R PRODOM; P0000995; FNITYPEII.

R SWART; SM0019; EGG; 2.

R SWART; SM0019; EGG; 2.

R SWART; SM0019; EGG; 2.

R SWART; SM00209; FNIT, 1.

R SWART; SM00209; FNIT, 1.

R PROSITE; PS00021; EGG; 2.

R PROSITE; PS00021; FIREONECTIN. 1; 1.

R PROSITE; PS00021; FIREONECTIN. 2; 1.

R PROSITE; PS00021; TRYPSIN. DOM; 1.

R PROSITE; PS00134; TRYPSIN. BR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 PWAS----EATYRNVTAEQARNWGLGGHAFCRNPDNDIRPWCFV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 PWNSATVLOOTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    databases,
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The main of the substitution of substitution 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 20
Q9BZW1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 PWNSATVLQQTY-HAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 RW----TVEATYRNWTEKQALSWGLGHHAFCRNPDNDTRPWCFVWSGDRLSWDYCGLEQC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Gaps
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Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;

"Molecular chracterization of coaggulation factor XII Mie.";

"Molecular chracterization of coaggulation factor XII Mie.";

Submitted (NOV-202) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0005576; F:cakridm ion binding; IEA.

R GO; GO:0005509; F:cakridm ion binding; IEA.

R GO; GO:0006508; P:trypsin activity; IEA.

R GO; GO:0006508; P:trypsin activity; IEA.

InterPro; IPR001903; Cys Ser trypsin.

InterPro; IPR001903; Cys Ser trypsin.

InterPro; IPR00181; EGF Ca.

InterPro; IPR00183; Fibranctn.

R InterPro; IPR00183; Fibranctn.

R InterPro; IPR00191; IEGF.

InterPro; IPR00154; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.1-MAR-2003 (TrEMBirel. 23, Created)
0.1-MAR-2003 (TrEMBirel. 23, Last sequence update)
0.1-OCT-2003 (TrEMBirel. 25, Last annotation update)
0.2-OCT-2003 (TrEMBirel. 25, Last annotation update)
Coagulation factor XII-Mie.
Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.8%; Pred. No. 1.2e-18;
Matches 49; Conservative 14; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          609 AA; 66783 MW; DF97D4DB2369B6D2 CRC64;
InterPro; IPR001314; Peptidase_S1A, Pfam; PF00008; EGF; 2. Pfam; PF00009; fm1; 1. Pfam; PF000040; fm2; 1. Pfam; PF000051; kringle; 1. Pfam; PF000051; kringle; 1. PRINTS; PR00013; kringle; 1. PRINTS; PR00013; kringle; 1. PRODOM; PR00013; kringle; 1. SWART; SW001013; kringle; 1. SWART; SW0019; EGF_CA; 2. SWART; SW0019; EGF_CA; 2. SWART; SW00058; FN1; 1. SWART; SW00058; FN1; 1. SWART; SW00059; FN2; 1. SWART; SW00059; RR; 1. PROSITE; PS01186; EGF_2; 1. PROSITE; PS01186; EGF_2; 1. PROSITE; PS01186; EGF_2; 1. PROSITE; PS01186; EGF_2; 1. PROSITE; PS01134; TRYPSIN_BRS; 1. PROSITE; PS01134; TRYPSIN_BRS; 1. PROSITE; PS01134; TRYPSIN_BRS; 1. NON TRK SEQUENCE 609 AA; 66783 MW; DP97D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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         SO OR NO OR 
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12 WCYVFKAGKYISEFCSTPACTKVAEDGDCYTGNGLAYRGTRSRTKSGFSCLPWNPVFLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 QQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKIYTALEEQRRALGLGKHNHCRNPDGDAQPWCHVWKDRQLTWEYCDVPQC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%; Score 197.5; DB 13; Length 202; 36.9%; Pred. No. 1.5e-13; ive 11; Mismatches 50; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0018; KRINGLE.
ProDom; PRO00195; KRINGLE.
PROSTE; PRO001010; KR.
PROSTE; PSO0021; KRINGLE 1; 1.
PROSTE; PSO0020; KRINGLE 2; 2.
PROSTE; PSO0010; KRINGLE 2; 2.
PROSTE; PSO0104; TRYPSIN_DOM; 1.
Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
NON_TER 202 202
SEQÜENCE 202 AA; 23148 MW; 049DB42941DB3AFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 202
202 AA; 23148 MW; 049DB42941DB3AFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS, 2010.1.21.
GO: GO: 0008233; F: peptidase activity; IEA.
GO: GO: 0008233; F: peptidase activity; IEA.
GO: GO: 0004295; F: trypsin activity; IEA.
GO: GO: 0005608; F: proteclysis and peptidolysis; IEA.
INTERPRO; IRR009003; Cys Ser trypsin.
INTERPRO; IRR00001; Kringle.
INTERPRO; IRR001254; Peptidase_SI.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Tissue-type plasminogen activator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
Kremen2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                TPA.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus
                                                                                                                          Q90675
               RESULT 22
Q90675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8AXX3
                                                                                           DDT THE BEAR WAY OF THE PARTY AND THE PARTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 CYEGNGHFYRGKASTDIMGRPCLPMNSAIVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 WCNS----GRAQCS-EGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 WCNCPKKFGGQHCEIDXSKTCYEGNGHFYRGKASTDTWGRPCLPWNSATVLQQTYHAHRS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
R Pfam, PP00051; kringle; 1.

R Pfam; PP00051; kringle; 1.

R PRINTS; PR00029; trypsin; 1.

R PRINTS; PR00028; Kringle; 1.

R SWART; SW00058; Kringle; 1.

R SWART; SW00050; Tryp SPC; 1.

R PROSITE; PS00021; Tryp SPC; 1.

R PROSITE; PS00021; KRINGLE 1; 1.

R PROSITE; PS00034; KRINGLE 2; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN ER; 1.

R PROSITE; PS00135; TRYPSIN ER; 1.

R PROSITE; PS00135; TRYPSIN ER; 1.

R PROSITE; PS00353; TRYPSIN ER; 1.

R PROSITE; PS00353; TRYPSIN ER; 1.

R PROSITE; PS00353; TRYPSIN ER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.9%; Score 229.5; DB 4; Length 395; 42.7%; Pred. No. 1e-16; Live 10; Mismatches 44; Indels 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

27.6%; Score 218.5; DB 4; Length 90;
Best Local Similarity 49.4%; Pred. No. 3.2e-16;
Matches 41; Conservative 5; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SEQUENCE FROM N.A. | Dou D.; | Public Prom N.A. | Dou D.; | Perduction of kringle fragment."; | Perduction of kringle fragment."; | Submitted (JTM-2000) to the EMBL/GenBank/DDBJ databases. | Submitted (JTM-2000) to the EMBL/GenBank/DDBJ databases. | EMBL; APS282802; AAMS2248.1; -. | SIMILARITY: CONTAINS 1 KRINGLE | PERUTS; PRO0001; KRINGLE | R. PRODOM; PRO00395; KRINGLE | R. SWART; SM00130; KR; 1. | R. SWART; R. SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 SAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 DALQLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 395 AA; 44323 MW; 3FBD4A2F0B7C11C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein, Kringle. SEQUENCE 90 AA; 9804 MW; A33887F9FDF4C7B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0AT-2003 (TrEMBLrel. 23, Last annotation update)
Plasminogen/activator kringle.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 RPWCYVQVGLKPLVQECMVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 КРИСУТ-ТИРККІУ БУСЬ В В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.9%
Best Local Similarity 42.7%
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Q8NG20;
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RESULT 21 Q8NG20

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441 LHQDPSAC------THIPPFDFKKE------NITRICYSGNGGFYQGWAN 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 VTASGIPCOKWS-----DOAPHLHRRTPQVFPELSDA-----ENYCRNPGGENERPWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.5%; Score 170.5; DB 13; Length 947; 32.4%; Pred. No. 7.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruiz i Altaba A., Thery C.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 4 TRINGLE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                947 AA; 105588 MW; E6C3FCC5796CC8BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Growth factor Livertine.
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.4%; Pred. No. 7.16
ive 13; Mismatches
                                                 INCEPTO INVOISSES IN INCEPTOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 YVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 YTK---DPSVTWEYCSVSPCGD 545
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0018; KRINGLE.
PRINTS; PRO0109; TYRKINASE.
PRODOM; PD000395; Kringle; 1.
ProDom; PD00001; Prot_kinase;
         Fz domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       091691 PRELIMINARY;
091691;
01-NOV-1996 (TremBirel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom, PD000395; Kringle Probom, PD000001; Prot Ki. SMART; SM00409; IG; 3. SMART; SM00408; IGc2; 3. SMART; SM00130; KR; 1. SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor, Kinase
SEQUENCE 947 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSSI
PROSITE; PSSI
PROSITE; PSSI
PROSITE; PSSI
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PROSITE; PSSI
                                       nterPro
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 HCEIDKSKICYEGNGHFYRGKAS-TDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDIINE=20538710; PubMed=11083926;
Ip F.C., Glass D.G., Gies D.R., Cheung J., Lai K.O., Fu A.K.,
Yancopoulos G.D., Ip N.Y.;
"Cloning and characterization of muscle-specific kinase in chicken.";
Mol. Cell. Neurosci. 16:661-673(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 HPELSE---CFTVNGRDYRGTVSQAGPEGTPCLYWNQTT--QHLYNAQSDPDGELGLGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oainus gatus (chicken).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                    MEDLINE=22308873; PubMed=12421700;
Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;
"Kremen proteins interact with Dickkopf1 to regulate anteroposterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gies D., Glass D.J., Yancopoulos G.D.;
SEQUENCE FROM N.A.
Gies D., Glass D.J., Yancopoulos G.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX144173; AAN05008.1; -..
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005874; C:miorotubule; IEA.
GO; GO:0005874; C:miorotubule; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:000598; F:transmembrane receptor activity; IEA.
GO; GO:0007713; F:protein-tyrosine kinase activity; IEA.
GO; GO:000775; F:protein-tyrosine kinase activity; IEA.
GO; GO:0007775; F:protein-mino-acid movephorylation; IEA.
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microtubule-based movement; IEA.
protein amino acid phosphorylation; IEA.
33; Beta_tubulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch
21.9%; Score 174; DB 13; Length 4;
1 Similarity 47.4%; Pred. No. 1.2e-10;
36; Conservative 6; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74D04DB1682CD15F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CGT-2003 (TrEMBLrel. 25, Last annotation update)
Muscle-specific receptor tyrosine kinase MuSK.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    947 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                          CNS patterning.";
Development 129:5587-5596(2002).
EMBL, AV150813; AAN64661.1; -..
InterPro; IPR000089; CUB.
InterPro; IPR000001; Kringle.
InterPro; IPR00289; WSC.
InterPro; IPR00289; WSC.
Pfam; PP00431; CUB; 1.
Pfam; PP00421; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01180; CUB; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
SEQUENCE 421 AA; 46274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 NYCRNPDNRRRPWCYV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 NYCRNPDADVQPWCYV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kringle; 1
                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0018; KRINGLE.
ProDom; PD000395; Kringle;
SMART; SM00120; KR; 1.
SMART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxiD=9031;
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Best Local 8
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Matches
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49; Gaps

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Query Match
Best Local Similarity 29.0%
Matches 42, Conservative
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                  SORRERE
                                                                                                                                                                                                                                                                                                                                                                                                      요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 WNSAT-----VLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQV------GL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ENYCRNPDGSEAPWCFTTLPGMRMAYCFQI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 WC----NCPKKFGGOHCEIDKSK-----TCYEGNGHFYRGKASTDIMGRPCLP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Pittle-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O., Pittle-Shepherd S.R., Voffman J., Waters D.J.; Folkman J., Waters D.J.; Mangiostatin is Detectable in the Urine of Dogs with Spontaneous Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 20.9%; Score 166; DB 13; Length 716; Local Similarity 31.1%; Pred. No. 1.6e-09; nes 42; Conservative 11; Mismatches 40; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Plasminogen (Fragment).
Canis familiaris (Dog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RGO; GO:0001809; F:thrombin activity; IEA.
RGO; GO:0007295; F:trypsin activity; IEA.
RGO; GO:0007295; F:trypsin activity; IEA.
RGO; GO:0007596; F:blood coagulation; IEA.
RILESPC: IPR003001; Pand pp.
RILESPC: IPR003001; Pan app.
RILESPC: IPR003004; Pan app.
RILESPC: IPR003124; Pan app.
RILESPC: IPR003124; Pan app.
RILESPC: IPR003124; Pan app.
RILESPC: IPR00314; Pan app.
REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; REMINESPEC: IPR00316; 
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1. - SIMILARITY: CONTAINS 4 KRINGLE DOWAINS.

EMBL; AV06988; AALS8519.1; -...

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0007596; F:blood coaqulation; IEA.

GO; GO:0007596; F:blood coaqulation; IEA.

GO; GO:0006508; P:protecolysis and peptidolysis; IEA.

InterPro; IPR000001; Kringle.

R Ffam; PR00001; Kringle.

PFam; PR000018; Kringle; 4.

PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 WDSQTPQSHRFLPEKYPCKGLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 KPLVQECMVHDCADG 134
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211 NRTPENFPCKN----LDENYCRNPDGETAPWCYTTNSEVRWEHCQIPSCESSPITTEYLD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 APASVPPEQTPVVQECYHGNGQSYRGTSSTTITGRKCQSWSSMT-----PHRHEKTPE 319
                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 -------CYBGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDAL-- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=9156378; PubMed=1645711;

Kanalas J.J., Makker S.P.;

L. Sindharas J. Maker S.P.;
Kanalas J.M.;
Kanala
                                                                                                                                                                                                                                                                                                                                                                                                            5 HOVPSNCDCLNGGTCVSNKYFSN----IHWC-NCPKKFGGQHCEIDKSKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                         20.9%; Score 165.5; DB 6; Length 359; 29.0%; Pred. No. 8.7e-10; tive 13; Mismatches 43; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
Bangert K., Johnsen A.H., Thorsen S.;
"Rat plasminogen: CDNA and gene structure.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 4.
SMART; SM00130; KR; 4.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
Glycoprotein; Kringle.
NON_TER 1 1
NON_TER 359 A3; 41172 NW; 776D35F4AB0BDD9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 --- OLGLGKHNYCRNPDNRRRPWCY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 HFPEAGL-TMNYCRNPDADKSPWCY 343
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296 CIRIGIPMADPINKNHKCYNSTGVDYRGTVSVTKSGRQCQPWNS-----QYPHTHTFTAL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NELHOVP-----PKKFGGQHCVSNKYFS-----NIHWCNC-----PKKFGGQH 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 C-----BIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDAL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REALINE-C57BL/6J; TISSUE=Adipose tissue;

RX MRDINE-C57BL/6J; TISSUE=Adipose tissue;

RX MRDINE-C55BL/6J; TISSUE=Adipose tissue;

RX The FANTOM Consortium,

The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

RT 60,770 full-length const.

RREL; ARC80886; Exact RAC80868.1;

NAC1981347520; RAC1.

RREL; ARC80886; RAC38068.1;

NGD; GO:0016020; C:membrane; IEA.

RGO; GO:0016020; C:membrane; IEA.

RGO; GO:0016020; C:membrane; IEA.

RGO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

RGO; GO:0004713; F:protein serine/threonine kinase.

RGO; GO:0004713; F:protein serine/threonine kinase.

RIME-FPC; IPRO00719; Protein serine/threonine kinase.

RIME-FPC; IRRO00719; Protein serine/threonine kinase.

REAM; PRO0047; RIMINGIE.

REAM; PRO0047; RIMINGIE.

REAM; PRO0069; PKINGIE.

REAM; PRO0069; PKINGIE.

RENDER; PRO00099; TKINGIE.

RENDER; PROD0099; TKINGIE.
                                                                                                                                                                                                                                                                                                                       Query Match 20.0%; Score 158.5; DB 4; Length 393;
Best Local Similarity 29.7%; Pred. No. 5.5e-09;
Matches 43; Conservative 14; Mismatches 51; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              SMART; SM00408; IGC2; 1.
SMART; SM0010; KR; 1.
PROSITE; PSS0038; FZ; 1.
PROSITE; PSS0031; IG_LIKE; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00070; KRINGLE 2; 1.
Glycoprotein; Immunoglobulin domain; Kinase; Kringle; Receptor.
SEQUENCE 393 AA; 43825 MW; 1F93DGBBBF53855 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor tyrosine kinase-like orphan receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 QLG--LGKHNYCRNPDNRRR-PWCY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Q8BNP9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 NRTPENPPCKN----LEENYCRNPDGETAPWCYTTDSQLRWEYCEIPSCGSSVSPDQSDS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 SVLPBQTPVVQECYQGNGKSYRGISSTINIGKKCQSW-----VSMTPHSHSKTPANFPDA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 HOVPSNCDCLNGGTCVSNKYFSN----IHWC-NCPKKFGGQHCEI------DKS-- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 -----KICYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRSDALQL--- 94
InterPro; IPR003966; Peptidase SIA pr.

InterPro; IPR001400; Somatotropin.

Pfam; PP00051; kringle; 5.

Pfam; PP00051; kringle; 5.

R Pfam; PP00052; trypsin; 1.

R PRINTS; PR00122; CHYMCTRYPSIN.

R RINTS; PR00129; Kringle; 5.

R RART; SM00403; KR; 4.

R SMART; SM00403; KR; 4.

R SMART; SM00403; KR; 4.

R SMART; SM00021; KRINGLE 1; 5.

R RART; SM00021; KRINGLE 2; 5.

R ROSITE; PS00103; KRINGLE 2; 5.

R ROSITE; PS00103; TryPSIN DM; 1.

R ROSITE; PS00103; TryPSIN DM; 1.

R ROSITE; PS00103; TryPSIN DM; 1.

R ROSITE; PS00103; TRYPSIN HIS; 1.

R ROSITE; PS00103; TRYPSIN HIS; 1.

R ROSITE; PS00103; TRYPSIN SRR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.8%; Score 165; DB 11; Length 812; 29.0%; Pred. No. 2.4e-09; tive 20; Mismatches 49; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BRB6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to receptor tyrosine kinase-like orphan receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberger R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
L. SIMILARITY: CONTAINS I KRINGLE DOMAIN.
R. BERL; BC006574; ARH06374.1; -..
GO; GO:0016301; Fixinase activity; IEA.
GO; GO:0016301; Fixinase activity; IEA.
GO; GO:0016301; Fixinase activity; IEA.
GO; GO:007275; Pickase activity; IEA.
GO; GO:007275; Pickase activity; IEA.
R. GO; GO:007275; Pickase activity; IEA.
R. GO; GO:00024; Fixinase activity; IEA.
R. InterPro; IPR007110; Ig-like.
R. InterPro; IPR007110; Ig-like.
R. InterPro; IPR00001; Kringle.
R. Pfam; PF01392; Fz; 1.
R. Pfam; PF00064; ig; 1.
R. Pfam; PF00064; ig; 1.
R. Pfam; PF00064; ig; 1.
R. ProDom; PD00018; KRINGLE.
R. ProDom; PD0000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 20 812 PLASMINOGEN.
SEQUENCE 812 AA; 90535 MW; 8C703C514105BC9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query, Match 20.8%
Best Local Similarity 29.0%
Matches 47; Conservative
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TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BRB6
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1098RB
AC 098RB
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                                                                                                                                                                                                                                                                                                                                                                            2 NELHQVP-----SNCDCLNGGTCVSNKYFS-----NIHWCNC-----PKKFGGQH 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Adipose tissue,

XX MEDLINE=22346483; PubMed=12466831;

A The FANTOM Consortium,

A the FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

XI MALLYSIS of the mouse transcriptome based on functional annotation of

XI MALLYSIS of the mouse transcriptome based on functional annotation of

XI MALLYSIS of the mouse transcriptome based on functional annotation of

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XI MALLYSIS OF CONSTRUCTOR OF THE ADIABLE OF TH
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                             Query Match 20.0%; Score 158.5; DB 11; Length 937; Best Local Similarity 29.7%; Pred. No. 1.4e-08; Matches 43; Conservative 14; Mismatches 51; Indels 37;
R SYART; SW00409; IG; 1.

SWART; SW00409; IG; 1.

SWART; SW00409; IG; 1.

SWART; SW00220; KR; 1.

SWART; SW00220; TKc; 1.

SWART; SW00219; TYKC; 1.

R SWART; SW00219; TKK; 1.

R PROSITE; PSS0039; IG LIKE; 1.

R PROSITE; PSS0001; KRINGLE 1; 1.

R PROSITE; PSS00109; RRINGLE 2; 1.

R PROSITE; PSS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PSS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor tyrosine kinase-like orphan receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                937 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 QLG--LGKHNYCRNPDNRRR-PWCY 114
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Q8BG10
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48 -----KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQTYHAHRS-----DA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 HOVPSNCDCINGGTCVSNKYFSN----IHWC-NCPKKFGGQHCBI------DKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 SVLPEQTPVVQECYQGNGKSYRGTSSTINTGKKCQSW----VSMTPHSHSKTPANFPDA
                                                                                                                                                                                                                                                                                       01-OCT 2003 (TrEMBLrel. 25, Created)
01-OCT 2003 (TrEMBLrel. 25, Last sequence update)
01-OCT 2003 (TrEMBLrel. 25, Last annotation update)
Abl-346.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Mammalia, Butherlas, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutherlas, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
11.1—Taxib=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
14-0CT-2003 (TrEMBLrel. 25, Last annotation update)
15-0CT-2003 (TrEMBLrel. 25, Last annotation update)
15-0CT-2003 (TrEMBLrel. 25, Last annotate)
15-0CT-2003 (TrEMBLrel. 25, Las
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STRAINAB, TISSUB-Body;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar C.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong Li.,
Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaranne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma Hang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.,

"Liver regeneration after PH.";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AN321159, AApp2560.1;

SEQUENCE 759 AA, 86056 MW; 1422BFACOSCGDFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
19.7%; Score 156; DB 11; Length 759;
Best Local Similarity 24.9%; Pred. No. 2.1e-08;
Matches 50; Conservative 20; Mismatches 47; Indels 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AA.
                             64 DADTGPWCFT---MDPSIRWEYCNLTRCSD 90
                                                                                                                                                                                                                                                                      759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                      Q7TP84
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Q7SXB3
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Q7TP84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 CYHGDGQSYRGSFSTTVTGRTCQSWSSMTPHQHKRTPENHPNDGLTM-----NYCRNPDA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTM-----NYCRNP
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MEDLINE=21181705; PubMed=11285247;

Goorelkova M., Kraft H.G., Enhholm C., Utermann G.;

Goorelkova M., Kraft H.G., Enhholm C., Utermann G.;

Single nucleotide polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";

Hum. Mol. Genet. 10:815-824(2001).

EMBL; AF158663; AAF03680.1;

EMBL; AF158662; AAF03680.1;

EMBL; AF158662; AAF03680.1;

InterPro; IPRO00001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
PRINTS; PR00122; CHYMOTRYPSIN,
PRINTS; PR00018; KRINGLE.
Probom; PD000395; Kringle; 2.
SWART; SM00130; KR; 2.
SWART; SM00020; Tryp SPc; 1.
PROSITE; PS00021; Tryp SPc; 1.
PROSITE; PS00010; KRINGLE 1; 2.
PROSITE; PS00135; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Glycoprotein; Hydrolase; Kringle; Lipoprotein; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 19.7%; Score 156; DB 4; Length 113; Similarity 37.8%; Pred. No. 2.7e-09; 34; Conservative 12; Mismatches 32; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
454 AA; 50041 MW; 974E30744C187B2F CRC64;
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113 AA; 12685 MW; F3D65681D9B5253A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%; Score 158; DB 6; 39.8%; Pred. No. 7.4e-09; iive 10; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 DNRRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 RRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam. PF00051, kringle.
PRINTS, PR00018, kringle; 1.
PRINTS, PR000185, Kringle; 1.
SMART, SM00130, KR, 1.
PROSITE; PS00021, KRINGLE; 1.
PROSITE; PS50070, KRINGLE; 1.
Glycoprotein, Kringle; 1.
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Best Local Similarity
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SEQUENCE
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Q9UIRS;
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RESULT 32

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RN 118 SEQUENCE FROM N.A.

RA EXPONENCE FROM N.A.

RA BECOME J. (Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,

RA Mitchell D., Robinson J.H.;

RA Hack Cells.,

RI Hela cells.,

RI Hela cells.,

RI Fibrinolysis 0:00-0(1991).

C. -: SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.

DR EMBL, MAZZO, AAASIG451.1; -.

DR EMBL, MAZZO, AAASIG451.1; -.

BR GO, GO:00004263; F:cdlcium ion binding; IEA.

GO, GO:00004263; F:chymorrypein activity; IEA.

BR GO, GO:00004293; F:chymorrypein activity; IEA.

DR GO, GO:00004293; F:chymorrym activity; IEA.

BR GO, GO:00004293; F:chymorrym activity; IEA.

BR GO, GO:00005009; F:thrombin activity; IEA.

BR GO, GO:00005009; F:trypein activity; IEA.

BR GO, GO:00005009; P:trypein activity; IEA.

BR InterPro; IPR000001; Kringle.

BR InterPro; IPR001254; Peptidase SI.

BR InterPro; IPR001264; Peptidase SI.

BR InterPro; IPR001264; Peptidase SI.

BR InterPro; IPR0016760; Febtidase SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 PCNIPRCSSPPPPGPMLQ-----CLKGRGENYRGKIAVTKSGHTCQRWN-----KQTP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 FSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLFWNSATVLQQTY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                     R PRINTS; PRO0018; KRINGLE.
R PRINTS; PRO1056; PROTHROMBIN.
R PRODOM; PRO001395; KRINGLE.
R SWART; SM00130; KR; 4.
R SWART; SM00020; TYPE SC: 1.
R PROSITE; PS00021; KRINGLE_1; 5.
R PROSITE; PS00013; KRINGLE_2; 5.
R PROSITE; PS0134; TRYPEIN_HIS; 1.
R PROSITE; PS0134; TRYPEIN_HIS; 1.
R PROSITE; PS0134; TRYPEIN_HIS; 1.
R PROSITE; PS0135; TRYPEIN_HIS; 1.
R GIVCOPROCE: 10; Hydrolase; Kringle; Protease.
C SEQUENCE 806 AA; 90981 NW; 95FAA86DC20064D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 806;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.4%; Score 154; DB 6; 30.5%; Pred. No. 3.8e-08; tive 9; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.8e-08;
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Pfam, PF00024; PAN; 1.
Pfam, PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 KDCIINNGEDYRGIQQKISSGSTCLSWRSLNL-----KFKDSQIGVGDHNFCRNPDG 74
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Paney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Yorskinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUB-Liver;

MEDLINE=98004511; PubMed=9342350;

Lawn R.M., Schwartz K., Patthy L.;

"Convergent evolution of apolipoprotein(a) in primates and hedgehog.";

Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).

- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.

EMBL; AF012297; AaB65760.1; -.

HSSP, P00747; 5HPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macropus eugenii (Tammar wallaby).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
NCBI_TaxID=9315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Indels
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANI=AB; TISSUE=Body;
Strani=AB; TISSUE=Body;
Stransberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOSSG75; AAH55675.1; -.
SEQUENCE Z63 AA; 28777 MW; BBEBC117EC7C8A58 CRC64;
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MERCES, SOLIS,
MERCES, SOLIS,
GO, GO.0005509; F.calcium ion binding; IEA.
GO; GO.0004263; F.chymotrypsin activity; IEA.
GO; GO.0003809; F.thrombin activity; IEA.
GO; GO.0004299; F.thrombin activity; IEA.
GO; GO.0004299; F.thrombin activity; IEA.
GO; GO.0005508; P.thrombin activity; IEA.
GO; GO.0005508; P.thrombin activity; IEA.
InterPro; IPRO00001; Kringle.
InterPro; IPRO00001; Kringle.
InterPro; IPRO01549; Peptidase_SI.
InterPro; IPRO01549; Peptidase_SI.
InterPro; IPRO01549; Peptidase_SIA.
InterPro; IPRO01549; PAN; I.
Pfam; PRO0051; PAN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 RRRPWCYVQVGLKPLVQE-CMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     018783
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CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 109
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MESSP; 801,977; --

MESSP; 801,977; --

R GO; GO:0004263; P:calcium ion binding; IEA.

GO; GO:0004263; P:chymcrrypain activity; IEA.

GO; GO:0004293; P:thrombin activity; IEA.

GO; GO:0004299; P:thrombin activity; IEA.

GO; GO:0005508; P:thrombin activity; IEA.

GO; GO:0005508; P:thrombin activity; IEA.

BC; GO:0005508; P:thrombin activity; IEA.

GO; GO:000509; P:thrombin activity; IEA.

BR InterPro; IPR00001; Kringle.

BR InterPro; IPR000134; Peptidase S1A.

InterPro; IPR00134; PR00114; A.

BR FAMP; PR000124; PAN; I.

BR FAMP; PR00125; PR0THROMBIN.

BR FAMP; PR00126; PROTHROMBIN.

BR SNART; SM00020; RR; MAP; I.

BR RRSITE; PS00013; KR; MAP; I.

BR RRSITE; PS00013; KR; MAP; I.

BR RRSITE; PS00013; KR; MAP; I.

BR RRSITE; PS00010; KRINGLE I; A.

BR RRSITE; PS00010; KRINGLE I; A.

BR RRSITE; PS00010; KRINGLE I; A.

BR RRSITE; PS00010; RRINGLE I; A.

BR RRSITE; PS00010; RRINGLE I; A.

BR RRSITE; PS00010; RRINGLE I; A.

BR RRSITE; PSS0040; TRYPSIN_DOM; I.

BR RRSITE; PS00010; RRINGLE I; A.

BR RRSITE; PS
                                                                                   11 CYHGDGQSYRGSFSTTVTGRTCQSWSSMT---PHWHQRTTEYYPNGGLTRNYCRNPDAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 WC----NCPKKFGGQHCEIDKSK------TCYEGNGHFYRGKASTDTMGRPCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocyte growth factor-like protein precursor.
Xenopus laevis (African clawed frog)
Xenopus laevis (African clawed frog)
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.7%; Pred. No. 4.8e-08;
Matches 39; Conservative 13; Mismatches 42; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                 717 AA.
                                                                                                                                                                      110 RPWCYVQVGLKPLV--QECMVHDC 131
                                                                                                                                                                                                                       RPWCYT---MDPSVRWEYCNLTRC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN 29 717 H. SEQUENCE 717 AA; 82017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     864 PTAPPELTPVVQDCYHGDGQSYRGTSSTTTTGKKCQSWSS-----MTPHRHQKTPENYPN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 NRIPENFPCKN----LDENYCRNPDGKRAPWCHIINSQVRWEYCKIPSCDSSPVSTEQLA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
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MEDLINE=21181705; PubMed=11285247;
AGOCIALXCAM M., Kraff H.G., Enhalm G.;
OgoralXcam M., Kraff H.G., Enhalm G.;
OgoralXcam M., Kraff H.G., Enhalm C.;
Clingle nucleotide polymorphisms in exons of the apo(a) kringles IV
Types 6 to 10 domain affect Lp(a) plasma concentrations and have
IT differents in Africans and Caucasians.";
Hum. Mol. Genet. 10:815-824(2001).
-!- SIMILARITY: CONTAINS 1 KRINGIE DOMAIN.
RR BRBL; AF158659; AAF03678.1; -.
RRBL; PRODO19; KRINGIE.
RRBL; PRODO130; KRINGIE.
RRBR; PROSITE; PSSO070; KRINGIE.
RRBR; PROSITE; PSSO070; KRINGIE.
RRBR; PROSITE; PSSO070; KRINGIE.
RRBR; PROSITE; PSSO070; KRINGIE.
RRBR; PRODO170; KRINGIE.
RRBR; PROSITE; PSSO070; KRINGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 ------KTCYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQTYHAHR---SDALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 HOVPSNCDCLNGGTCVSNKYFSN----IHWCNCP-KKFGGOHCEI---DKS-----
PRINTS; PRO0016; KRINGLE.
PRINTS; PRO11505; PROTHROMBIN.
PROD00395; Kringle; 5.
SWART; SM00130; KR; 5.
SWART; SM000473; PAN AP; 1.
PROSITE; PS00020; Tryp SPC; 1.
PROSITE; PS00014; KRINGLE; 5.
PROSITE; PS00134; TRYPEIN DOM; 1.
PROSITE; PS00134; TRYPEIN HIS; 1.
PROSITE; PS00135; TRYPEIN HIS; 1.
SMOOTH PROSITE; PS00135; TRYPEIN HIS; 1.
PROSITE; PS00135; TRYPEIN HIS; 1.
PROSITE; PS00135; TRYPEIN HIS; 1.
PROSITE; PS00135; TRYPEIN HIS; 1.
PROSITE; PS00135; TRYPEIN HIS; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%; Score 153; DB 4; Length 113;
larity 39.3%; Pre6. No. 5.7e-09;
Conservative 8; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
19.4%; Score 154; DB 4; Length 810,
Best Local Similarity 28.0%; Pred. No. 3.8e-08;
Matches 45; Conservative 20; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 LGLGKHNYCRNPDNRRRPWCYVQVGLKPLV--QECMVHDCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12815 MW; 4F80ADF8708548CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                810 PLASMINOGEN.
90555 MW; B05C7D4B0D020B3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 AGL-TMNYCRNPDADKGPWCFT---TDPSVRWEYCNLKKCS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ©9UIR7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Kringle; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apolipoprotein(a) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN 20 8
SEQUENCE 810 AA;
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Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
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320 VRPQDCYHG 328
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Best Local S
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Q8AV69
ID Q8AV69
                                            RESULT 40
Q13208
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259 WCYTTDPNVEREF----CHITKCKKQRISNIEITSTCFKERGEGYRGKANTTTSGIPCQR 314
                                                           77 ATVLQQTYHAHRSDALQLGLG--KHNYCRNPDNRRRPWCY-----VQVGLKPLVQEC--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QIPHQHRFTPEKYACKDLRENFCRNPDGSEAPWCFTLRPGMRVGFCYQIRRCTDD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 WC-NCPKKFGGQHCEIDK-----SKTCYEGNGHFYRGKASTDTMGRPCLPWNS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 WNSATVLQQTYHAHRSDALQL---GLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                          01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
01-07T-3 (Similar to MST1 (Macrophage stimulating 1 (Hepatocyte prowth factor-like))).
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SUBMITTED ().

SUBMITTED ().

SUBMITTED ().

- SIMILARITY: BELONGS TO PERTIDASE FAMILY SI.

- SIMILARITY: CONTAINS 4 KRINGLE DOWAINS.

REAL; AL137798; CAC17639.1; - .

RESP: POOT44; F. FLYPSHIN activity; IEA.

RO; GO:0004263; F:peptidase activity; IEA.

RO; GO:0004263; F:peptidase activity; IEA.

RO; GO:0004269; F:trypsin activity; IEA.

RITERPRO; IPR003001; Kiingle.

RITERPRO; IPR003001; Kiingle.

RITERPO; IPR001124; Peptidase SI.

RITERPO; IPR001124; Peptidase SI.

RITERPO; REP00034; FAYPSIN; I.

REPRO; ROWO35; KINGLE.

REPRO; REPOWSS; FAYNGLE.

REPRORS; RR00435; KRINGLE.

REPRORS; RR00435; KRINGLE.

REPRORS; RR00436; KRINGLE.

REPRORSITE; PSC0021; KRINGLE.

REPRORSITE; PSC0040; TRYPSIN'DOM; 1.

REPRORSITE; PSC040; TRYPSIN'DOM; 1.

REPRORSITE; PSC040; TRYPSIN'DOM; 1.

REPRORSITE; PSC040; TRYPSIN'DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 19.1%; Score 151.5; DB 4; Length 648; l Similarity 27.9%; Pred. No. 5.5e-08; 36; Conservative 18; Mismatches 46; Indels 29
                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                131 CAD 133
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxiD=9606;
                                                                                                                           369 ĆTĎ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265
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                                                                                                                                                                      RESULT 39
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REPUBLICE FROM N.A.

WEDUINE=20191171; PubMed=10728827;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 WC-NCPKKFGGQHCEIDK-----SKTCYEGNGHFYRGKASTDTMGRPCLPWNS
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                                                                                                                                                                                                                                                                            Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.0%; Score 150.5; DB 4; Length 567; 27.9%; Pred. No. 6.2e-08; ive 17; Mismatches 47; Indels 29
                                                                               01-NOV-1996 (TrEMBirel. 01, Created)
01-NOV-1996 (TrEMBirel. 01, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
Hepatocyte growth factor-like protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    930 AA.
567 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 VRPQDCYHG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 -MVHDCADG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                          Homo sapiens (Human)
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250 WCYTTDPNVEREF----CHITKCIEKQRISNIEITSTCFKERGEGYRGKANTTTSGIPCQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 PWNSATVLQQTYHAHRSDALQL---GLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECKVH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 RWDT-----QAPHVHRFLPEKYPCKGLDE-NYCRNPVGSBAPWCFTTLKNMRMAYCFQIK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 WC----NCPKKFGGQHCEIDK-----SKTCYEGNGHFYRGKASTDTMGRPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleost.
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Kenopodinae, Kenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.8%; Score 149; DB 13; Length 709; 30.6%; Pred. No. 1.1e-07; ive 14; Mismatches 42; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; ...
PRINTS; ...
PRODOM; PD000395; ...
RAMAR; SM00131; PAN AP; 1.
JR SWART; SM00020; Tryp SPC; 1.
JR SWART; SM00020; Tryp SPC; 1.
DR PROSITE; PS00021; RTNINGLE; 4.
PROSITE; PS00070; KRINGLE; 2; 4.
PROSITE; PS00070; RRINGLE; 2; 4.
PROSITE; PS00040; TrypSIN DOM; 1.
The last respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; sdrausberg R.; ed (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Similar to macrophage stimulating 1 (Hepatocyte growth factor-like).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
                                                                                                              709 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR009003; Cys_Ser_trypsin
InterPro, IPR000001; Kringle.
InterPro, IPR003014; PAN.
                                                                                                                                                                                                                                                                                        frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003609; Pan app.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR003966; Peptidase_S1A.
Pfan; PP00051; kringle; 4.
                                                                                                                                                                                                                                                                                     Kenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 22, (TrEMBLrel. 22,
                                                                                                                                                                                       (TrEMBLrel. 24,
                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                               -OCT-2003 (TrEMBLrel,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8K0Q8;
Q8K0Q8;
01-OCT-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 00042
GO; GO: 00042
GO; GO: 00075
GO; GO: 00065
InterPro; IP
                                                                                                                                                            01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PI
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                                                                                                              Q7ZTN9
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Q8K0Q8
                                                           RESULT 42
Q7ZTN9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAH---RSDALQLGLGKGNYCRNP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 OCYNGTGTDYRGSVSVTKSGHQCQPMS-----HQVPHSHSLSNADYPEIG-GGHSYCRNP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 CDCLNGGTCVSNKY-----FSNIHWCNC-----PKKFGGQHC-----EIDKSK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDING=12399314; MEDINE=22286220; PubMed=12399314; MEDINE=22286220; PubMed=12399314; Miratani I., Taira M.; Mibasa H., Shibata M., Hiratani I., Taira M.; "The Xenopus receptor tyrosine kinase Xror2 modulates morphogenetic movements of the axial mesoderm and neuroectoderm via Wnt
                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein serine/threonine kinase activity, IEA.
protein-tyrosine kinase activity, IEA.
transmembrane receptor activity, IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.0%; Score 150.5; DB 13; Length 930; 28.0%; Pred. No. 1.1e-07; ive 18; Mismatches 44; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, ABB091137 EAGL6209.1, --
EMBL, ABB091137 EAGL6209.1, --
EMBL, EABC91137 EAGL6209.1, --
GO, GO:0005524, F:parbelming; IEA.
GO, GO:0004674; F:parcein serine/threonine kinase activity
GO, GO:0004913; F:parcein-tyrosine kinase activity; IEA.
GO, GO:0004988; F:transmembrane receptor activity; IEA.
GO, GO:000725; P:development, IEA.
GO, GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                930 AA; 104081 MW; C68454572411A8B6 CRC64;
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IRR003599; Ig_
InterPro; IRR007110; Ig-11ke,
InterPro; IRR003588; Ig-2:
InterPro; IRR00001; KrIngle,
InterPro; IRR000719; Prot kinase,
InterPro; IRR001249; Ser_Ehr_pkinase.
InterPro; IRR001245; Tyr_pkinase.
                                                                                                                                                      Kenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         elopment 129:5227-5239(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00109; KRINGLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ptam; PF00047; ig; 1.
Pfam; PF00051; kringle; 1
Pfam; PF00069; pkinase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Conservative
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                                                                                                                                                                                                                       Xenopodinae; Xenopus,
NCBI_TaxID=8355;
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Best Local Similarity
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SMART; SM00408; I
SMART; SM00130; K
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PRINTS;
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Matches
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NC-----PKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 SHRLSSTEFPELG-GGHAYCRNPGGQMEGPWCFTQ-NKNVRVELCDVPPCSPRDG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 18.8%; Score 149; DB 11; Length 944; I Similarity 36.5%; Pred. No. 1.6e-07; 42; Conservative 11; Mismatches 36; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C5/BL/6J; TISSUB=Forelimb;
MEDLINB=223546683; PubMed=12466851;
The FANTOM Consortium
the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBBSP6, PRELIMINARY; PRT; 944 AA. QBBSP6, 01-NAR-2003 (TrEMBLrel. 23, Created) 01-NAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor tyrosine kinase-like orphan receptor 2.
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Best Local Similarity
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        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 NC-----PKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AHR---SDALQLGLGKHNYCRNPDNRRR-PWCYVQVGLKPLVQECMVHDCA--DG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 SHRLSSTEFPELG-GGHAYCRNPGGQMEGPWCFTQ-NKNVRVELCDVPPCSPRDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
[1]
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.8%; Score 149; DB 11; Length 801;
Best Local Similarity 36.5%; Pred. No. 1.3e-07;
Matches 42; Conservative 11; Mismatches 36; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        801 AA; 89201 MW; 3A5928326C8B885D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor tyrosine kinase-like orphan receptor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            944 AA
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SEQUENCE
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RESULT 44 **Q8C3W2**

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Gaps

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50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKKHNYCRNPDNRR 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 CYHGDGQSYRGSFSTTVTGRTCQSWSSMI---PHWHQRITEYYPNGGLTRNYCRNPDAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                         18.7%; Score 148; DB 4; Length 105; 38.1%; Pred. No. 1.8e-08; Live 8; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 18.5%; Score 147; DB 4; Length 113; Similarity 36.0%; Pred. No. 2.6e-08; 31; Conservative 14; Mismatches 33; Indels
                                                                                                                                                                                         105 AA; 11882 MW; GECBGC02CD30EFA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 113
113 AA, 12697 MW; 51D4461D9C66312E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 RPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                   110 RPWCYVQVGLKPLV--QECMVHDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                   SPWCYT---MDPNVRWEYCNLTQC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01.MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01.MAR-2003 (TrEMBLrel. 23, Last ann
Apolipoprotein(a) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
Glycoprotein; Kringle; Lipoprotein.
NON TER 113 113
SEQÜENCE 113 AA; 12697 MW; 51D44
                                                                                                               PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
Glycoprotein; Kringle; Lipoprotein.
NON TER
                      InterPro; IPR000001; Kringle.
Pfam; PF00051; Kringle; 1.
PRINTS; PR00018; KRINGLE.
Prochom; PD000395; Kringle; 1.
SWART; SM00130; KR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00051, Kringle, 1.
PRINTS, PR0018, KRINGLE.
ProDom, PD000395, Kringle, 1.
SMART, SM00130, KR; 1.
                                                                                                                                                                                                                               Query Match
Best Local Similarity 38.15
Matches 32; Conservative
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SEQUENCE
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Matches
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Q9UIR6
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'Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 NCMRIGIPAERLGRYH-----ACYNGSGADYRGMASTTKSGHQCQPW----ALQHP-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch
1 Similarity 36.5%; Pred. No. 1.6e-07;
42; Conservative 11; Mismatches 36; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 NC-----PKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AHR---SDALQLGLGKHNYCRNPDNRRR-PWCYVQVGLKPLVQECMVHDCA--DG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 SHRLSSTEFPELG-GGHAYCRNPGGQMEGPWCFTQ-NKNVRVELCDVPPCSPRDG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-21181705; PubMed=11285247;

MEDLINE-21181705; PubMed=11285247;

Gorelkova M., Kraft H.G., Enrholm C., Utermann G.;

Gorelkova M., Kraft H.G., Enrholm C., Utermann G.;

Single nucleotide polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";

Hum. Mol. Genet. 10.815-824 (2001).

-! - SIMLLARITY: CONTAINS I KRINGLE DOMAIN.

EMBL; AF158655; AAF03677.1; -INDINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50038; FZ; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS508021; KRĪNGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50010; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
SEQUENCE 944 AA; 105053 MW; IBBD416BE3170401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TYEWBLrel. 13, Created)
01-MAY-2000 (TYEWBLrel. 13, Last sequence update)
01-MAR-2003 (TYEWBLrel. 23, Last annotation update)
APOAlpoprotein(a) (Fragment).
           60,770 full-length cDNAs.";

Mature 420:563-573(2002)

EMBL; AK0311121-BAC27258.1;

MGD; MG1:1347521; BAC27258.1;

MGD; MG1:1347521; BAC27258.1;

MGD; MG1:1347521; BAC27258.1;

InterPro; IPR000024; Fz domain.

InterPro; IPR000109; Fr domain.

InterPro; IPR0002109; Ser thr pkinase.

InterPro; IPR0002109; Ser thr pkinase.

InterPro; IPR0002109; Ser thr pkinase.

InterPro; IPR000210; Ser thr pkinase.

InterPro; IPR000210; Fz domain.

InterPro; IPR000210; Fz domain.

Pfam; PR00001; Fz domain.

Pfam; PR00001; Fz domain.

Pfam; PR00001; Fz domain.

PR0000; PR000010; Fr domain.

PR0000; PR000010; Fr domain.

SMART; SM00100; TYRKINASE.

PR0000; PR000010; Fr domain.

SMART; SM00100; TYRK; 1.

SMART; SM00210; TYRK; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q9UIR8
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Q90865, Q90865,

RESULT Q90865

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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Heatcocyte growth factor-like 1.
MST1 OR HGFL1.
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                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi B.,
"Expression of HGF/SF, HGF1/MSP and c-met suggests new functions
during early chick development.",
Dev. Genet. 17:90-101(1955).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 HR-SDALQLGLGKHNYCRNPD-NRRRPWCYVQVGLKPLV--QECMVHDCAD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                          ol-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocyte growth factor-like/macrophage stimulating protein.
HGFI/MSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PRO0722; CTYMOTRYPEIN: 1.
PRINTS, PR00722; CTYMOTRYPEIN.
PRINTS, PR0018; KRINGLE.
PRODON; PR000189; KRINGLE.
SWART; SM00130; KR; 4.
SWART; SM00020; TRYP, SPC; 1.
SWART; SM00020; TRYP, SPC; 1.
PROSITE; PS00021; KRINGLE 1; 4.
PROSITE; PS00040; KRINGLE 2; 4.
PROSITE; PS0040; TRYPSIN_DOW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .le-07;
es 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X84047; CAA58862.1; -. MINOLE DOWNING.
HSSP; PO0747; ICEA.
MEROPS; S01.977; -CEA.
MEROPS; S01.977; -CEA.
GO; GO:0004263; F:edymotrypsin activity; IEA.
GO; GO:0004263; F:edymotrypsin activity; IEA.
GO; GO:0006238; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPRO00001; Kringle.
InterPro; IPRO0001; Kringle.
InterPro; IPRO01314; Peptidase S1.
InterPro; IPRO01254; Peptidase S1.
Fram; PPO0051; Kringle; 4.
Pfam; PPO0051; Kringle; 4.
Pfam; PPO0051; Kringle; 4.
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Q90ZN6;
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 36.9
les 41; Conservative
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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RESULT 49 Q90ZN6 ID Q90ZN AC Q90ZN DT 01-DE

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98 NCDLYEMKVYVRKCIVGKGEDYRGKVSTTTSGRTCQQWWS-----KFPHDHRWTPSATNG 152
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Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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Canorhabditidae; Peloderinae; Caenorhabditidae; Redecrea; Rhabditidae; Relogentiae; Caenorhabditidae; Caenorhabditidae; Caenorhabditise; Caenorhabditise; Caenorhabditise; Caenorhabditise; Caenorhabditise; Caenorhabditise; Caenorhabditidae; Caenorhabditidae; Caenorhabditidae; Caenorhabditidae; Caenorhabditise; Caenorhabditidae; Caenorhabditise; C
                                                                                                                                                                                                                                                                 Query Match
18.5%; Score 146.5; DB 13; Length 709;
Best Local Similarity 35.9%; Pred. No. 2.1e-07;
Matches 37; Conservative 12; Mismatches 33; Indels 21;
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308 STALQSSPVAEVNRGHLTHWCYVNSGTQYEGTVAQTSSGKQCAPWIDST--SRDFNVHRF 365
                                                                                                                                                        366 PEL---MNSKNYCRNPGGKKSRPWCY----SKPWGQEBYCDVPQC 403
                                                                                                              90 DALQLGLGKHNYCRNPDNRR-RPWCYVQVGLKPLVQE--CMVHDC 131
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Job time : 23.362 secs
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**X COGA M., Take-uchi M., Tameishi T., Ohshima Y.,

**I "Control of DAF-7 TGF expression and neuronal process development by a

receptor Pyrosine Kinase KIN-8 in C. elegans.";

**Submitted (FEB-1999) to the EMBL/Geneank/DBJ databases.

- 1- SIMILARITY: CONTAINS 1 KRINGLE DOWAIN.

**BMBL, Z3559; CAB46439.2, -...

**R EMBL, Z3599; CAB461003.1; -...

**R EMBL, Z3599; CAB61003.1; -...

**R EMBL, Z3599; CAB61003.1; -...

**R MASSP, P11324.7 CAC29085.1; -...

**R MSSP, P11324.7 CAC29085.1; -...

**R MSSP, P11322.1 FGF.**

**R MSSP, P1
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R PRINTS; PRO0109; TYRKINASE.
R PRODOM; PRO00001; FARINASE.
R PODOM; PRO00001; FARINGLE.
R PROSON; PRO00001; FARINGLE.
R SMART; SM00130; KR; 1.
SMART; SM00130; KR; 1.
SMART; SM00130; KR; 1.
R PROSITE; PSS0835; IG_LIKE; 1.
R PROSITE; PSS0835; IG_LIKE; 1.
R PROSITE; PSS00101; FRINGLE 1; FALSE NEG.
R PROSITE; PSS00101; PROTEIN KINASE ATP; 1.
R PROSITE; PSS00101; PROTEIN KINASE DOM; 1.
R PROSITE; PSS00109; PROTEIN KINASE DOM; 1.
R PROSITE; PSS00109; PROTEIN KINASE DOM; 1.
R PROSITE; PSS00109; PROTEIN KINASE TYR; 1.
R TYROSING-PROCEIN KINASE TYR; 1.
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Best Local Similarity 25.5%; Pred. No. 4.6e-07;
Matches 42; Conservative 25; Mismatches 55; Indels 43; Gaps
                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
               Berks M ;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                Mortimore B.J.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
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InterPro; IRR000101; Ig-like.
InterPro; IRR000101; Kringle.
InterPro; IRR000001; Kringle.
InterPro; IRR0001045; Prot Kinase.
InterPro; IRR001045; Tyr Dkinase.
InterPro; IRR001045; Tyr Dkinase.
InterPro; IRR001045; Tyr Dkinase.
Fam; PR00011; Kringle; I.
                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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May 25, 2004, 14:43:00 ; Search time 33.0105 Seconds (without alignments) 1155.508 Million cell updates/sec
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1 SNELHQVPSNCDCLNGGTCV......QVGLKPLVQECMVHDCADGK 135
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003bs:* geneseqp2004s:*

Description	Aae16545 Human uro	549	2 Human	95	Aae16547 Human uro	Aap50871 Sequence	4	Aar05117 UK-S3 as	Aaw13634 Human nat	Aar10057 Pro-uroki	Aar10058 Pro-uroki	Aar40225 PUK, 2/19	Aar62997 Pro-uroki	Aar63008 Pro-uroki	Aar62999 Pro-uroki	Aar62994 Pro-uroki		Aar63001 Pro-uroki	Aar63006 Pro-uroki	Aar62992 Pro-uroki	Aar63002 Pro-uroki	_	Aar62995 Pro-uroki	Aar63000 Pro-uroki	Aar63004 Pro-uroki
SUMMARIES	AAE16545	AAE16549	AAG75492	ABP41795	AAE16547	AAP50871	AAR06244	AAR05117	AAW13634	AAR10057	AAR10058	AAR40225	AAR62997	AAR63008	AAR62999	AAR62994	AAR63003	AAR63001	AAR63006	AAR62992	AAR63002	AAR63007	AAR62995	AAR63000	AAR63004
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11 2 AAR6299 11 2 AAR6300 11 2 AAR6299 11 2 AAR6299 11 2 AAR6299 11 2 AAR9283 11 3 AAR9283 12 2 AAR1033 24 2 AAR1033 11 1 AAR1033 24 2 AAR1033 11 1 AAR9601	431 1 AAP60783 431 1 AAP71058 431 1 AAP71698 431 1 AAP71698 431 1 AAP71698 431 1 AAP71698 431 1 AAP71698 431 1 AAP91886 431 1 AAP912109 431 1 AAP92119 431 2 AAX33121 431 3 AAX99229 431 5 AAU99229 431 5 AAU99229 431 6 ABE71076 431 7 AD760538 431 7 AD760538	ntry) plasminogen activator applasminogen activator atherosolerosis; heart atherosolerosis; heart ann; amqioqenic disorden; glaucoma; diabetic si glaucoma; diabetic srine contraction disorteress syndrome; amino tress syndrome;
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The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, upulmonary fibrosis, asthma, tumour cell angiogenesis, tumour cell metastasis, glaucoma, invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, clasorderic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sequence is human urokinase-type plasminogen activator (uPA) amino terminal fragment (ATF) and connecting peptide
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                                                                                                                                                                                                                                                                                                                                                                        Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
adult respiratory distress syndrome; amino terminal fragment; ATF; male impotence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, colon cancer, colon cancer antigen, diagnosis, detection, colorectal carcinoma, chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 793; DB 5; Length 143; 100.0%; Pred. No. 3.4e-54; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 24; Fig 1H; 117pp; English
                                                                                                                                                                                                         20-JUN-2000; 2000US-0212874P.
                                                                                                                                                                      13-JUN-2001; 2001WO-US018976
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                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a composition comprising one or more domains of urckinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell angiogenesis, tumour cell metastasis, glaucoma, invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, clasorder, male impotence, respiratory disease or condition such as asthma, adult respiratory diserses syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sequence is human urokinase-type plasminogen activator (uPA) amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human uPA amino terminal fragment (ATF) and connecting peptide.
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100.0%; Pred. No. 3.2e-54;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 1D; 117pp; English
                                                                                                              13-JUN-2001; 2001WO-US018976
                                                                                                                                                20-JUN-2000; 2000US-0212874P
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                                                                                                                                                                                     UYPE-) UNIV PENNSYLVANIA,
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Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                           Higazi AA;
                                                                                                                                                                                                                                                           WPI; 2002-122240/16.
N-PSDB; AAD27078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 135 AA;
                                       WO200197752-A2.
   Homo sapiens
                                                                           27-DEC-2001
                                                                                                                                                                                                                           Cines DB,
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated mucleic acid melecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased care expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the mucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37704 and AAB7779 represent carcinomas and cancers. AAH37196 to AAH37704 and AAB7779 represent pages 666 to 682 and page 7053 of the sequence listing were missing at time of pubblication, meaning no sequences are present for SBQ ID NO:1027 to 1052
                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:2927.
                                                                                                                                                                                                                                       Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 7707-7708; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP41795 standard; protein; 337 AA
                                                                                                                                                                                                                                       Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ovarian antigen HVVCB79,
                                                                                                                                                  99US-0157137P.
                                                                                                                  28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 100.
Matches 135; Conservative
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to 1052, 7921 and 7922
                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                      2001-235357/24.
                                                                                                                                                                                                                                                                                        N-PSDB; AAH34897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 337 AA;
                                               WO200122920-A2,
                                                                                                                                                  29-SEP-1999;
                  Homo sapiens
                                                                                                                                                                   03-NOV-1999;
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                                                                                 05-APR-2001
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87 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 146
                                                                                                                                                                                                                                       KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                          9
                                                                                                                                                      SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 86
                                                                                                                   SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                              Gaps
                                                              .,
100.0%; Score 793; DB 4; Length 337; 100.0%; Pred. No. 7.3e-54; ive. 0; Mismatches 0; Indels (
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27 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                               1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                     Conservative
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Matches 135; Conser
                                                                                                                                                                                                                                                                                                                                  Sequence 337 AA;
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                                                                                                                                                                                                                                                                                                                                                                         Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (AB954131-AB956305), and also encompasses polypeptides 90% identical and polymocleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens, and the use of ovarian antigens, and the use of ovarian prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, calsorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertility, disorders (e.g., mastitis, oophoritis and captured; shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginately, immune disorders (e.g., congenital and acquired.

Shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginated disorders (e.g., anaemia), cardiovascular disorders.

Confortalated disorders (e.g., anaemia), cardiovascular disorders.

Confortalated disorders. Ovarian antigen polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which continue represents a human ovarian antigen of the printed

Colypeptides may be used as food additives or to prepare antibodies

Colypeptides may be used as food additives or to prepare antibodies

Colypeptides may be used as food additives or to prepare antibodies

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Colypeptides may be used as food additives or to prepare antibodies

Colypeptides may be used as food additives or to prepare antibodies

Colypeptides may be used as food additives or to prepare antibodies

Colypeptides may be used as food additives o Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases. infertility; pregnancy disorder; annountation; polycytic ovary syndrome; pCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; mune disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromesome mapping; forenelic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 10q24. Claim 11; SEQ ID NO 2927; 2922pp; English. 07-JUN-2001; 2001WO-US018569 07-JUN-2000; 2000US-0209467P (HUMA-) HUMAN GENOME SCI INC Rosen CA; WPI; 2002-147878/19. N-PSDB; ABQ54872. WO200200677-A1. Homo sapiens. 03-JAN-2002. Birse CE,

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RESULT 6
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                        KASTDIWGRPCLPWINSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 146
                                                                                                                                                                                                                                                                                                                                                                 Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atroke; hypotension; atroke; hypotension; and disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; ucerine contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome; scuPA deltal36-143; single chain urokinase; mutean; metein.
KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                              Human urokinase-type plasminogen activator scuPA delta136-143 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
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llarity 100.0%; Pred. No. 8.6e-54;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                            AAE16547 standard; protein; 403 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 22; Fig 1F; 117pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2000; 2000US-0212874P
                                                                          PLVQECMVHDCADGK 135
                                                                                                             147 PLVQECMVHDCADGK 161
                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cines DB, Higazi AA;
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Best Local Similarity
Matches 135; Conservat
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Gaps

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Length 403; Indels

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Zymogen AAP50871 is the inactive precursor form of human urokinase. Urokinase zymogen is cleaved into the two-chain form composed of characteristic urokinase H (molecular wt.of 30,000) and L (molecular wt.of 20,000) chains when treated with catalytic amounts of plasmin. The patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a single chain molecular structure, and selective affinity for fibrin. It is a thrombolytic agent which manifests its plasminogen activator activity on cleavage by proteolytic enzymes (e.g. plasmin) and has higher affinity for fibrin than known forms of urokinase
                                 61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                       61 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
    9
                                                                                                                                                                                                                                                                                     Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese Patent Application No.37119/84).
1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKRGGQHCEIDKSKTCYBGNGHFYRG
                                                                                                                                                                                                                                                                                                                                  Thrombolytic agent; plasminogen activator activity; fibrin affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "potential cleavage site which generates the chain form from the zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New urokinase zymogen - useful as thrombolytic agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suyama T;
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                  AAP50871 standard; protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kasai S, Arimura H, Mori K,
                                                                                                                         121 PLVQECMVHDCADGK 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83JP-00170354.
83JP-00195051.
                                                                                            121 PLVQECMVHDCADGK 135
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148. .279
158. .159
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Disulfide-bond
Disulfide-bond
Disulfide-bond
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Disulfide-bond
Disulfide-bond
Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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17-OCT-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP139447-A.
                                                                                                                                                                                                                               AAP50871;
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us-09-880-503-4.rag

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The polypeptide is a deriv. of mature urokinase, designated UK-83 which has 2 amino acid substns. which result in an N-linked glycosylation site giving the new protein improved stability and activity. See also AAROS113-17. (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
       61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide(s) with added carbohydrate chains - formed by modification aminoacid sequence, used to improve physio:chemical properties and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Itoh
                                                                                                                                                                                                                                                                                                              /label= synthetic_mutation
/note= "old seq (Leu)"
Misc-difference 155
                                                                                                                                                                                                                                                                                                                                                                      /label= synthetic_mutation
/note= "old seq (Pro)"
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                                                                                                                           AAR05117 standard; protein; 411 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yasumura S,
                                                         121 PLVQECMVHDCADGK 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLVQECMVHDCADGK 135
                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                       UK-S3 as encoded by pUKS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 135, Conservative
                                                                                                                                                                                                                                                Urokinase; glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki K, Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-165029/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 411 AA;
                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1989;
                                                                                                                                                                                25-MAR-2003
04-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activities.
                                                                                                                                                      AAR05117;
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                                                                                                                                  KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                  61 KASTDIWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urokinase precursor-lipid composite - used as thrombolytic agent, having prolonged half-life in the blood, enhanced bio:availability and improved activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                             1 SNELHQVPSNCDCLNGGICVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                       SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYBGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By forming a precursor-lipid composite, the half-life of this thrombolytic agent in the blood may be increaced, exhibiting improved activity without abnormal acceleration of fibrinolytic activity. Composis useful as a thrombolytic agent in treatment of cerebral thrombosis, myocardial infarction etc
                                                                                                                                                                                                                                                                                                                                                                                          Urokinase precursor; fibrinolysis; thrombolytic; cerebral thrombosis; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
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                              Length 411;
                                                       Indels
                         100.0%; Score 793; DB 1;
100.0%; Pred. No. 8.7e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                 AAR06244 standard; protein; 411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tamanouchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig 1; 11pp; English.
                                                                                                                                                                                                             121 PLVQECMVHDCADGK 135
                                                                                                                                                                                       PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90EP-00300772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89JP-00016406
89JP-00121405
                                                                                                                                                                                                                                                                                                                                                                Urokinase precursor protein
                                        Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ueda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-233117/31
                         Query Match
Best Local Similarity
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Les 135; Conserv
 Sequence 411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1989;
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                                                                                                                                                                                                                                                                                                             AAR06244;
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Best Local Si
Matches 135,
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KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UK-T4 is one example of a plasminogen activator which differs from natural human pro-urckinase at positions 153 and 155 (Leu substituted by ser; Pro substituted by Thr, respectively). The derivative has decreased susceptibility to thrombin compared to natural type pro-UK and higher specific activity. See also AAQ10168 and AAQ10170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New plasminogen activator almost identical to natural pro:urokinase thrombin resistant and used for prophylaxis-treatment of cerebral thrombosis or myocardial infarction.
                                                                                                                                                                                                                                                                                                                         UK-T4; plasminogen activator; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                     Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 793; DB 2;
100.0%; Pred. No. 8.7e-54;
iive 0; Mismatches 0;
                                                                                                                                                                              AAR10057 standard; protein; 411 AA.
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                                                                                       121 PLVOECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90EP-00111471
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                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                         PLVQECMVHDCADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yasamura S, Nishi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-008678/02.
N-PSDB; AAQ10169.
                                                                                                                                                                                                                                                                                                                           pro-urokinase; UK-T4
cerebral thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 411 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-1989;
                                                                                                                                                                                                                                                     18-MAR-1991
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                                                         121
                                                                                                                                                                                                                   AAR10057;
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AAR10058
ID AAR10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of human prourokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence is that of the wild-type hPUK protein, including the EGF domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                          10. .42
/label = EGF domain
/note= "in Claimed variants, at least part of the EGF
domain is deleted (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent.
                                                                                                                                                                                                                                Human, prourokinase, hPUK, variant, half-life, increase, EGF,
epidermal growth factor domain, deletion, thrombolysis, fibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 793; DB 2;
100.0%; Pred. No. 8.7e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               20. .31
/label= second_loop
33. .42
/label= third_loop
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                       AAW13634 standard; protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             (0. .19
/label= first_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amatsuji Y, Kasai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90EP-00109472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89JP-00126433
90JP-00042020
121 PLVQECMVHDCADGK 135
                                                                                                                                                          (first entry)
                                                                                                                                                                                              Human native prourokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-350146/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 411 AA;
                                                                                                                                                          04-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1989;
22-FEB-1990;
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L8-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanabe T,
Airmura H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP398361-A.
                                                                                                                         AAW13634;
                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                      AAW1363
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KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant human pre:urokinase - by replacing specified aminoacid(s) in N-terminal for providing longer half-life in blood and higher thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGQQHCEIDKSKTCYEGNGHFYRG
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 Pro, Gly, or Tyr in the region 10 to of the human PUK can be replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0, Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                       /note= "Thr encoded by AGT (sic)"
                                                                                                                                                                                                                                        /note= "Thr encoded by TAC (sic)"
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100.0%; Pred. No. 8.7e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 14-16; 26pp; Japanese.
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/note= "Ser, Asn,
in the N-terminal
Thr, Pro or Ala"
                                                                 /label= EGF
10. 19
10. 19
20. 31
/label= Loop_1
/label= Loop_2
33. 42
/label= Loop_3
                                                                                                                                                                                                                                                                                                                                            92JP-00030178
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-277461/35.
N-PSDB; AAQ48228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 411 AA;
                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                        Misc-difference
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21-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UK-33 is one example of a plasminogen activator which differs from natural human pro-urckinase at positions 153 and 155. (Leu substituted by Asn; Pro substituted by Thr, respectively). The derivative has decreased susceptibility to thrombin compared to natural type pro-UK and higher specific activity. See also AAQ10168 and AAQ10169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                            New plasminogen activator almost identical to natural pro:urokinase thrombin resistant and used for prophylaxis-treatment of cerebral thrombosis or myocardial infarction.
                                                                                                  UK-S3; plasminogen activator; myocardial infarction;
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                                                                   derivative UK-S3 with Asn(153) and Thr(155)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 793; DB 2;
100.0%; Pred. No. 8.7e-54;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 9; 84pp; English.
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Matches 135; Conservative
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                                                                                                  pro-urokinase; UK-S:
cerebral thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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WO9501427-A1 12-JAN-1995. 28-JJN-1994; 02-JUL-1993;

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61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                    reduced fibrinogenolysis;
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Best Local Similarity 100.0%; Pred. No. 8.7e-54; Matches 135; Conservative 0; Mismatches 0; Indels
                                                                                         Pro-urokinase mutant Ser175 His187 His300 Ala301 His313
                                                                                                                                             Pro-urokinase; thrombolysis; fibrin clot lysis; reduced non-specific plasminogen activation; systemic bleeding; mutant Ser175 His187 His300 Ala301 His313.
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/note= "flexible loop"
325. .341
352. .380
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   (revised)
(first entry)
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21-SEP-1995
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REXERVED SOURCE SERVED 
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Best Local Similarity 100.0%; Pred. No. 8.7e-54;
Matches 135; Conservative 0; Mismatches 0;
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/note= "flexible loop"
325. .341
352. .380
                                                                                                                             location/Qualifiers
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Liu J,

WPI; 1995-060991/08

Sequence 411 AA;

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Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis; non-specific plasminogen activation; systemic bleeding; mutant His 299 Ala300.
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No. 8.7e-54;
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/note= "flexible loop"
325. .380
352. .380
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Pred.
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                                                                                                                                                                                                                                                                       Pro-urokinase mutant His299 Ala300.
                                                                                                                                                             AAR62994 standard; protein; 411
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                                                    PLVQECMVHDCADGK 135
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Best Local Similarity
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                                                AAR62999 standard; protein; 411 AA.
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                                                                                                                                                          Pro-urokinase mutant His313
                                                                                                              (revised)
(first entry)
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Matches 135; Conservative
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the case with the wild type protein. (Updated on 25-MAR-2003 to correct
PN field.)
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                                                             Score 793; DB 2;
Pred. No. 8.7e-54;
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/note= "flexible loop"
325. 341
352. 380
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Best Local Similarity 100.
Matches 135; Conservative
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21-SEP-1995
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                                                                           KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                             SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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/note= "flexible loop"
325. .341
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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                      AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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                                        Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation.
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100.0%; Pred. No. 8.7e-54;
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Matches 135; Conservative
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         AAR62991 is the wild type pro-urokinase, from which the new mutants the described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and nonspecific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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100.0%; Pred. No. 8.7e-54;
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61 XASTDIMGRPCLPWNSAIVIQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                           AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and nonspecific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct
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                                                      (NEWE-) NEW ENGLAND DEACONESS
                                                                                                                                                                                   Claim 5; Fig 1; 46pp; English
 94WO-US007278
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                                                                                                             WPI; 1995-060991/08
                                                                                   Gurewich V;
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28-JUN-1994;
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21-SEP-1995
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                                                                                   Liu J,
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61 KASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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100.0%; Pred. No. 8.7e-54;
tive 0; Mismatches 0;
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(first entry)
325. .341
352. .380
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AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and nonspecific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation. Claim 16; Fig 1; 46pp; English

Sequence 411 AA;

1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG ö Length 411; 100.0%; Score 793; DB 2; Length 4 100.0%; Pred. No. 8.7e-54; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 135; Conservative δ

KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120 61 KASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 61 d ò 셤

121 PLVOECHVHDCADGK 135 121 ò

standard; protein; 411 AA AAR62995 AAR62995; RESULT 23

(revised)
(first entry) 25-MAR-2003 21-SEP-1995

Pro-urokinase mutant Ala300 Ala301.

Pro-urokinase, thrombolysis, fibrin clot lysis, reduced fibrinogenolysis, non-specific plasminogen activation; mutant Ala300 Ala301; systemic bleeding.

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AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thrombolism, but have a reduced fibrinogenolysis activity and nonspecific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct
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KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120 KASTDIMGRPCLEWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 1 SNELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHPYRG AAR63000 standard, protein, 411 AA. PLVQECMVHDCADGK 135 PLVQECMVHDCADGK 135 (revised) (first entry) 25-MAR-2003 21-SEP-1995 61 61 121 AAR63000; RESULT 24 AAR63000 g ઠે a ò

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Length 411; Indels

100.0%; Score 793; DB 2; 100.0%; Pred. No. 8.7e-54; iive 0; Mismatches 0;

Best Local Similarity 100. Matches 135; Conservative

Query Match

Sequence 411 AA;

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Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis; non-specific plasminogen activation; systemic bleeding; mutant Ser175 His187 Gly306 Ala313.
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activation.
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     AAR63004 standard; protein; 411 AA.
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Pro-urokinase mutant Ser175 His187
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                                                                                                                                                                                                 Pro-urokinase, thrombolysis, fibrin clot lysis, reduced fibrinogenolysis, non-specific plasminogen activation, mutant His300 Ala301;
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                                                                                    AAR62996 standard; protein; 411 AA.
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 PLVQECMVHDCADGK 135
                         PLVQECMVHDCADGK 135
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Best Local Similarity 100.6
Matches 135; Conservative
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                                            61 KASTDÍTMGRPCLÞWNSATVLÓQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                       KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
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note= "flexible loop"
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specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the waild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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Local Similarity 100.0%; Pred. No. 8.7e-54;
les 135; Conservative 0; Mismatches 0;
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                                                                                  Sequence 411 AA;
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                                                                                                                 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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                                 Score 793; DB 2;
Pred. No. 8.7e-54;
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Best Local Similarity 100.0%; P. P. Matches 135; Conservative 0;
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                  AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and nonspecific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                              Length 411;
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100.0%; Pred. No. 8.7e-54;
ive 0; Mismatches 0;
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           Fig 1; 46pp; English.
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Best Local Similarity 100.
Matches 135; Conservative
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21-SEP-1995
          Claim 11;
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                                                                                                                                                               described in AAR62992-K63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thrombolem, but have a reduced fibrinogenolysis activity and nonspecific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                  type pro-urokinase, from which the new mutants
                                                               Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro-urokinase; plasminogen activator; fusion drug; drug delivery; platelet; cardiovascular disease; thrombolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "disulfide bond between Cys102 and Cys126"
133. .158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "disulfide bond between Cys50 and Cys131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cy842"
                                                                                                                                                                                                                                                                                                                                                                         ..
0
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                                                                                                                                                                                                                                                                                                                                         Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note≈ "disulfide between Cys11 and Cys19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "disulfide bond between Cys33 and
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                   Score 793; DB 2;
Pred. No. 8.7e-54;
; Mismatches 0;

    .45
    /label= Growth_factor_domain

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Kringle_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1, .132
/label= A-chain
                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                       135; Conservative
                                                                                                                 Claim 5; Fig 1; 46pp;
                                                                                                                                                  wild
                                WPI; 1995-060991/08.
Gurewich V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR92926 standard;
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      Sequence 411 AA;
                                                                                                                                                  is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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N-terminal; pro-uPA; urokinase plasminogen activator; receptor; uPAR; anti-reneer; anti-metastatic; anti-prollferative; anti-atherosclerotic; anti-thrombotic; anti-angiogenic; anti-inflammatory; anti-athhitic; anti-fibrotic; apoptotic; asocropic; anti-fibrotic; ophthalmological;

thrombolytic Homo sapiens cocation/Qualifiers

Disulfide-1 Disulfide-1

Disulfide-Disulfide-Disulfide-

Disulfideisulfide-

isulf isulf:

Urokinase plasminogen activator (uPA)

(first entry)

29-AUG-2000

AAY92836;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SNELHQVPSNCDCLANGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A portion of the A-chain (pref. amino acids 1-132) of pro-urckinase (AAR92926) can be linked to a drug, e.g. hirudin, somatostatin or their analogues (see also AAR929257-33) and used in the prodn. of new fusion drugs. The constructs can be obtd. by expression of the appropriate nucleotide sequences in transformed host calls. When administered to a patient, the A-chain binds the fusion drug to the platelet outer membrane, i.e. to the site of thrombosis or vascular injury. Cleavage sites for thrombin and/or plasmin with the fusion drug allow the release of the drug at the target site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        targeted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                           note= "disulfide bond between Cys325 and Cys341"
                                                                                                                                                                                                                                                             352
/note= "disulfide bond between Cys352 and Cys380"
                note= "disulfide bond between Cys148 and Cys279"
[56. .157
                                                                                                                                                                                note= "disulfide bond between Cys197 and Cys268"
                                                                                                                                                                                                             note= "disulfide bond between Cys293 and Cys362"
                                                                                                                                                 note= "disulfide bond between Cys189 and Cys205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion product of plasminogen activator A chain and drug - platelets, useful for treatment of cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 793; DB 2;
100.0%; Pred. No. 8.7e-54;
ive 0; Mismatches 0;
                                          56. .157
note= "thrombin cleavage site"
58. .159
note= "plasmin cleavage site"
59. .411
label= B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                              NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
 'label= Linker_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 39-40; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                     95WO-US009848.
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                                                                                                                                                                                                                                                                                                                                                                                                 94US-00286748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-129123/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT18237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 411 AA;
              Disulfide-bond
                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                        Disulfide-bond
                                             Cleavage-site
                                                                       Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                    15-FEB-1996
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98US-00181816

29-OCT-1998;

28-OCT-1999;

11-MAY-2000.

WO200026353-A1 Disulfide-bond Disulfide-bond

(ANGS-) ANGSTROM PHARM INC.

WPI; 2000-365605/31.

Mazar AP,

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The present sequence shows the wild-type urokinase plasminogen activator (UPA). Cyclic peptides based on the amino acids residues 20-30 (the receptor-binding region) of UPA are claimed. These cyclic peptides target the UPA receptor (UPAR), allowing therapeutic or diagnostic agents to be delivered to UPAR-expressing cells The cyclic peptides are used, coptionally when linked to a therapeutic agent, to inhibit migration, invasion and proliferation of cells, or anglogenesis, or to induce apoptosis. Particularly they are used, in human or veterinary medicine, to treat diseases characterized by these processes, e.g. solid tumors, leukaemia or lymphoma (or their metastases); benigh hyperplasis; atherosclerosis; restenosis; ischeemia; deep vein thrombosis; neovascular glaucher cretinopathy; arthritis; fibrosis; bone fracture etc., most particularly growth, invasion and metastasis of tumors. When labeled, the cyclic peptides can be used for diagnostic detection of uPAR (a marker of metastasis) on cells, tissues etc., in vivo or in vitro, and when immobilized they are used to isolate uPAR or cells that express them. The cyclic peptides are stable, soluble in water, bind strongly to attachment of therapeutic or diagnostic agents without significantly affecting their binding. Since they target uPAR, they should have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cyclic peptide, useful for treatment or diagnosis of e.g. tumors and other diseases involving cell proliferation or migration, targets the urokinase plasminogen activator receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       affecting their binding. Since they target uPAR, they should hav
relatively low systemic toxicity and only low doses are required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 793; DB 3; Length 411;
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AAY92836 standard; protein; 411 AA.

RESULT 32 AAY92836 ID AAY9 XX

121 PLVQECMVHDCADGK 135

Length 411;

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us-09-880-503-4.rag

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Seguence 411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke, hypotension; servoke, hypotension; attoke, therombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory distance; male impotence; adult respiratory distress syndrome; tcuPA; scuPA; two chain urokinase; single chain urokinase.
                                                                                                                   KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                       61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                     SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                         1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                             Human urokinase-type plasminogen activator tcuPA and scuPA protein.
                              ö
            Pred. No. 8.7e-54;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     AAE16544 standard; protein; 411 AA.
100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Fig 1C; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2000; 2000US-0212874P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2001; 2001WO-US018976.
                                                                                                                                                                                               PLVQECMVHDCADGK 135
                                                                                                                                                                               PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYPE-) UNIV PENNSYLVANIA.
                            135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cines DB, Higazi AA;
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N-PSDB; AAD27077.
            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                   AAE16544;
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This recombinant single-chain urine-plasminogen activator (scu-PA), is encoded by a structural gene inserted into plasmid pBR332 (from which the infoloom and/or tet resistance genes have been removed), following insertion of a multiple cloning site (see AAQ10281), a terminator and a synthetic Trp promoter. The resultant expression construct can be used to produce high yields of this scu-PA protein which can be refolded to therappeutically active recombinant scu-PA. This is used in the treatment of e.g. cardiac infarction, pulmonary embolism or arterial occlusive disease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                    61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                      61 KASTDIMGRPCLEWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                     9
                                                                                                                                                                          9
                                                                                                                                                                       1 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                  1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single chain urine plasminogen activator; enterobacteriaceae; scu-PA; cardiac infarction; pulmonary embolism; arterial occlusive disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New plasmids for expressing urine plasminogen activator - in enterobacteriacae have operon contg. promoter, ribosome binding site, synthetic gene and terminator, etc.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant single-chain urine plasminogen activator.
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100.0%; Score 793; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.7e-54;
Matches 135; Conservative 0; Mismatches 0;
; Score 793; DB 5;
; Pred. No. 8.7e-54;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR10334 standard; protein; 412
      100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
      Query Match
Best Local Similarity 100.
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-023590/04.
N-PSDB; AAQ10282.
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05-APR-1991
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Query Match
Best Local Similarity 100.
Matches 135; Conservative
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                                                                                                                                                                  Sequence 424 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1990;
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11-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW24578;
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                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                          Urokinase, inhibitor resistant, plasminogen; human; whey acid protein, plasminogen activator; protesse; WAP, plasmin, proteolytic enzyme; clot lysis; heart attack; heart muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the modified full length urokinase of the invention, including the whey acid protein (WAP) signal peptide. This sequence had residues 179-184 of the wild type urokinase sequence (see AAW24578) deleted. This modified urokinase cleaves plasminogen, and has lower binding affinity for plasminogen activator inhibitor-1 than the corresponding unmodified urokinase. Urokinase is one of two types of mammalian plasminogen activators (PA), the other being tissue type PA.
                          SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                    KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179. .424
/note= "P-domain"
197. .198
/note= "site of 6 residue (Arg-His-Arg-Gly-Gly-Ser)
deletion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deletion-modified urokinase protein - with increased resistance to inhibition by plasminogen activator inhibitor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "whey acid protein signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Kringle-1 domain"
                                                                                                                                                                                                                                                                                                                                                                                          Inhibitor resistant modified urokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iocation/Qualifiers
                                                                                                                                                                                                                                                                   standard; protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "urokinase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "E-domain"
                                                                                                                                          PLVQECMVHDCADGK 135
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                                                                                                                                                                        PLVQECMVHDCADGK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Col; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , .430
/note= "...
                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61. .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-372062/34.
N-PSDB; AAT80076.
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11-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                 RESULT 35
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PAs catalyse the conversion of the circulating zymogen plasminogen to the broad spectrum protease plasmin by limited proteolysis. The modified urokinase can be used for clot lysis, specifically to dissolve heart attack-causing clots before they cause permanent damage to heart muscle. The urokinase mutant is more resistant to inhibition by plasminogen extivator inhibitors than the unmodified urokinase. It can be selectively expressed and secreted from the mammary glands of transgenic animals. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYBGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note= "deleted in modified urokinase of the
                                                                                                                                                                                                                                                                                                                                              Length 424;

    .19
/note= "whey acid protein signal peptide"

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                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                              100.0%; Score 793; DB 2; 100.0%; Pred. No. 9e-54;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW24578 standard; protein; 430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "urokinase"
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/note= "Kringle-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179. .430
/note= "P-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "E-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibitor resistant urokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLVQECMVHDCADGK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00942157
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Ë Suyama

Nishida M,

Rimura H,

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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The inventors claim a method of producing single-chain pro-urokinase by using as template, mRNA obtd. from cells of an established human kidnay-derived cell line. The urokinase is used to treat thrombosis and embolic diseases as well as in the treatment of diseases in combination with
                                                                                                                                                                                                                                Glycosylated single-chain pro-urokinase - prepd. by cultivating animal cells transformed by DNA prepd. from m RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 793; DB 1;
100.0%; Pred. No. 9.1e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 8-10; 64pp; English.
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21. .431
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                                                                                         Nagai M,
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HODOGAYA CHEM IND CO LTD.
SAGAMI CHEM RES CENTRE.
CENTRAL GLASS CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli; high molecular urokinase
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NIPPON SODA CO.
TOYO SODA MFG CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                 (GREC ) GREEN CROSS CORP.
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                                                                                         Kaneda
                                                                                                                                             WPI; 1985-224693/37.
N-PSDB; AAN50138.
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N-PSDB; AAN60703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anticancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human urokinase
                                                                                         Hiramatsu R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
23-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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(HODO
(SAGA
(CENG
(NIPS
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      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                     This sequence represents the full length urokinase, including the whey acid protein (WAP) signal peptide. This sequence has residues 179-184 of the urokinase sequence deleted to craste the modified urokinase of the invention. The modified urokinase (see AMX24579) cleaves plasminogen, and has a lower binding affinity for plasminogen activator inhibitor-1 than the corresponding unmodified urokinase. Urokinase is one of two types of mammalian plasminogen activators (PA), the other being tissue type PA. PAS catalyse the conversion of the diroulating zymogen plasminogen to the circulating zymogen plasminogen to the urokinase can be used for clot lysis, specifically to dissolve heart attack-causing clots before they cause permanent damage to heart muscle. The urokinase mutant is more resistant to inhibition by plasminogen captivator inhibitors than the unmodified urokinase. It can be selectively expressed and secreted from the mammary glands of transgenic animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzyme; thrombosis therapy; embolic disease; single-chain pro-urokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNELHÖVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence and noncoding region of the
                                                    Deletion-modified urokinase protein - with increased resistance to inhibition by plasminogen activator inhibitor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 793; DB 2; Length 430; 100.0%; Pred. No. 9.1e-54; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .20
label= signal peptide
                                                                                                                                       Disclosure; Col 15-18; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
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UK structural gene (Sequence II)
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label= A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79. .431
label= B chain
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85JP-00017969,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLVOECMVHDCADGK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 135; Conser
N-PSDB; AAT80075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-1984;
31-JAN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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RESULT 37

q δ 엄 ò g 9 80

Gaps

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Indels

Length 431;

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The TPA portion of the claimed hybrid polypeptide (see FT) may consist of x bringles from Vterminal first serine to 219th glycine of human TPA, 1 kringle from 128th serine to 219th glycine to thuman TPA or half a kringle from 161st methionine to 219th glycine (see AAP70257). The C-terminal and for the hybrid polypeptide may contain an AA sequence from 150th glutamine to C-terminal 411th leucine of prourokinase (see AAP70258).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 KASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid modified form of prourokinase - having high fibrin selectively and resistant to cleavage to the two-chain form.
              Hybrid plasminogen activator-like polypeptide - having a region for affinity to fibrin from tissue plasminogen activator and a region from prourokinase.
                                                                                                                                                                                                                                                                                                                                                              1 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                              21 SNELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KASTDIMGRPCLPWNSAIVLOQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                          100.0%; Score 793; DB 1; Length 431; 100.0%; Pred. No. 9.1e-54; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
21. .431
/label= Mature product
                                                                                  Disclosure; Fig 2(1-5); 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP71491 standard; protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Fig 1; 18pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87EP-00301567
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87US-00012023
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(first entry)
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified prourokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1987-251560/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibrin selectivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mao JI;
                                                                                                                                                                                                                                                         Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1986;
19-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-1987.
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15-MAY-1991
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                                                                                           The claimed gene product may be expressed in a transformed E.coli host, for the efficient production of high molecular human urokinase. The N-terminal of the protein expressed by the transforming plasmid is replaced with a codon frequently used in E.coli. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                        61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                              81 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                   SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardiovascular disease treatment; fibrin affinity; thrombolytic; enzyme;
            Human urokinase gene - has N-end of aminoacid sequence coded by codon used in Escherichia coli.
                                                                                                                                                                                                                                                                                                     SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                   100.0%; Score 793; DB 1; Length 431; 100.0%; Pred. No. 9.1e-54; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Numao N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wada M, Yamada M, Yokoyama M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of human prourokinase and leader.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |label= prourokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP70258 standard; protein; 431 AA.
                                                          Disclosure, Fig 2; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) SAGAMI CHEM RES CENTRE.
) NIPPON SODA CO.
) CENTRAL GLASS CO LTD.
) TOYOO SODA MFG CO LTD.
) NISSAN CHEM IND LTD.
) NISSAN CHEMICAL INDS KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .20
|abel= leader
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87JP-00018626.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLVOECHVHDCADCK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                 Matches 135; Conservative
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N-PSDB; AAN70390.
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                 correct PA field.
                                                                                                                                                                                                  Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-1987;
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19-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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(CENG) (TOYJ) T
(NISC) N
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120

us-09-880-503-4.rag

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The amino acid LNS at position 158 of the mature protein is replaced by MET and the amino acid LLE at position 160 is replaced by SER, achieved by site-directed mutagenesis or by chemial modification. The modified PUK has a single polypeptide chain, high fibrin activity and is resistant to cleavage to the two-chain form to an extent greater than its original unmodified form. The therapeutic specificity of single-chain PUK can be increased without decreasing librinolytic activity. The single chain form can have high fibrin activity and thus does not cause general bleeding in
                                                                                                                                                                                                                               81 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid modified form of prourokinase - having high fibrin selectively and resistant to cleavage to the two-chain form.
     fibrinolytic activity. The single chain form can have high fibrin activity and thus does not cause general bleeding in the body but rather can be localised to the site of the blood clot directly. See also AAN71368-69
                                                                                                                                                                                                                KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                                                                          SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                    21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                 Gaps
                                                                                                                                 ó
                                                                                                     Length 431;
                                                                                                                                 Indels
                                                                                                     100.0%; Score 793; DB 1;
100.0%; Pred. No. 9.1e-54;
ive 0; Mismatches 0;
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/label=_sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified prourokinase (MET/SER).
                                                                                                                                                                                                                                                                                                                                                                      AAP71698 standard; protein; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COLB ) COLLABORATIVE RES INC
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87US-00012023.
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                                                                                                                                                                                                                                                                         PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                PLVQECMVHDCADGK 155
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                               Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prourokinase, fibrin, PUK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1987-251560/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mac JI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAN71368
                                                                          Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-1987;
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19-FEB-1987;
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                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                          61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                             Amino acid modified form of prourokinase - having high fibrin selectively and resistant to cleavage to the two-chain form.
                                                                                                                                                          9
                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The amino acid LVS at position 158 of the mature protein (see tag b) is replaced by another amino acid, achieved by site-directed mutagenesis or by chemial modification. The modified PUK has a single polypeptide chain, high fibrin activity and is resistant to cleavage to the two-chain form to an extent greater than its original unmodified form. The therapeutic specificity of single-chain PUK can be increased without decreasing
The modified prourokinase product has a single polypeptide chain, high fibrin selectivity and resistance to cleavage into the two-chain form. The modification is at the codon for Lys158. (Updated on 31-OCT-2002 to add missing OS field.)
                                                                                                                                                                        21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKRGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                      1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                              Gaps
                                                                                                                              ÷
                                                                                                     Length 431;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "amino acid other than LYS"
                                                                                                100.0%; Score 793; DB 1;
100.0%; Pred. No. 9.1e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //label= sig peptide
21. 431
/label= mat protein
178. 178
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                                                                                                                                                                                                                                                                                                                                                                AAP71663 standard; protein; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COLB ) COLLABORATIVE RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86US-00833179.
87US-00012023.
                                                                                                                                                                                                                                                                    PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87EP-00301567
                                                                                                                                                                                                                                                                                             141 PLVQECMVHDCADGK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibrin; PUK
                                                                                            Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified prourokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1987-251560/36.
N-PSDB; AAN71338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vovis GF, Mao JI;
                                                                     Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prourokinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-1987;
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19-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Peptide
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The patent is for the prodn. of human single chain urokinase-type plasminogen activator (UTPA). Mutants of scu-PA are especially those which render the protein protease resistant. Such scu-PA mutants are covalently modified at sites of proteolysis by proteases occuring in blood such as thrombin or plasmin, so that thay are no longer susceptable to protease hydrolysis at these locations. The target sites include Lys135 to Lys136 (cleavage at this site generates the so-called low molecular weight form of scu-PA or LUX), Arg156 to Phe157 (susceptible to thrombin attack) and Lys158 to Ile159 (cleavage at this site by plasmin
                                                                                                                                                    KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                       21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain urokinase plasminogen activator (SCU-PA); human Hep3 cells; glyceraldehyde-3-phosphate dehydrogenase gene; thrombosis prevention; thrombosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                 Deduced AA sequence of the single chain urokinase plasminogen activator (SCU-PA) cDNA insert prepared from human Hep3 cells.
                                                                                            1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodn. of human single chain urokinase-type plasminogen activator culturing yeast strain transformed with hybrid vector contg. yeast expression control sequences.
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                                     Length 431;
                                                                Indels
                                 100.0%; Score 793; DB 1;
100.0%; Pred. No. 9.1e-54;
ive 0; Mismatches 0;
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1. .20
21. .411
                                                                                                                                                                                                                                                                                                                AAP80430 standard; protein; 431 AA.
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87GB-00014059.
87IE-00003299.
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                                                                                                                                                                                                            121 PLVQECMVHDCADGK 135
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                                                                                                                                                                                                                                 PLVQECMVHDCADGK 155
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(first entry)
                                             Similarity 100.
35; Conservative
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N-PSDB; AAN80981.
       Sequence 431 AA;
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16-JUN-1987;
04-DEC-1987;
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14-SEP-1990
                                                  Best Local Sim:
Matches 135;
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Protein
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                                                                                                                                                                                                               81 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid modified form of prourokinase - having high fibrin selectively and resistant to cleavage to the two-chain form.
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                                                                                                                                                    SNEIHQVPSNCDCLNGGICVSNKYFSNIHWCNCPKKFGGOHCEIDKSKICYEGNGHFYRG
                                                                                                                                 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                           KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                       Gaps
the body but rather can be localised to the site of the blood clot directly. See also AAN71368-69 and AAN71338
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                                                                           Length 431;
                                                                                                       0; Indels
                                                                      100.0%; Score 793; DB 1;
100.0%; Pred. No. 9.1e-54;
ive 0; Mismatches 0;
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/label= sig_peptide
21. .431
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87US-00012023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified prourokinase (ALA).
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                                                                     Query Match
Best Local Similarity 100.
Matches 135; Conservative
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N-PSDB; AAN71369.
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                                            Sequence 431 AA;
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19-FEB-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               generates tuc-PA). Suitable scu-PA mutants have site specific substitutions, insertions or deletions of residues at one or more of these target sites. Especially preferred are those mutants in which one amino acid residue or both amino acid residues forming the target sites are deleted or in which at least one of these amino acid residues is replaced by another amino acid residue so that the resulting mutants are resistant to proteolytic attack. The UTPA proteins exhibit the blological activity of natural human UTPA without any refolding procedure being or treatment of thrombosis or other conditions where it is desired to produce local fibrinolytic or proteolytic activity. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .20
/label= signal peptide
21. .431
/label= pro-urokinase
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Best Local Similarity
Matches 135; Conserv
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03-DEC-1990
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The Arg at position 2 is encoded by TGA(sic). Possible error in the specification. Should read CGA ? The pro-UK gene was derived from plasmid but3. The cDNA was synthesised using urokinase mRNA isolated from a human kidney cell line. Pro-UK was cloned into a SV40 promoter-contg. plasmid ,down - stream of the promoter. This plasmid was then ligated to a DHFR-gene contg. plasmid so that pro-UK and DHFR are inserted in opposite directions. The recombinant plasmid was used to transform CHO-K1 cell derived DHFR gene-deficient host cells to produce glycosylated single-chain pro-UK. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KASTDIMGRPCLEWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wt. plasminogen activator; prourokinase; dissolve blood
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/note= "Mature prourokinase."
/note= 170. .179
/note= "Preferred initiation region for the low
                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                    100.0%; Score 793; DB 1; Length 431; 100.0%; Pred. No. 9.1e-54; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLVÓECMVHDCADGK 155
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Best Local Similarity 100.
Matches 135; Conservative
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N-PSDB; AAN91740.
                                                                                                                                                                                                                                                       Sequence 431 AA;
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31-OCT-2002
16-APR-1990
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WPI; 1989-068869/09.
N-PSDB; AAN91075.
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         A low mol. wt. polypeptide plasminogen activator (PA) is claimed which is formed from amino acids 150-411 of prourokinase. The preferred intiation region for the low mol. wt. PA is indicated (see FT). A low mol wt. PA can be injected into blood in the body in vivo to dissolve clots without harm. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR
                                                                                                                                                                                                                       KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                            SNETHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                             Gaps
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0
                                                                                                                    Score 793; DB 1; Length 431;
Pred. No. 9.1e-54;
Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "May be replaced by a non-basic AA in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Pro, Gly, Ala or Val in new deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .155 note= "Incorporated into new deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Lys or Arg in new deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              new
                                                                                                                                                                                                                                                                                                                                                                                                                             Human prourokinase; antithrombotic; derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Undefined residue in
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) CENTRAL GLASS CO LTD.

) HODOGAYA CHEM KK.

) NIPPON SODA CO.

NISSAN CHEM IND LTD.
                                                                                                                    Query Match
Best Local Similarity 100.0%; P
Matches 135; Conservative 0;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Natural human prourokinase
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                                                                                               Sequence 431 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                            A human prourokinase (PU) deriv. is new which is based upon residues 2-155 of natural human prourokinase. The new deriv. is produced by E. col 2103/gbwT90_RPK in culture. It is a fast-acting drug for the treatment and prevention of thrombosis. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
Antithrombotic fast-acting pro-urokinase deriv. - produced by culture E coli transformant contg. new plasmid of PMUT9Q family.
                                                                                                                                                                                                                                                                                                                                           KASTDIMGRPCLPWNSAIVLOQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK
                                                                                                                                                                                                                                                                            1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New non glycosylated, secreted plasminogen activator - pref. with asparagine replaced or deleted, useful for treating blood clots, expressed in non mammalian cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGE 195; plasminogen activator; blood clot lysis.
                                                                                                                                                                                                                Length 431;
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                                                                                                                                                                                                          Query Match
100.0%; Score 793; DB 1;
Best Local Similarity 100.0%; Pred. No. 9.1e-54;
Matches 135; Conservative 0; Mismatches 0;
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/label= signal sequence
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                                                75pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-glycosylated prourokinase.
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88US-00211279
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N-PSDB; AAN93079.
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                                              Disclosure, Fig 1;
                                                                                                                                                                               Sequence 431 AA
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27-JUN-1990
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to CCA; Gln(346), CAA to CAG. See also AAQ06045-Q06048 and AAQ06392. (Updated on 25-MAR-2003 to correct PA field.)
                                                           Query Match
Best Local Similarity 100.
Matches 135; Conservative
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N-PSDB; AAQ04107.
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                                          Sequence 431 AA;
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12-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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Best Local S:
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       myocardial infarction. DNA encoding the protein was sequenced from plasmid pCGB195, a subclone of two inserts isolated by screening a cDNA library prepd. From kidney cell RNA. One of the original inserts, clone CGF31 (tag c) started in the middle of the signal sequence. Mutants of the sequence, pref. in which goc (Ala) replaces aat (Asn) at nucleotides 1002-1004 (residue 302) are used to transform hosts for the prodn. of non-glycosylated prourokinase. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.coli strain C600SF8 was transformed with recombinant plasmid containing ds DNA derived from human pharynx cancer cell strain Detroit 562. 10000 colonies were screened and one positive clone was identified. Plasmid pUX1 was isolated and found to contain the coding region and 3' non-coding region of pro-UX downstream of Cys(41). Four silent substitutions were identified c.f. Holmes et al., Biotechnology, vol.3, p.923 (1985) as follows: (aic) Asn(254), AAC to AAT; Leu(340), CTA to CTG; Pro(345), CCC
                                                                                                                                                                                                                                     KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                        KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
                                                                                                                                                                                  SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                    SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of recombinant protein, esp. human pro:urokinase - from milk of transgenic animals using promoter of bovine alpha S1 casein chromosomal
                                                                                                                                                                Gaps
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                                                                                                                                       Length 431;
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                                                                                                                                    100.0%; Score 793; DB 1;
100.0%; Pred. No. 9.1e-54;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 431 AA.
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JIKKEN DOBUTSU CHUO KENK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pro-Urokinase; transgenic mice
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(EXPE-) CENT INST EXPER ANIMP
(JIKK-) JIKKEN DOBUTSU CHUO P
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Matches 135; Conservative
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                                                                                                            Seguence 431 AA;
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24-JAN-1991
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61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strains and
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100.0%; Pred. No. 9.1e-54;
ive 0; Mismatches 0;
100.0%; Score 793; DB 2;
100.0%; Pred. No. 9.1e-54;
ive 0; Mismatches 0;
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promoter PTRP and Shine-Dalgarno sequence MS-2.
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                                                                                                                                                                                                                                                                                        PLVQECMVHDCADGK 135
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(first entry)
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Search completed: May 25, 2004, 14:52:54 Job time : 36.0105 secs

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May 25, 2004, 14:53:05 ; Search time 24.61 Seconds (without alignments) 1530.046 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                     793
1 SNELHQVPSNCDCLNGGTCV.....QVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1149313 seqs, 278921704 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries
                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                     US-09-880-503-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
		ф			-		
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	
. 4	793	100.0]] 4	. 6	US-09-880-503-4	Sequence 4, Appli	
7	793	100.0		σι	US-09-984-186-12	Sequence 12, Appl	
m	793	100.0	138	14	US-10-237-667-12	Sequence 12, Appl	
4	793	100.0	138	14	US-10-237-708-12	Sequence 12, Appl	
5	793	100.0	138	14	US-10-237-866-12	Sequence 12, Appl	
9	793	100.0	138	14	US-10-237-871-12	Sequence 12, Appl	
7	793	100.0	138	14	US-10-237-624-12	Sequence 12, Appl	
œ	793	100.0	138	16	US-10-702-536-12	Sequence 12, Appl	
o,	793	100.0	138	16	US-10-702-636-12	Sequence 12, Appl	
10	793	100.0	143	σ	US-09-880-503-8	Sequence 8, Appli	
11	793	100.0	337	14	US-10-106-698-6266	Sequence 6266, Ap	
12	793	100.0	337	15	US-10-264-049-2927	Sequence 2927, Ap	
13	793	100.0	403	σ	US-09-880-503-6	Sequence 6, Appli	
14	793	100.0	411	σı	US-09-880-503-3	Sequence 3, Appli	
15	793	100.0	431	σ	US-09-264-468B-1	Sequence 1, Appli	

quenc	equence 34	equence 16	equence 4	equence 16	equence 2.	equence 4.	equence 3	equence 3	equence 594, Ap	equence 149, Ap	equence 2	equence 562, Ap	equence 266, Ap	equence 1, Appl	Sequence 53	Juence 1,	Semience 37	equence 36	equence 1.	equence 3.	squence 1,	equence 9	equence 2	equence 9	equence o	equence 9.	equence 5	equence 2	equence 1	equence 3	equence 1	equence 1.	equence 1	equence 3	equence 3,	equence 1	equence 3	equence 2	equence 4	equence 2	equence 1	equence 3	equence 1	equence 1	equence 1	equence 1	equence 1	equence 2	equence 4	equence 2	equence /	, aniianha
US-10-411-037-3	US-10-411-02	US-10-171-311-	1 US-10-193-656-4	1 US-10-301-822-1	US-10-131-985-21	S US-10-295-02	S US-10-410-962-34	5 US-10-411-049-3	2 US-10-087-192	4 US-10-247-671-1	5 US-10-407-821-2	2 US-10-282-174-	5 US-10-360-101-26	S US-10-401-077-1	-261-080-01-30 2	110-09-080-303	08-09-880-303-3 7 TR-10-424-999-3	2 US-10-424-999-3	2 US-10-424-999-1	2 US-10-425-000-	5 US-10-233-675A-	2 US-10-424-999-9	2 US-10-425-000-	5 US-10-233-675A-	2 US-10-424-999-5	2 US-10-424-999-6	5 US-10-233-675A-	5 US-10-233-675A-	2 US-10-424-999-18	2 US-10-425-000-38	5 US-10-233-675A-	2 US-10-424-999-1	5 US-10-423-000-3 5 US-10-233-675A-	2 US-10-424-999-35	2 US-10-424-999-3	2 US-10-424-999-1	2 US-10-425-000-3	5 US-IU-233-6/5A-1	2 US-10-425-000-4	5 US-10-233-675A-	2 US-10-424-999-1	2 US-10-425-000-35	S US-10-233-675A-	Z US-10-424-999-1	Z 03-10-423-000-3 5 US-10-233-675A-	2 118-10-424-999-1	5 US-10-233-675A-	2 US-10-424-999-2	2 US-10-425-000-40	5 US-10-233-675A-	2 US-10-424-999-	-WC/9-83-01-80 C
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ALIGNMENTS

US-09-880-503-4
; Sequence 4, US20020131964A1
; Sequence 10.0220020131964A1
; GENERAL INFORMATION:
; APELICANT: CINES, Douglas B
; APELICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 KASTDIMGRPCLPWNSATVIQQIYHAHRSDALQIGIGKHNYCRNPDNRRRPWCYVQVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SNELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                                                                  1 SNELHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                                                        ò
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PREPARATION THEREOF AND PHARMACEUTICAL
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                       Length 138;
                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                       100.0%; Score 793; DB 9;
100.0%; Pred. No. 3.7e-72;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA.

APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/PR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-38,619
       REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Ahone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-10-237-667-12
US-10-237-667
; Sequence 12, Application US/10237667
; Publication No. US20030022308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Pournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
; Patrice
Yeh, Patrice
                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-984-186-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                           TELECOMMUNICATION INFORMATION
TELEPHONE: (610) 454-383
TELEFAX: (610) 454-3808
                                                                                                                                               LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 PLVQECMVHDCADGK 138
                                                                          TELEFAX: (610) 454-:
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 135; Conservative
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KASTDIMGRPCIPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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100.0%; Pred. No. 3.6e-72;
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COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-0ct-2001
CLASSIFICATION NUMBER: US/08/797,689
FILING DATE: 31-0AN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-0AN-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-0AN-1992
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-0AN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 29-7AN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
    TISSUE CONTRACTABILITY
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTION OF 18
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NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09984186
Patent No. US20020151011A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            .
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-4
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US-09-984-186-12
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61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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100.0%; Pred. No. 3.7e-72;
ive 0; Mismatches 0;
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COMPUTER: LOSA

ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: SYSTEM: ASTEM: ASTE
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REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-10-237-866-12
; Sequence 12, Application US/10237866
; Publication No. US20030036171A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Gournier, Alain
Guitton, Jean-Dominique
; Jung, Gerard
; Jung, Resince
Yeh, Patrice
Yeh, Patrice
                                                                                                     | LENGTH: 138 amino acids | LENGTH: 138 amino acids | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-10-237-708-12
                                           454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                       TELEFAX: (610) 454-31
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PLVQECMVHDCADGK 135
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Best Local Similarity 100.
Matches 135; Conservative
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 KASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SNELHQVPSNCDCLNGGTCVSNXYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 63
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 793; DB 14; Best Local Similarity 100.0%; Pred. No. 3.7e-72; Matches 135; Conservative 0; Mismatches 0;
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COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION OF CURROWN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: R 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: P 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: P 92/01064
FILING DATE: SB-JAN-1993
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REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSER: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Publication No. US20303036170A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
TELECOMMUNICATION INFORMATION
                                                                                      INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 138 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
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US-10-237-667-12
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                  Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                           100.0%; Score 793; DB 14;
100.0%; Pred. No. 3.7e-72;
ive 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
FILING DATE: 10-SEP-2002
CLASSIFICATION: CURKNOWN:
PRIOR APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/56,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PS/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 31-JAN-1993
APTLICATION NUMBER: PCT/FR93/00085
FILING DATE: 329-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph. D., Julie K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-871-12
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Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
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US-10-237-624-12
; Sequence 12, Application US/10237624
; Publication No. US20030082747A1
; GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
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       INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 PLVQECMVHDCADGK 138
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.(
Matches 135; Conservative
                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 63
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.7e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0
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REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                   | EINGTH: 138 amino acids | TYPE: amino acids | TYPE: amino acid | TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-10-237-866-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/10237871
Publication No. US20030036172A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Gutton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (610) 454-38:
TELEFAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 PLVQECMVHDCADGK 138
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61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 63
                                                                                                                                                                                                                                                                                                                                                                                          1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
                                                                                                                                                                                                                                                                                                                          Gaps
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US-10-702-636-12
Sequence 12, Application US/10702636
Publication No. US20040086977A1
GENERAL INFORMATION:
CENERAL INFORMATION:
CONTAINS
HOPELCANT:
CHILLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES.
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                                                                                                                                                                                                                                                   Query Match 100.0%; Score 793; DB 16; Length 138; Best Local Similarity 100.0%; Pred. No. 3.7e-72; Matches 135; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERBUCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                           MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-702-536-12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                     LENGTH: 138 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454-3808
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKGHNYCRNPDNRRPWCYVQVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                1 SNEIHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG
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al Similarity 100.0%; Score 793; DB 14; Length 138;
al Similarity 100.0%; Pred. No. 3.7e-72;
135; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                   Indels
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COMPUTER: Macintosh
SOFTWARE: Wach 5:1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/702,536
FILING DATE: O7-NOV-2003
CLASSIFICATION SATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1994
APPLICATION NUMBER: FR 92/01064
APPLICATION NUMBER: PCT/FK93/00065
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PCT/FK93/00065
FILING DATE: 28-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: SMITP Ph. D. , Julie K.
REFERENCE/DOCKET NUMBER: P39,619
TELECOMMUNICATION INFORMATION:
METERALICATION NUMBER: P38,619
TELECOMMUNICATION INFORMATION:
METERALICATION INFORMATION:
MET
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CORRESPONDENCE ADDRESS:
ADDRESSES: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: COllegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids

LYPE: amino acids

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-237-624-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/10702536 Publication No. US20040086976A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
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Best Local Similarity
Matches 135; Conserv
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                      Length 337;
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Publication No. US20040005579A1
GENERAL INPORMATION:
FILE REFRENCE:
FILE REFRENCE:
FILE REPRINCE:
FILE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 4360
NUMBER OF SEQ ID NOS: 4360
SOFFWARE: Patentin Ver. 3.1
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100.0%; Score 793; DB 14;
Best Local Similarity 100.0%; Pred. No. 9.7e-72;
Matches 135; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 6266
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US-09-880-533-6
; Sequence 6, Application US/09880503
; Patent No. US20020131964A1
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Matches 135; Conservative
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ORGANISM: Homo sapiens
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US-10-106-698-6266
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LENGTH: 337
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Publication No. US20030109690A1
GENERAL INFORMATION:
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA0055P1
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
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APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEY: 2.1
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                                                                                                                                       100.0%; Score 793; DB 16;
100.0%; Pred. No. 3.7e-72;
ive 0; Mismatches 0;
                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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, Sequence 8, Application US/09880503

; Patent No. US20020131964A1

; GENERAL INFORMATION:
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                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 135; Conservative
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Best Local Similarity 100.
Matches 135, Conservative
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ORGANISM: Homo sapiens
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US-10-106-698-6266
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US-10-702-636-12
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Sequence 3, Application US/09880503

Patent No. US2002011964A1

GENERAL INFORMATION

APPLICANT: HIGAZI, Abd Al-Roof

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

TITLE OF INVENTION: TISSUE CONTRACTABILITY

TITLE OF INVENTION TISSUE CONTRACTABILITY

TITLE OF INVENTION UNMER: US/09/880,503

CURRENT FILING DATE: 2001-06-13

PRIOR PELICATION NUMBER: US 60/212,847

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 3

LENGTH: 411
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GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILLE REFERENCE: 9596-33
CURRENT APPLICATION NUMBER: US 60/212,847
PRIOR APPLICATION NUMBER: US 60/212,847
NUMBER OF SEQ ID NOS: 18
SOFWARE: PATENTIN DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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Best Local Similarity 100.0%; Pred. No. 1.2e-71;
Matches 135; Conservative 0; Mismatches 0; Indels
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100.0%; Score 793; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.2e-71;
Matches 135; Conservative 0; Mismatches 0; Indels
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CORGANISM: Homo sapiens
US-09-880-503-6
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US-09-880-503-3
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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Sequence 2, Application US/10076421
Publication No. US2020193304A1
GENERAL INFORMATION:
APPLICANT: WADA, MARNBU
APPLICANT: WADA, NAOKO
ITILE OF INVENTION: ANTI-HIV AGENTS
FILE REFERENCE: HAYAK-9
CURRENT APPLICATION NUMBER: US/10/076,421
CURRENT FILING DATE: 2002-05-17
PRIOR PELICATION NUMBER: JP 2001-42655
PRIOR PELICATION NUMBER: JP 2001-184284
PRIOR PELICATION NUMBER: JP 2001-184284
PRIOR PELING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 2
LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PLVQECMVHDCADGK 135
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; ORGANISM: Homo sapiens
US-10-076-421-2
                                                                           , ORGANISM: Homo sapiens
US-10-411-026-34
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(Sequence 34, Application US/10411026

(Sequence 34, Application US/10411026

(Publication NO US200040063911A1

(RENERL INFORMATION: US20040063911A1

(RENERL INFORMATION: Decrees, Shawn

(APPLICANT: Decrees, Shawn

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PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APLICATION NUMBER: US 60/391,292
PRIOR PILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
PRIOR PLANG DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 34
LENGTH: 431
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; ORGANISM: Homo sapiens
US-10-411-037-34
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121 PLVQECMVHDCADGK 135
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US-10-131-985-21
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## APPLICANT: Hoersh, Sebastian

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: DEMYIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

TITLE OF INVENTION: OF CERVICAL CANCER

FILE REFERENCE: MRI-035

CURRENT PELLOATION NUMBER: US/10/171,311

CURRENT FILING DATE: 2002-06-13

PRIOR APPLICATION NUMBER: US 60/298,159

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-06-13

PRIOR PLING DATE: 2001-11-14

NUMBER OF SEQ ID NOS: 238

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 184

TENGTH: A31
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Publication No. US20030096733A1
GENERAL INFORMATION:
APPLICANT: WY, TOR
APPLICANT: HOLMDAHL, Rikard
APPLICANT: LI, Jinan
ITILE OF INFORMATION:
FILE REFERENCE: 3810/1J577-US3
CURRENT APPLICATION NOWBER: US/10/193,656
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR PLING DATE: 2001-07-10
PRIOR PAPLICATION NUMBER: US 60/304,490
PRIOR FILING DATE: 2001-07-10
PRIOR PELING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-13
SOFTWARE: PARCHIN VEXEION 3.1
SEQ ID NO 4
LENGTH: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 793; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.3e-71;
Matches 135; Conservative 0; Mismatches 0;
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100.0%; Score 793; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.3e-71;
Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P00749
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1). (431)
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CORGANISM: Homo sapiens

US-10-171-311-184
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APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Morahan, John E.
APPLICANT: Morahan, John E.
APPLICANT: Hibodeau, Stephen N.
APPLICANT: HERAPY OF COLON CANCER
ITILE OF INVENTION: THERAPY OF COLON CANCER
ITILE OF INVENTION: THERAPY OF COLON CANCER
ITILE OF INVENTION: THERAPY OF COLON CANCER
ITILE OF INVENTION: HOWER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 228
SOFTWARE FEASEG FOR Windows Version 4.0
                                                                                                              61 KASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                     81 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKRNYCRNPDNRRRPWCYVQVGLK 140
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SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 161, Application US/10301822; Publication No. US20030148410A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/10131985
Publication No. US20030199440A1
GENERAL INFORMATION:
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APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
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81 KASTDIMGRPCLPWNSAIVIQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
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APPLICANT: Mack, David.H.
APPLICANT: Mateon, Susan R.
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
TITLE OF INVENTION: Methods of Diagnosis of Cancer,
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE OF INVENTION: MUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR PELLING DATE: 2000-10-11-13
PRIOR PELLING DATE: 2001-11-15
PRIOR PELLING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-11-29
PRIOR PELLING DATE: 2001-11-10
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PELLING DATE: 2002-01-10
PRIOR PELLING DATE: 
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           Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1386
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 414
LENGTH: 431
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100.0%; Pred. No. 1.3e-71;
tive 0; Mismatches 0;
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Publication No. US20030232350A1
GENERAL INFORMATION:
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
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Best Local Similarity 100.0
Matches 135; Conservative
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; ORGANISM: Homo sapiens
US-10-295-027-414
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions ar

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

FILE REFERENCE: 08501-012500US

CURRENT APPLICATION UWBER: US/10/295,027

CURRENT FILING DATE: 2002-11-13
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100.0%; Pred. No. 1.3e-71;
ive 0; Mismatches 0;
FILE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131,985
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/726,295
PRIOR FILING DATE: 2000-11-30
PRIOR PLING DATE: 1999-12-29
PRIOR PLING DATE: 1999-12-29
NUMBER OF SEC ID NOS: 60
SOFTWARE: PatentIn Ver: 2.1
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PRIOR FILING DATE: 2000-09-15
PRIOR PELING DATE: 2000-09-15
PRIOR PELING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR PLUCATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR PLUCATION NUMBER: US 60/34,393
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-2-14
PRIOR PLUCATION NUMBER: US 60/34,336
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-09
PRIOR PLING DATE: 2002-01-09
PRIOR PLING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PLING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/375,250
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PRING DATE: 2002-01-08
PRIOR PRING DATE: 2002-01-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
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Publication No. US20030232350A1
GENERAL INFORMATION:
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
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Watson, Susan R
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Best Local Similarity 100.
Matches 135; Conservative
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ORGANISM: Homo sapiens
US-10-131-985-21
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PLVQECMVHDCADGK 155
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Best Local Similarity 100.
Matches 135; Conservative
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ORGANISM: Homo sapiens
US-10-411-049-34
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APPLICANT: DeFrees, Shawn
APPLICANT: Eayer, Robert
APPLICANT: Eayer, Robert
APPLICANT: Chen, Xi
APPLICANT: Hakes, David
APPLICANT: GENERAL CATYN
TITLE OF INVENTION: GLYCOCOUNTGATION OF G-CSF
TITLE OF INVENTION UNMERR: US 60/328,523
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-05
PRIOR FILING DATE: 2002-06-15
PRIOR PILING DATE: 2002-06-15
PRIOR FILING DATE: 2002-06-15
PRIOR FILING DATE: 2002-06-16
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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Best Local Similarity 100.0%; Pred. No. 1.3e-71;
Matches 135; Conservative 0; Mismatches 0; Indels 0
       Length 431;
                                                                          Indels
Query Match
100.0%; Score 793; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-71;
Matches 135; Conservative 0; Mismatches 0;
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Publication No. US20040077836A1
GENERAL INFORMATION:
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CRGANISM: Homo sapiens
US-10-410-962-34
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PRIOR APPLICANTON NUMBER: US 60/346,594

PRIOR PLINE DATE COLL 10.

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APPLICANT NUMBER: US 60/346,394

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TITLE OF INVENTION: INTERPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURITIS IN RABBITS FILE REFERENCE: UTSN:02205
CURRENT APPLICATION NUMBER: US/10/407,821
CURRENT PEDELICATION NUMBER: US/10/407,821
PRIOR FILING DATE: 2002-09-27
SOFTWARE: PALENCHIN VOICE: 2012-09-27
SOFTWARE: PALENCHIN VOICE: 2012-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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APPLICANT: Wang, Xn
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Tanzi, Lars
APPLICANT: Bertram, Lars
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Backer, Deborah Lynne
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASES
TITLE OF INVENTION: NEUROBER: US 60/339,525
PRIOR PELLING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR PELLING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-09
PRIOR PILING DATE: 2001-11-204
PRIOR PILING DATE: 2001-11-304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.7%; Score 783; DB 15; Length 411; 99.3%; Pred. No. 1.2e-70; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 562, Application US/10282174; Publication No. US20030224380A1; GENERAL INFORMATION:
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APPLICANT: Velicelebi, Gonul
APPLICANT: Elliot, Kathryn J.
APPLICANT: Wang, Xin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 PLVQECMVHDCADGK 135
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Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-407-821-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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99.7%; Score 791; DB 14; Length 431;
Best Local Similarity 99.3%; Pred. No. 2e-71;
Matches 134; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 149, Application US/10247671
; Publication No. US20030194721A1
; Publication No. US20030194721A1
; GENERAL INFORMATION:
   APPLICANT: Shiffman, Dov
   APPLICANT: Raser, Matthew R.
   APPLICANT: Kaser, Matthew R.
   TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
   FILE REFERENCE: PA-0050 US
   CURRENT APPLICATION NUMBER: US/10/247,671
   CURRENT PILING DATE: 2002-09-18
   PRIOR APPLICATION UNMBER: 60/323,784
   PRIOR FILING DATE: 2001-09-19
   NUMBER OF SEQ ID NOS: 186
   SOFTWARE: PERL PROGRAM
   SEQ ID NOS: 186
   SEQ ID NOS: 186
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) OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
US-10-247-671-149
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                       Score 793; DB 12;
Pred. No. 1.3e-71;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                   NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 594
LENGTH: 437
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US-10-407-821-2
Sequence 2, Application US/10407821
; Publication No. US20030219386A1
                                                                                                                                                                                                                                                                                                                                       100.0%;
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PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 135; Conservative
                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-594
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ORGANISM: Homo sapiens
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Best Local Similarity
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136 RGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 RGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 RPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 RPCLAWNAPAVIQKPYNAHRPDAISLGLGKANYCRNPDNQKRPWCYVQIGLRQFVQECMV 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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TITLE OF INVENTION: HUMAN TISSUE UROKINASE TYPE PLASMINOGEN TITLE OF INVENTION: ACTIVATOR PRODUCTION
FILE REFERENCE: 12133-006001
CURRENT APPLICATION NUMBER: US/10/401,077
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/371,013
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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| Publication No. US20201825861
| Publication No. US20201825861
| APPLICANT: Morris, David W. |
| APPLICANT: Morris, David W. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: CANCER |
| TITLE OF INVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.1%; Score 595.5; DB 15; Best Local Similarity 77.9%; Pred. No. 1.6e-51; Matches 106; Conservative 7; Mismatches 18; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 LKPLVQECMVHDCADG 134
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                                                                                                                                                                                                                                                                                                                           LENGTH: 650
TYPE: PRT
CRGANISM: Homo sapiens
US-10-401-077-1
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ORGANISM: Mus musculus
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Best Local Similarity
Matches 91; Conserv
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Publication No. US20040009550A1
Publication No. US20040009550A1
APPLICANT: No.1, Gert N.
APPLICANT: Leenhouts, Cornelis J.
APPLICANTON INVERS: US/10/360,101
CURRENT APPLICATION NUMBER: US/10/360,101
PRIOR FILING DATE: 2002-05-24
NUMBER: OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 KASTDIMGRPCLEWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 SNEIHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFXGQHCBIDKSKTCYBGNGHFYRG
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                                                                                                                                                                                                                                                                                             Length 431;
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                                                                                                                                                                                                                                                                                   Score 777; DB 12; Length 4
Pred. No. 5.2e-70;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Pred. No. 2.2e-69;
0; Mismatches 0;
                                                                                                                   NAME/KEY: VARIANT

CCATION: 15, 58, 141, 214, 231, 274, 366

OTHER INFORMATION: Xaa = Any Amino Acid

US-10-282-174-562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: sequence of urokinase US-10-360-101-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10401077
Publication No. US20040002137A1
GENERAL INFORMATION:
APPLICANT: Hung, Paul Porwen
APPLICANT: Wu, Bryan T. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 VGLKPLVQECMVHDCADGK 159
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.5%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 XLVQECMVHDCADGK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PLVQECMVHDCADGK 135
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Best Local Similarity 97.1%;
Matches 135; Conservative
                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 31
US-10-360-101-266
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LENGTH: 445
LENGTH: 431
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OTHER INFORMATION: Abrogen D43
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
Publication No. US20040052810A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 88; Conservat
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US-10-424-999-36
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                                 Sequence 1, Application US/09880503
Sequence 1, Application US/09880503
Sequence 1, Application US/09880503
SERENT USECO131964A1
SEPLICANT: USECO131964A1
SEPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: TISSUE CONTRACTABILITY
TITLE OF INVENTION: TISSUE CONTRACTABILITY
TITLE OF INVENTION: USECO13
TITLE OF INVENTION UNBER: US/09/880,503
CURRENT APPLICATION NUMBER: US 60/212,847
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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Patent No. US2020131964A1
GENERAL INFORMATION
APPLICANT: CIRES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT PILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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Best Local Similarity 100.0%; Pred. No. 7.8e-44;
Matches 88; Conservative 0; Mismatches 0;
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64.3%; Score 510; DB 9;
Best Local Similarity 100.0%; Pred. No. 8.5e-44;
Matches 88; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
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; ORGANISM: Homo sapiens
US-09-880-503-9
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Homo sapiens US-09-880-503-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
US-10-424-999-37
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; Sequence 37, Application US/10424999

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Sequence 36, Application US/10424999
Publication No. US20040052810A1
General Information:
General Information:
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
CURRENT APPLICATION NUMBER: 12013-04-29
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENTH: 221
GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
APPLICANT: Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and M.
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REPERRNCE: ST01027-A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR PILING DATE: 2002-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Petentin version 3.2
SEQ ID NO 3.7
LENGTH: 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.2%; Score 501; DB 12; Length 91; Best Local Similarity 92.6%; Pred. No. 6.5e-43; Matches 88; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch
     63.2%; Score 501; DB 12; Length 2:
1 Similarity 92.6%; Pred. No. 1.7e-42;
88; Conservative 1; Mismatches 2; Indels
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; OTHER INFORMATION: TrxA-Abrogen D43 fusion protein
[05-10-404-999-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 HNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCAD 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 HNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCAD 91
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Sequence 9, Application US/10424999
Publication No. US20040052810A1
GENERAL INFORMATION:
APPLICANT: Neablt, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Glanche, Francis
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REFERENCE: ST01027-A
CURRENT APPLICANTON NUMBER: US/10/424,999
FRICH APPLICANTON NUMBER: 10/233,675
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SEQ ID NOS: 70
SEQ ID NO 9
LENGTH: 87
                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
APPLICANT: Pron, Timochy
APPLICANT: Pron, Timochy
APPLICANT: Brockstedt, Dirk
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and M
TITLE OF INVENTION: Them To Inhibit Angiogenesis
FILE REPERRNCE: ST01027
CURRENT APPLICATION NUMBER: US/10/233,675A
CURRENT APPLICATION NUMBER: 60/316,300
PRIOR APPLICATION NUMBER: 60/316,300
PRIOR PILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD
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US-10-424-999-9
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63.2%; Score 501; DB 15;
Best Local Similarity 97.7%; Pred. No. 5.7e-42;
Matches 86; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.1%; Score 500; DB 12; 98.9%; Pred. No. 7.8e-43; tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: fusion protein human abrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 NRRRPWCYVQVGLKPLVQECMVHDCADG 134
61 NRRRPWCYVQVGLKPLVQECMVHDCADG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NRRRPWCYVQVGLKPLVQECMVHDCADG 88
                                                                                                                 ; Sequence 17, Application US/10233675A; Publication No. US20030228298A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 98.9<sup>3</sup>
Matches 86; Conservative
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US-10-424-999-9
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                                                                                               APPLICANT: Neebli, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REFERENCE: STOLO7.A
CURRENT APPLICATION NUMBER: US/10/424,999
PRIOR PELING DATE: 2003-04-29
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Neebit, Mark
APPLICANT: Generon, Bearrice
APPLICANT: Cameron, Bearrice
APPLICANT: Cameron, Bearrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
FILE REFERENCE: ST01027-B
CURRENT APPLICATION NUMBER: US/10/425,000
FRICE REPERION NUMBER: 10/233,675
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR APPLICATION NUMBER: 10/233,675
ANDMER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 687
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Pred. No. 5.7e-42;
2; Mismatches 0;
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                                   Sequence 17, Application US/10424999
Publication No. US20040052810A1
GENERAL INFORMATION:
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Publication No. US20040052777A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 86; Conserv
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Matches 86; Conserv
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LENGTH: 687
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LENGTH: 687
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Sequence 6.2. Application US/10424999
| Sequence 6.2. Application World Color 
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Sequence 5, Application US/10424999;
Publication No. US20040052810A1
GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
FILE REPRENCE: ST01027-A
CURRENT FILING DATE: 2003-04-29
CURRENT FILING DATE: 2003-04-29
PRIOR PILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.2
SEQ ID NO S
LENGTH: 86
47 SKTCYEGNGHFYRGKASTDTWGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
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                                          48 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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                                                                                                                                                                                   61 NRRRPWCYVOVGLKPLVOECWYHDCAD 87
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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| Publication No. U820030228298A1
| Publication No. U820030228298A1
| GENERAL INFORMATION
| APPLICANT: Neablt, Mark
| APPLICANT: Brockstedt, Dirk
| TITLE OF INVENTION: Them To Inhibit Angiogenesis
| FILE REFERENCE: STO1027
| CURRENT APPLICATION NUMBER: US/10/233,675A
| PRIOR APPLICATION NUMBER: 60/316,300
| PRIOR PILING DATE: 2002-09-04
| NUMBER OF SEQ ID NOS: 27
| SEQ ID NO 9
                                                                                                                                                                                                                                                            Sequence 29, Application US/10425000
Publication No. US2004005277A1
GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
TITLE OF INVENTION: Anglogenesis
TITLE OF INVENTION: Anglogenesis
CURRENT APPLICATION NUMBER: US/10/425,000
CURRENT FILING DATE: 2003-04-29
FRIOR APPLICATION NUMBER: 10/233,675
PRIOR APPLICATION NUMBER: 10/233,675
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.2
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CTHER INFORMATION: human derived fusion protein

US-10-233-675A-9
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                      107 NRRRPWCYVQVGLKPLVQECMVHDCAD 133
                                                                                           NRRRPWCYVQVGLKPLVQECMVHDCAD 87
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; ORGANISM: Artificial Sequence
; FEATURE:
; COTHER INFORMATION: Human abrogen (D43)
US-10-425-000-29
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ORGANISM: Artificial Sequence
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Sequence 18, Application US/10424999
Publication No. US20040052810A1
GENERAL INFORMATION:
APPLICANT: Neeblt, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
CURRENT APPLICATION NUMBER: US/10/424,999
PRIOR PILING DATE: 2003-04-29
PRIOR FILING DATE: 2003-09-04
NUMBER OF SEQ ID NOS: 70
                                                                                                                                                                                                          1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
                                                                                                                                                           48 KTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDN
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US-10-233-675A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nesbit, Mark
APPLICANT: Nesbit, Mark
APPLICANT: Fong, Timothy
APPLICANT: Brocketedt, Dirk
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding '
TITLE OF INVENTION: Them To Inhibit Angiogenesis
TITLE OF INVENTION: Them To Inhibit Angiogenesis
CURRENT APPLICATION NUMBER: US/10/233,675A
CURRENT FILING DATE: 2002-09-04
PRIOR PRIOR APPLICATION NUMBER: 60/316,300
PRIOR FILING DATE: 2001-09-04
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                                                                                                              Indels
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                                                                                      9.7e-43;
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Pred. No. 9.7e-43;
                                                                            100.0%; Preu. ...
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Publication No. US20030228298A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
Matches 86; Conservative 0;
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SOFWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 86
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ORGANISM: Artificial Sequence
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                                                       Query Match
Best Local Similarity 100.
Matches 86; Conservative
             US-10-233-675A-5
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Publication No. US20030228298A1
GENERAL INFORMATION:
Publication No. US20030228298A1
GENERAL INFORMATION:
PAPLICANT: Nebbit, Mark
APPLICANT: Fong, Timothy
APPLICANT: Brockstedt, Dirk
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for INTEL OF INVENTION: Them To Inhibit Angiogenesis
FILE REFERENCE: STOIO27
CURRENT APPLICATION NUMBER: US/10/233,675A
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/316,300
PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
APPLICANT: Blanche, Francis
APPLICANT: Blanche, Francis
APPLICANT: Blanche, Francis
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
FILE REPERENCE: STO1027-B
CURRENT APPLICATION NUMBER: US,10/425,000
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: 10/233,675
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.2
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                                                                       48 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 107
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                                                                                                                 1 KTCYEGNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDN 60
                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.9%; Score 499; DB 12; Length 86; 100.0%; Pred. No. 9.7e-43; ive 0; Mismatches 0; Indels
                               Indels
Best Local Similarity 100.0%; Pred. No. 9.7e-43; Matches 86; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human derived abrogen
                                                                                                                                                                        108 RRRPWCYVQVGLKPLVQECMVHDCAD 133
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Publication No. US20040052777A1
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 86; Conservative
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LENGTH: 86
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us-09-880-503-4.rapb

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US-10-425-000-38
Sequence 38 Application US/10425000
Publication No. US20040052777A1
GENERAL INFORMATION:
APPLICANT: Nesbit, Mark
APPLICANT: Cameron. Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Angiogenesis
TITLE OF INVENTION: Angiogenesis
TITLE OF INVENTION: Angiogenesis
TITLE OF INVENTION: Angiogenesis
FILE REFERENCE: ST0127-8
CURRENT FILING DATE: 2003-04-29
CURRENT FILING DATE: 2003-04-29
PRIOR PELICATION NUMBER: 10/233,675
PRIOR PELICATION NUMBER: 10/233,675
NUMBER OF SEQ ID NOS: 105
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                    47 SKICYEGNGHFYRGKASIDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPD 106
                                                                                                                                                                                                                                 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
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62.8%; Score 498; DB 12; Length 68
Best Local Similarity 98.9%; Pred. No. 1.2e-41;
Matches 86; Conservative 1; Mismatches 0; Indels
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62.8%; Score 498; DB 12;
Best Local Similarity 98.9%; Pred. No. 1.2e-41;
Matches 86; Conservative 1; Mismatches 0;
; ORGANISM: Artificial Sequence
; FRATURE:
. OTHER INFORMATION: Fusion protein human abrogen
US-10-424-999-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
COMBARIEN INFORMATION: Human derived fusion protein
US-10-425-000-38
                                                                                                                                                                                                                                                                                              107 NRRRPWCYVQVGLKPLVQECWVHDCAD 133
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Search completed: May 25, 2004, 15:03:41 Job time : 25.61 secs

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Sequence 12, Application US/08797689

Patent No. 5876969

GENERAL INFORMATION:

APPLICANT: Fleer, Rainhard

APPLICANT: Fleer, Alain

APPLICANT: Fleer, Alain

APPLICANT: Jung, Gerand

APPLICANT: Jung, Gerand

APPLICANT: Web, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE FOLYPEPTIDES,

TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES

ITLLE OF INVENTION: CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA
                                                           Sequence 43, Appl
Sequence 50, Appl
Sequence 38, Appl
Sequence 4, Appli
Patent No. 5185259
Patent No. 5344773
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 13, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 1, Appli
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Sequence 3, A
Sequence 10,
Sequence 10,
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Sequence 51,
Sequence 55,
   Sequence 2
Patent No.
Patent No.
Patent No.
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Sequence 6
Sequence 8
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Sequence 6
Sequence 1
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RESULT 1
US-08-797-689-12
Sequence 12, Appl
Sequence 13, Appl
Sequence 96, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Patent No. 5219569
Sequence 1, Appli
Patent No. 5188829
                                                                                              May 25, 2004, 14:48:05 ; Search time 9.34706 Seconds (without alignments) 745.636 Million cell updates/sec
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793
1 SNELHQVPSNCDCLNGGTCV.....QVGLKPLVQECMVHDCADGK 135
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Sequence 96,
Sequence 1, 1
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-984-186-12
US-09-101-272G-93
US-08-101-272G-98
US-08-153-799-18
US-08-153-799-18
US-09-403-736-2
US-09-403-736-2
US-09-101-272G-1
S188829-1
US-09-101-272G-96
US-09-101-272G-96
US-09-101-272G-96
US-09-101-272G-96
US-09-101-272G-96
US-09-101-272G-96
US-09-101-272G-96
US-08-560-098A-48
US-08-560-098A-48
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US-08-560-098A-48
US-08-560-098A-48
US-08-560-098A-48
US-08-560-098A-48
US-08-560-098A-48
US-08-560-098A-49
US-08-560-098A-44
US-08-560-098A-44
US-08-967-024C-24
US-08-967-024C-24
US-08-967-024C-25
US-09-5101-272G-65
US-09-5101-273G-65
US-09-5101-273G-65
US-09-5101-273G-65
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Maximum Match 100%
Listing first 75 summaries
                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 138;
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// Sequence 73, Application US/09101272G

// Patent No. 6509445

// GENERAL INFORMATION:
// APPLICANT: Nissin Food Products Co., Ltd.
// TITLE OF INVENTION: CANCEROUS METASTABIS INHIBITOR
// TITLE REPERENCE: 050979

// CURRENT APPLICATION NUMBER: US/09/101,272G

// CURRENT PILING DATE: 1998-07-08

// PRIOR PLING DATE: 1996-01-08

// NUMBER OF SEQ ID NOS: 107

// SEQ ID NO : 107
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                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UEL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INPORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION UNMBER: P.38,619
REFERENCE/DOCKET NUMBER: P.38,619
TELECOMMUNICATION:
OPERATING SYSTEM: System 7.1
SOFWRARE: Word 5.1 [Patentin]
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <a href="https://www.number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-number-num
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MOLECULE TYPE: protein
US-09-984-186-12
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; OTHER INFORMATION: ATF domain of uPA
US-09-101-272G-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454-3808
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Best Local Similarity 100.
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 793; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.2e-72;
Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                        FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: RF 92/01064
FILING DATE: 31-JAN-1992
APPLICATION DATA: APPLICATION DATA:
APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P.38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
        MEDIUM TYPE: Langer COMPUTER: Macinicoh COMPUTER: Macinicoh COPERATING SYSTEM: System 7.1 SOFTWARE: Word S.1 (Patentin) CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/797,689 TILING DATE: 3.1-AN-1997
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Fournier, Alain
Guitten, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-09-984-186-12
Sequence 12, Application US/09984186
Patent No. 6686.79
GENERAL INFORMATION:
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CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (610) 454-3839
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ADDRESSEE: Rhone-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-797-689-12
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61 KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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Sequence 18, Application US/08286748B
Sequence 18, Application US/08286748B
Sequence 18, Application General Sequence 18, Application Sequence 19, Application Composition Composition Sequence 11TLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF TITLE OF INVENTION: OR DRUGS BY PLATELETS FOR THE TREATMENT OF NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 793; DB 1; Length 411; 100.0%; Pred. No. 1.4e-71;
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COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,748B
FILING DATE: August 5, 1994
CLIASSIFICTATION DATA:
APPLICATION NUMBER:
                 COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1)
                                                                                      CURRENT ADDICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: PESEC, J. PETER
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04353/00300
TELECHMONICATION NUMBER: 04353/00300
TELECHMONICATION NUMBER: 04353/00300
TELECHMONICATION INFORMATION:
RECORDING CHARACTERISTICS:
LENGTH 111
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Best Local Similarity 100.
Matches 135; Conservative
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US-08-087-163-1
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US-08-286-748B-18
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                                        0; Gaps
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100.0%; Score 793; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.7e-72;
Matches 135; Conservative 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Pred. No. 6.4e-72; Matches 135; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 98. Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
ADPLICANT: Missin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 050979
CURRENT APPLICATION WHMBER: US/09/101,272G
CURRENT PLING DATE: 1988-07-08
PRIOR APPLICATION NUMBER: LP 1059/1996
PRIOR APPLICATION NUMBER: LP 1059/1996
PRIOR SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 98
LENGTH: 208
TYPE: RT
CREAMISM: Attificial Sequence
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| Sequence 1, Application US/08087163|
| Sequence 1, Application US/08087163|
| Patent No 472692|
| GENERAL INFORMATION:
| APPLICANT: Liu, Jian-Ning APPLICANT: Liu, Jian-Ning APPLICANT: Gurewich, Victor TITLE OF INVENTION: PRO-UROKINASE MUTANTS NUMBER OF SEQUENCES: 1
| CORRESPONDENCES: 1
| CORRESPONDENCES: 1
| CORRESPONDENCES: 1
| STREET: 225 Franklin Street
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                    121 PLVQECMVHDCADGK 135
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STATE: Massach
COUNTRY: U.S.A
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APPLICANT: DO. RELATION PROBLEM APPLICANT: SORION PROBLEM APPLICANT: SORION, Paule APPLICANT: SORION, Paule APPLICANT: SORION, Paule APPLICANT: SORION, Taladdine APPLICANT: SORIA, Taladdine APPLICANT: SORIA, Jeanette APPLICANT: SERRICAUDET, Michel APPLICANT: YEH, Patrice APPLICANT: YEH, Patrice APPLICANT: YEH, Patrice For The Treatment of Tumors TILLE OF INVENTION: For The Treatment of Tumors TILLE OF INVENTION: NUMBER: US/09/403,736
CURRENT FILING DATE: 1999-110-26
PRIOR APPLICATION NUMBER: BCT/EP98/02491
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/044,980
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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100.0%; Score 793; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.4e-71;
Matches 135; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09403736
Patent No. 6638502
FELECOMMUNICATION INFORMATION
                                                                    TELEX: 219484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PLVQECMVHDCADGK 135
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                                                                                                                                            : 411 amino acids
amino acid
                                       (908) 771 6159
                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-153-799-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNBLHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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100.0%; Score 793; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.4e-71;
Matches 135; Conservative 0; Mismatches 0; Indels
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Patent No. 5766883
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
                                             04547/013001
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1999
PRIOR APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1999
RPIOR APPLICATION NUMBER: DCT/GB90/00650
FILING DATE: 26-APR-1990
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-CCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
     REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0454
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PLVQECMVHDCADGK 135
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-286-7488-18
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61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                     5219569-2;
Patent No. 5219569
; Patent No. BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GORDON A.
TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-71;
Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/766,858
FILING DATE: 16-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 725,468
FILING DATE: 22-APR-1985
          140 PLVQECMVHDCADGK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PLYQECMYHDCADGK 135
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Best Local Similarity 100.0
Matches 135; Conservative
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OTHER INFORMATION:
NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                           LENGTH: 430
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                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:2
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  61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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COTHER INFORMATION: /label= modified
OTHER INFORMATION: /note= "six amino acids deleted in mutant"
US-07-94Z-157A-3
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100.0%; Score 793; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.5e-71;
Matches 135; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                            STREET: 1100 Peacher STREET: 1100 Peacher STREET: 1100 Peacher STATE: Georgia COUNTRY: USA ZIP: 3030-4530 COMPUTER: BEADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/942,157A FILING DATE: 19920908
                                                                                                                                                                  Sequence 3, Application US/07942157A
Patent No. 5648253
GENERAL INFORMATION:
APPLICANT: Wel, Cha-Mer
TITLE OF INVENTION: Inhibitor-Resistant Urokinase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= peptide
/note= "WAP signal"
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CLASSIFICATION: 435
PLORASIFICATION: 435
PLORATION DATE: 435
PFILING DATE: 20-205-1990
ATTORNEY/AGENT INFORMATION:
NAME: Paber, Patrea L.
REGISTRATION NUMBER: 31.284
REFERENCE/DOCKET NUMBER: 751108Cont
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                                      121 PLVQECMVHDCADGK 135
                                                                         121 PLVQECMVHDCADGK 135
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AMINO ACID
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acide
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NAME/KEY: Peptide
LOCATION: 1..19
OTHER INFORMATION: /
OTHER INFORMATION: /
FEATURE:
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TOPOLOGY:
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121 PLVQECMVHDCADGK 135

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61 KASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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| Patent No. 6277818
| GENERAL INFORMATION |
| APPLICANT: MAZAR, Andrew P. |
| TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR |
| TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR |
| TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR |
| TITLE OF INVENTION: UNMERR: 329042001300 SIDN 1-7 |
| CURRENT APPLICATION NUMBER: 09/181,816 |
| CURRENT PLING DATE: 1998-10-29 |
| NOMBER OF SEQ ID NOS: 7 |
| SOFTWARE: PATENTIN VEr. 2.0 |
| SOFTWARE: PATENTIN VER. 2.0 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.4%; Score 788; DB 4; Length 201; Best Local Similarity 100.0%; Pred. No. 2e-71; Matches 134; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.4e-70;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                 HELECANT: Missin Food Products Co., Ltd.,
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: Q50079
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: US/09/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Version 3.1
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: ATFHI-CL chimeric protein
                                                                                                                                                                      Sequence 96, Application US/09101272G; Patent No. 6509445; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                            122 PLVQECMVHDCADG 135
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              121 PLVQECMVHDCADG 134
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Best Local Similarity 99.3
Matches 134; Conservative
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US-09-101-272G-96
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KASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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                                     81 KASIDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGRGNYCRNPDNRRRPWCYVQVGLK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 431;
                                                                                                                                                                                                                                                                            APPLICANT: KOBAYASHI, YO-ICHI;OMORI, MUNEKI;YAMADA, CHIKAKO TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE NUMBER OF SEQUENCES: 23 CURRENT APPLICATION DATA;
APPLICATION DATA;
APPLICATION DATA;
FILING DATE: 18-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.4%; Score 788; DB 4; Length 194; 100.0%; Pred. No. 2e-71; ve 0; Mismatches 0; Indels
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Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
ITILE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFREENCE: Q50970
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT PILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 793; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.5e-71;
Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: ATFHI chimeric protein US-09-101-272G-80
                                                                                           PLVQECMVHDCADGK 135
                                                                                                                                      141 PLVQECMVHDCADGK 155
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 134; Conservative
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;Patent No. 5188829
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5188829-1
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US-09-101-272G-80
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LENGTH: 194
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61 KASTDIMGRPCLPWNSATVLQOTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
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ZIP: 20005
COMPUTER: READABLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 17-NOV-1995
PTILING DATE: 17-NOV-1995
PTILING DATE: 17-NOV-1994
ATTORNEY/ADRENT INFORMATION:
NAME: EVANS, JOSEPH 17-NOV-1994
ATTORNEY/ADSTON NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REPERENCE DOCKET NUMBER: 148/42448
TELEPHONE: (202) 628-8840
TELEPHONE: (202) 628-8840
TELEPHONE: (202) 628-8844
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
TENNEY/ATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 411;
                                                                                                                                                                                              Sequence 48, Application US/08560098A

Patent No. 5976841

GENERAL INFORMATION:
APPLICANT: WINDUT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEGUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: Sevenson, MCKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i, Indels
                                                                                                                                                                                                                                                                                                                                         STATE: DC Street, N.W., Suite 700 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
98.6%; Score 782; DB 2;
Best Local Similarity 99.3%; Pred. No. 1.8e-70;
Matches 134; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 17
US-08-142-590B-25
; Sequence 25, Application US/08142590B
                                                           121 PLVQECMVHDCADGK 135
                                                                                                 121 LLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLVQECMVHDCADGK 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                           US-08-560-098A-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KASTDIMGRPCLPMNSAYVLQQTYHAHRSQALQLGLGKCHNYCRNPQNRRRPWCYYQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                   ENERAL INFORMATION:
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and
APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and
ITILE OF INVENTION: UROXINASE PLASMINOGEN ACTIVATOR FRAGMENTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STREET: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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97.0%; Score 769; DB 3; Length 157;
Best Local Similarity 97.0%; Pred. No. 1.2e-69;
Matches 131; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-560-098A-47

Sequence 47, Application US/08560098A

Sequence 47, Application US/08560098A

PAPLICANT: WHENDT, Stephan

APPLICANT: WHENDT, Stephan

APPLICANT: HINZEL-WIELAND, Regina

APPLICANT: PEFFENS FORCE JOSE

TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, MCKeown, Edwards & Lenahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evenson, McKeown, Edwards & Lenahan
1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                              COMPUTER: USAS

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: DE PC COMPACIBLE
COMPUTER: DE PC COMPACIBLE
COMPUTER: DE PC COMPACIBLE
CONTRARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,590B
FILING DATE: 25-OCT-1993
PFILING DATE: 02-APR-1993
PFILING DATE: 02-APR-1993
PFILING DATE: 02-APR-1993
ATTORNEY/AGENT INPORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: MGP-009CP
FILECPHONE: (617) 227-7400
TELEPAK: (617) 227-7400
TELEPAK: (617) 227-541
INPORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 PLVOECMVHDCADGK 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1200 G St.
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-142-590B-25
                                                                                                                                                                                                                                                            COUNTRY:
Patent No.
GENERAL IN
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Sequence 83, Application US/08720012

Patent No. 5747291

GENERAL INFORMATION:

APPLICANT: STEPFENS, GERD J.

APPLICANT: SCHNEIDER, JOHANNES

APPLICANT: ALINEL OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH

TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH

TITLE OF INVENTION: IMPROVED FIRENCLYTIC CHARACTERISTICS AND THROMBIN

TITLE OF INVENTION: IMPROVED FIRENCLYTIC CHARACTERISTICS AND THROMBIN

TITLE OF INVENTION: IMPROVED FIRENCY

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:

ADDRESSEB: Evenson, McKeown, Edwards & Lenahan

STREET: 1200 G Street, N. W. Suite 700

CITY: Washington, D.C.

CONTRY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 365;
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COUNTRY: U.S.
ZIP: 2005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,012
FILING DATE: 27-SEP-1996
CLASSIFICATION NUMBER: US 08/093,741
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSSEPH D.
REGISTRATION NUMBER: 26,269,7375
REGISTRATION NUMBER: 26,269,7315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
64.8%; Score 514; DB 1; 1
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 89; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 NRRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NRRRPWCYVQVGLKPLVQECMVHDCADGK 89
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/41345
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPERBUE/DOCKET NUMBER: 26,269
REPERBUE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                  TELEFAX: (202)628-8844
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   : 365 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)628-8844
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY:
US-08-093-741-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-720-012-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 PWNSATVLQQTYHAHRSDALQLGLGRGRHNYCRNPDNRRRPWGYVQVGLKPLVQEGWVHDCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 83, Application US/08093741

Patent No. 5681721

GENELL INFORMATION:
APPLICANT: STEFFENS, GERD J.
APPLICANT: WINNIT, STEFFENS
APPLICANT: STEFFENS, GERD J.
APPLICANT: STEFFENS, GERD J.
APPLICANT: WINNIT, STEFFENS
APPLICANT: SAUNDERS, DEREK J.
TITLE OF INVENTION: INFOVED FIBER J.
TITLE OF INVENTION: INFROVED FIBER INCLYTIC CHARACTERISTICS AND THROMBIN NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSED: EVENEON, MCKEOWN, Edwards & Lenahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
CIDE: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
FILING DATE: 17-NOV-1995
FILING DATE: 17-NOV-1994
ATTONBEY/AGENT INFORMATION:
FILING DATE: 17-NOV-1994
ATTONBEY/AGENT INFORMATION:
FREENEW-COMMUNICATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
TELLEPAN: (202) 628-8844
INFORMATION FOR SEQ. ID NO: 47:
SEQUENCE CHARACTERISTICS:
FWATTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.9%; Score 515; DB 2; Length 432; Best Local Similarity 75.6%; Pred. No. 1e-43; Matches 93; Conservative 8; Mismatches 16; Indels
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,741
FILING DATE: 20-UUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Evenson, McKeown, Edwards & Lenahan: 1200 G Street, N. W. Suite 700 Washington, D.C.
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20-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-560-098A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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62 NRRRPWCYVQVGLKPLVQECMVHDCADGK 90
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                                                                                       RESULT 22
US-08-967-024C-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
US-08-967-024C-25
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                                                                                                                                                                                          47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHANRSDALQLGLGKHNYCRNPD 106
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                                                                                                                                                                                                                                1 SKTCYEGNGHFYRGKASIDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 60
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                                                                                                                                                                  Gaps
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 0892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BANS, Joseph D.
NAME: BANS, JOSEPh D.
TELECOMMUNICATION NUMBER: 148/42448
TELECOMMUNICATION NUMBER: 148/42448
TELECOMMUNICATION NUMBER: 148/42448
TELEFAX: (202) 628-8844
INFORMATION POR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TUDENGTH: 393 amino acids
                                                                                                                       Score 514; DB 1; Length 365;
                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/08560098A

Sequence 44, Application US/08560098A

Patent No. 5976641

APPLICANT: WIRNDT, Stephan
APPLICANT: HINZEL-WIELAND, Regina
APPLICANT: STEFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties

NUMBER OF SEQUENCES, 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
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                                                                                                                                                           Indels
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                                                                                                               Cuery Match

Guery Match

Best Local Similarity 100.0%; Pred. No. 1.1e-43;

Matches 89; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                     107 NRRRPWCYVQVGLKPLVQECMVHDCADGK 135
                                                                                                                                                                                                                                                                                                       61 NRRRPWCYVQVGLKPLVQECMVHDCADGK 89
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SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                            linear
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Best Local Similarity
Matches 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UK
                                                                                                                                                                                                                                                                                                                                                                                  US-08-560-098A-44
                                          TYPE: ami
TOPOLOGY:
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US-08-720-012-83
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47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 106
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                                                                                APPLICANT: WNENDT, Stephan
APPLICANT: STEPFENS, Gerd Josef
APPLICANT: JANOCHA, Blke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 393;
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Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: WISNOT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOCHA, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                              STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: 2005
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
                                                                                                                                                                                                                                                                                           : Evenson, McKeown, Edwards & Lenahan 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 514; DB 3; I
Pred. No. 1.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 89; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 NRRRPWCYVQVGLKPLVQECMVHDCADGK 135
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PRIOR APPLICATION DATA:
APPLICATION UNDER: P 44 2 665.8
APPLICATION UNDER: P 94 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPD. P.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 628-8800
; Sequence 24, Application US/08967024C; Patent No. 6133011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 393 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-967-024C-24
                        Patent No. 6133011
GENERAL INFORMATION:
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59 RGKASTDIMGRPCLPWNSATVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                             1 EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 BLHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCBIDKSKTCYEGNGHFY
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| Sequence 51, Application US/08560098A
| Patent No. 3978641
| GENERAL INFORMATION:
| APPLICANT: WINDIT, Stephan
| APPLICANT: HINZEL-WIELAND, Regina APPLICANT: PRINZEL-WIELAND, Regina APPLICANT: Profession of TITLE OF INVENTION: Coagulation-inhibiting Properties (UMBER OF SEQUENCES)
| UNDER OF SEQUENCES:
| ADDRESSEE: Evenson, MCKeown, Edwards & Lenahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
APPLICATION UNMBER: US/08/560,098A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
42.3%; Score 335.5; DB 2;
Best Local Similarity 46.3%; Pred. No. 1.1e-25;
Matches 62; Conservative 17; Mismatches 50;
                                                                                                                                                                                                   103 RNPDNRRRPWCYVQVGLKPLVQECMVHDC 131
                                                                                                                                                                                                                                                              61 RNPDNRRRPWCYVQVGLKPLVQECMVHDC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

PAPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EYANS, JOSEPh D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH 477 anino acids
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197 SKFILEFCSVPVCS 210
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SKTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPD 61
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; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
US-09-101-272G-62
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                                                                                                CITY: Washington
STATE: DC
ZIP: Z0005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6.3 Application US/09101272G

Patent No. 6509445

GENERAL INFORMATION:
APPLICANT N.48sin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPERENCE: 050979

CURRENT APPLICATION NUMBER: US/09/101,272G

CURRENT PLING DATE: 1996-01-08

PRIOR APPLICATION NUMBER: JP 1059/1996

PRIOR APPLICATION NUMBER: JP 1059/1996

NUMBER OF SEQ ID NOS: 107

SOFTWARE: Patentin Version 3.1

FROM PRIOR OF SECTION OF SEC
CORRESFONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
64.8%; Score 514; DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.2e-43;
Matches 89; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/ASET INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148/42444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 148/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE TRANSCERISTICS:
LENGTH: 393 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-967-024C-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-101-272G-62
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42 OCHSVPVKSCSEPRČFNGGTČQQALYPSDF-VČQČPEGPAGKCČEIDTRATCYEDQGISY 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 BLHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin
TITLE OF INVENTION: Specific Properties
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSER Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER: ISA PC compatible
OPERATING SYSTEM: PC c
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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41.4%; Score 328.5; DB 2;
Best Local Similarity 46.3%; Pred. No. 6.1e-25;
Matches 63; Conservative 14; Mismatches 54;
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FILING DATE: 1 March 1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS;
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amino acid
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Patent No. 236700
| Fatent No. 236700
| GENERAL INFORMATION:
| TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue Pl
| TORRESPONDENCE ADDRESS: 16
| CORRESPONDENCE ADDRESS: 16
| TORRESPONDENCE ADDRESS: 16
| CORRESPONDENCE ADDRESS: 16
| TORRESPONDENCE ADDRESS: 16
| TORRESPONDENC
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
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GENERAL INFORMATION:
APPLICANT: NIKE, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: SASAKI, HITOSHI
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES:
CORRESPONDENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
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41.4%; Score 328.5; DB 1
Best Local Similarity 46.3%; Pred. No. 6.1e-25;
Matches 63; Conservative 14; Mismatches 54
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OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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AMINO ACID
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59 RGKASTDIMGRPCLPWNSAIVLQQIYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA, ;PATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
41.4%; Score 328.5; DB 6; Length 5
Best Local Similarity 46.3%; Pred. No. 6.3e-25;
Matches 63; Conservative 14; Mismatches 54; Indels
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41.4%; Score 328.5; DB 6
Best Local Similarity 46.3%; Pred. No. 6.1e-25;
Matches 63; Conservative 14; Mismatches 54
                       APPLICATION NUMBER: US/08/88,451
FILING DATE: 06-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 770,510
FILING DATE: 03-OCT-1991
APPLICATION NUMBER: 384,608
FILING DATE: 24-JUL-1989
APPLICATION NUMBER: 240,856
FILING DATE: 02-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
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SAITO, YOSHIMASA
SASAKI, HITOSHI
HAYASHI, MASAKO
NOTANI, JOUJI
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         CURRENT APPLICATION DATA:
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HUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Patent No. 5200340
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5200340-6
                                                                                                                                                                                                                                               , LENGTH:527
5520913-1
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APPLICANT:
APPLICANT:
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5200340-6
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                                                                                                                                                                                                         Gaps
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; APPLICANT: GOEDDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 41.4%; Score 328.5; DB 6; Length 527; Best Local Similarity 46.3%; Pred. No. 6.1e-25; Matches 63; Conservative 14; Mismatches 54; Indels 5
                                                                                                                                                              Length 527;
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; PATENT NO. 5520913
; PATENT NO. 5520913
; PAPLICANT: ANDERSON, STEPHEN; BENNETT, WILLIAM F.; BOTSTEIN.
; DAVID; HIGGINS, DEBORAH L.; PAONI, NICHOLAS F.; ZOLLER, MARK J.
; TITLE OF INVENTION: TISSUE PLASMINGEN ACTIVATOR HAVING
; ZYMOGENIC PROPERTIES
; NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                      54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEHAR, GORDON A.
TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
                                                                                                                                                           DB 5;
                                                                                                                                                      Query Match

41.4%; Score 328.5; DB E
Best Local Similarity 46.3%; Pred. No. 6.1e-25;
Matches 63; Conservative 14; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15.
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/07/489,855
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12,694
FILING DATE: 09-FEB-1987
APPLICATION NUMBER: 483,062
FILING DATE: 07-APR-1983
APPLICATION NUMBER: 398,003
FILING DATE: 14-UL-1982
APPLICATION NUMBER: 374,860
FILING DATE: 05-MAY-1982
TYPE: AMINO ACID

TYPE: AMINO ACID

CT-US91-01025A-2

Querv
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5185259-8
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17 QCHSVPVKSCSEPRCFNGGTCQQALYFSDF-VCQCPEGFAGKCCEIDTRATCYEDQGISY 135
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| Sequence 38, Application US/08883795A
| Patent No. 5985607
| GENERAL INFORMATION:
| APPLICANT: Delcuve, Genevieve
| APPLICANT: Delcuve, Genevieve
| APPLICANT: Delcuve, Genevieve
| TITLE OF INVENTION: Recombinant DNA Molecules and Expression
| TITLE OF INVENTION: Recombinant DNA Molecules and Expression
| TITLE OF INVENTION: Recombinant DNA Molecules and Expression
| TITLE OF INVENTION: Recombinant DNA Molecules and Expression
| TITLE OF INVENTION: Recombinant DNA Molecules and Expression
| TITLE OF INVENTION: Recombinant County of the Compatible COUNTRY: Canada
| STREET: Ontario COUNTRY: Canada
| ZIP: MRSH 372
| COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: BatentIn Release #1.0, Version #1.25
| COMPUTER: Detection DATA: COMPUTER: Detection DATA: COMPUTER: Detection DATA: CASSIFICATION NUMBER: 105/08/883,795A
| FILING DATE: 27-JUN-1997 | TLASSIFICATION NUMBER: 40,261
| REFERENCE/DOCKET NUMBER: 7841-062
| TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION |
| TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: TELECOMMUNICATION INFORMATION |
| TELECOMMUNICATION |
| TEL
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41.4%; Score 328.5; DB 2; Length 562;
Best Local Similarity 46.3%; Pred. No. 6.5e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5
                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                         PADLICATION NUMBER: US/08/560,098A
PILICATION NUMBER: US/08/560,098A
PILICATION DATE: 17-NOV-1995
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1894
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 LKPLVQECMVHDCADG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (202) 628-8844 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 562 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 562 amino acids
amino acid
                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-560-098A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 328.5; DB 2; Length 562; ; Pred. No. 6.5e-25; 14; Mismatches 54; Indels 5;
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Sequence 50, Application US/08560098A

Patent No. 5976841

GENERAL INFORMATION:
APPLICANT: WIENDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
CITY: USA
ZIP.
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                    SEE: P.C.
: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-;
TELEPHONE: 703-413-3000
TELEFAX: 703-413-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24,618
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-413-220
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 46.3%;
Matches 63; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 562 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-811-949-43
                                                                                                                                                                                                                        CITY: ARLIN STATE: VA COUNTRY: US ZIP: 22202
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US-08-560-098A-50
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59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FOSTER, DONALD C., MULVIHILL, BILEEN R., O'HAKA, PATRICK J., PINGEL, KURT, YOSHITAKE, SHINJI TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 41.4%; Score 328.5; DB 6; Length Best Local Similarity 46.3%; Pred. No. 6.5e-25; Matches 63; Conservative 14; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Indels
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Patent No. 5344773

APPLICANT; WEI, CHA-MER; HSIUNG, NANCY; REDDY, VEENURI B.;

LEMONIT, JEFFREY F.; DACKOWSKI, WILLIAM; DOUGLAS, RICHARD;

COLE, EDWARD S.; PURCELL JR., RICHARD D.; LAU, DAVID TAI-YUI

TILLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN

ACTIVATOR PRODUCED BY RECOMBIANT DNA

NUMBER OF SEQUENCES: 6

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.4%; Score 328.5; 46.3%; Pred. No. 6.5
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NUMBER OF SEQUENCES: 34

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/53,412

FILING DATE: 22-MAY-1987
   FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12,694
APPLICATION NUMBER: 483,052
FILING DATE: 07-AER-1983
APPLICATION NUMBER: 398,003
FILING DATE: 14-UTI-1982
APPLICATION NUMBER: 374,860
FILING DATE: 05-MAY-1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 LKPLVQECMVHDCADG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 562
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                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 RGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDSKPWCYVFKA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09703695A

Patent No. 6593097

GENERAL INFORMATION.

APPLICANT: Xu, Yuan

TITLE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS
FILE REFERENCE: P1788H.

CURRENT APPLICATION NUMBER: US/09/703,695A

CURRENT FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: US 60/163,607

PRIOR PILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ELHQVP-SNCD----CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
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**Patent No. 5185259
**Patent Goeddel, David V.; Kohr, William J.; Pennica, Diane; Vehar, Gordon A.; Tille OP Invention: Truncated Human Tissue Plasminoden; Tille OP Invention: Truncated Human Tissue Plasminoden
                                                                                                                                                                                                                                                                                                                                            Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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46.3%; Pred. No. 6.5e-25;
                                                                                                                                                                                                                                                                                                                                                                         .5e-25
                                                                                                                                                                                                                                                                                                                                     ; Score 328.5;
; Pred. No. 6.5e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATOR
NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/489,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 LKPLVQECMVHDCADG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 LKPLVQECMVHDCADG 134
                                                                                                                                                                                                                    MOLECULE TYPE: protein (tPA) US-08-883-795A-38
                 LU NO. 3
LU NO. 3
LYPE: amino acids
STRANDEDNESS: sir
TOPOLOGY: 1, SIRCOLOGY: 1, SIRCO
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.3%;
Matches 63; Conservative 1.
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 63; Conserv
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US-09-703-695A-4
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1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 300, DB 3; Length 233;
Pred. No. 1.7e-22;
2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL NO. 0219712

GENERAL INFORMATION:

APPLICANT: Rosenberg, Steven

APPLICANT: Stratton-Thomas, Jennifer

APPLICANT: Stratton-Thomas, Jennifer

TILLE OF INVENTION: Expression of Urokinase Plasminogen

TILLE OF INVENTION: Activator Inhibitors

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,745
FILING DATE: 10-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/070,153
FILING DATA:
APPLICATION NUMBER: US 08/070,153
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
                                                                                                                     CURRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,745
FILING DATE: 10-AAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/070,153
APPLICATION NUMBER: 31,259
REGISTRATION NUMBER: 31,259
REGISTRATION NUMBER: 31,259
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10-601-2706
TELEFAX: 510-663-3542
                                                                : Floppy disk
IBM PC compatible
NYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-438-745-17; Sequence 17, Application US/08438745; Patent No. 6248715
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 510-655-00-1 IS: INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 233 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 37.8%;
1 Similarity 77.9%;
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-438-745-15
                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4560 Horto
CITY: Emeryville
STATE: CA
COUNTRY: USA
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                                                                                                              OPERATING SYSTEM:
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                                                                   MEDIUM TYPE:
                                                                                           COMPUTER:
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Best Local Si
Matches 53
  COUNTRY
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                                                                                                                                                                                                         DB 6; Length 562;
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TOLUNAY, H.ESER; WARREN, THOMAS G.; WUN, TZE-CHEIN
TILLE OF INVENTION: MODIFIED TISSUE PLASMINOGEN ACTIVATOR
WITH MODIFIED GLYCOSYLATION SITE
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/203,047
FILING DATE: 06-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15. Application US/08438745

Sequence 15. Application US/08438745

Batent NO. '6246715

GENERAL INFORMATION:
APPLICANT: Rosenberg, Steven
APPLICANT: Stratton-Thomas, Jennifer
TITLE OF INVENTION: Expression of Urokinase Plasminogen
TITLE OF INVENTION: Activator Inhibitors
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Indels
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                                                                                                                                                                                                                       6.5e-25;
ches 54;
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44.9%; Pred. No. 3.3e-24;
tive 16; Mismatches 54.
                                                                                                                                                                                                       Query Match
Best Local Similarity 46.3%; Pred. No. 6.5e
Matches 63; Conservative 14; Mismatches
APPLICATION NUMBER: US/07/782,686 FILING DATE: 01-00T-1985 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 656,770 FILING DATE: 01-0CT-1984
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Emeryville
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Best Local Similarity 44.9;
Matches 61; Conservative
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LENGTH: 562
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LENGTH: 562
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1 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
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PCT-US94-05669A-15

Sequence 15, Application PC/TUS9405669A

Sequence 15, Application PC/TUS9405669A

SEQUENCEAL INFORMATION:
TITLE OF INVENTION: Expression of Urokinase Plasminogen
TITLE OF INVENTION: Activator Inhibitors

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA

ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OSPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSIET OF THE TAMENT OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 233;
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37.8%; Score 300; DB 3; Length 23:
Best Local Similarity 77.9%; Pred. No. 1.7e-22;
Matches 53; Conservative 2; Mismatches 13; Indels
FILE REFERENCE: 23533-0005
CURRENT APPLICATION NUMBER: US/09/219,019
CURRENT FILING DATE: 1998-12-23
PRIOR PELING DATE: 1998-05-10
PRIOR FILING DATE: 1995-05-10
PRIOR FILING DATE: 1995-05-10
PRIOR PILING DATE: 1995-06-01
PRIOR PILING DATE: 1993-06-01
PRIOR PILING DATE: 1993-06-01
PRIOR PILING DATE: 1993-06-01
SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 17

LENGTH: 233
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NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERCE/DOCKET NUMBER: 0939.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 233 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein PCT-US94-05669A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-09-219-019-17
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Sequence 15, Application US/09219019
Sequence 15, Application US/09219019
Sequence 15, Application US/09219019
Sequence 15, Application US/08341
SEPERAL INFORMATION: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR
TITLE OF INVENTION: INHIBITORS
FILE REFERENCE: 23333-0005
CURRENT APPLICATION NUMBER: US/09/219,019
CURRENT APPLICATION NUMBER: US/09/219,019
FRIOR APPLICATION NUMBER: 08/18,263
PRIOR FILING DATE: 1994-07-26
PRIOR APPLICATION NUMBER: 08/280,288
PRIOR FILING DATE: 1994-07-26
PRIOR PEPLICATION NUMBER: 08/070,153
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VOY: 2.1
TYPE: PRIOR PATENTIN VOY: 2.1
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US-009-219-019-17
US-009-219-019-17
Sequence 17, Application US/09219019
Fatent No. 6268341
Fatent No. 6288341
FARBERAL INFORMATION:
FAPPLICANT: ROSENBERG, STEVEN
FAPPLICANT: STRATTON-THOMAS, JENNIFER R.
FAPPLICANT: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR
FITTLE OF INVENTION: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.8%; Score 300; DB 3; Length 233; Best Local Similarity 77.9%; Pred. No. 1.7e-22; Matches 53; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.8%; Score 300; DB 3; Length 233; Best Local Similarity 77.9%; Pred. No. 1.7e-22; Matches 53; Conservative 2; Mismatches 13; Indels
                                                   100.6860
           REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0939,
TELECOMMULATION INFORMATION:
TELEPHONE: 510-601-2706
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 anino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-438-745-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 KMANANKĠ 96
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US-09-219-019-15
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1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKQGGSGSGGPDYE 90
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37.8%; Score 300; DB 3; Length 235;
Best Local Similarity 77.9%; Pred. No. 1.7e-22;
Matches 53; Conservative 2; Mismatches 13; Indels
                                                                                                                                       COMPUTER REALABLE FORD

MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,745
FILING DATE: U-MAY-1995
CLASSIFICATION = 14
PRIOR APPLICATION NUMBER: US 08/070,153
ATPONENTY/AGENT INPORMATION:
NAME: GTEENT NPORMATION:
NAME: GTEENT NPORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 13:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-438-745-13
                                                                                                                     OMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Homo sapiens
US-09-219-019-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KASTDTMG 68
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CILL.
STATE: CA
COUNTRY: USA
TO: 94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-219-019-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKQGGSGSGDFDYE 88
                           29 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKQGGSGSGDFDYE 88
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chiron Corporation
TITLE OF INVENTION: Expression of Urokinase Plasminogen
TITLE OF INVENTION: Activator Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryille
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.9%; Pred. No. 1.7e-22;
Matches 53; Conservative 2; Mismatches 13; Indels
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Patent No. 6248715

GENERAL INFORMATION:
APPLICANT: Rosenberg, Steven
APPLICANT: Stratton-Thomas, Jennifer
TITLE OF INVENTION: Expression of Urokinase Plasminogen
TITLE OF INVENTION: Activator Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 9460B
COMPUTER READABLE FORM:
MEDILW TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: DEM PC compatible
COMPUTER: 19-MAY-1994
CURSTRIATION NUMBER: PCT/US94/05669A
FILING DATE: 19-MAY-1994
CTLLSSTRICATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 0939.100
TELECOMMUNICATION INFORMATION:
TELEFAK: 510-655-3542
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
LENGTH: 233 amino acids
LENGTH: CALLEDAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein PCT-US94-05669A-17
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                                                                                             61 KASTDTMG 68
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                                                                                                                                                                                                                                                                                               -05669A-17
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DB 3; Length 235;

37.8%; Score 300;

Query Match

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UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
                                                                                                                                                                                                                                                                                                                     OPERATING SYSIEM: PC-DOS/MS-DOS
OPERATING SYSIEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,915
FILING DATE: 12-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGRAT INFORMATION:
NAME: WIRASHIGE, KATE H.
NAME: WIRASHIGE, KATE H.
NEGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 32904-20001.00
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
36.9%; Score 293; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: RADER, FISHMAN & GRAUER
STREET: 1233 20TH STREET NW, SUITE 501
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
group(11..19, 13..31, 33..42)
                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NV
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READBELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              upplication US/09285783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
          FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
US-08-747-915-5
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                                                                                     1 SNELHQVPSNCDCLNGGICVSNKYPSNIHWCNCPKKFGGQHCEIDKSKTCYBGNGHFYRG 60
                                                                                                                               31 SNELHOVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKQGGSGSGDFDYE 90
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                                                                                                                                                                                                                                                                                                                                               Sequence 13. Application PC/TUS9405669A
GENERAL INFORMATION:
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Expression of Urokinase Plasminogen
TITLE OF INVENTION: Activator Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
             Best Local Similarity 77.9%; Pred. No. 1.7e-22; Matches 53; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOUTWARE: Patentlin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/05669A FLING DATE: 19-MAY-1994 ATTORNEY/AACHION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 0939
REFERENCE/DOCKET NUMBER: 0939
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-651-354
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTER/SICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.00 ouery Match
Best Local Similarity 77.9
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) MOLECULE TYPE: protein PCT-US94-05669A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMANANKG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KASTDIMG 68
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                                                                                                                                                                                                                                          91 KMANANKG 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: E
                                                                                                                                                                                                                                                                                                                       RESULT 48
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APPLICANT: Jones, Terence R. APPLICANT: Haney, David N. APPLICANT: Varga, Janos TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO

Sequence 5, Application US/08747915 Patent No. 5942492

GENERAL INFORMATION:

```
Varga, Janos
TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
                                                                                                                         1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKT 49
Length 49;
                                          0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,783
FILING DATE: 05-Agr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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Search completed: May 25, 2004, 15:00:01 Job time : 10.3471 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 25, 2004, 14:47:10 ; Search time 15.9649 Seconds (without alignments) 1662.947 Million cell updates/sec

US-09-880-503-5 1508 1 KPSSPPEELKFQCGQKTLRP.....VSHFLPWIRSHTKBENGLAL 276 score: Title: Perfect sc Seguence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description			u-plasminogen acti		u-plasminogen acti	u-plasminogen acti	u-plasminogen acti		t-plasminogen acti		t-plasminogen acti	t-plasminogen acti	t-plasminogen acti		t-plasminogen acti		hepatocyte growth	coagulation factor	coagulation factor	brain-specific ser	plasma hyaluronan-	plasma hyaluronan-	prostasin (EC 3.4.	plasma kallikrein	plasma kallikrein	hepsin (EC 3.4.21.	1 (EC 3.4	(EC	(EC 3
SUMMARIES	ç	1D	UKHU	UKBAY	UKPG	JN0560	S18932	UKMS	A35005	UKHUT	A35029	A29941	JS0599	JS0600	JS0598	A34369	78055	KFHU12	A4668B	S28941	845281	JC5759	JC5878	JC4795	A57014	KOMSPL	KQHUP	S00845	855066	TRBOTR	B61545
	6	a ;	Н	М	Н	Н	Н	٦	Н	Н	н	Н	N	(7	7	Н	N	н	Н	7	7	7	7	1	,-	Н	н	Н	N	Н	7
	1	rength	431	433	442	433	432	433	434	562	559	559	431	394	477	477	477	615	655	603	593	761	558	560	343	638	638	417	248	229	460
		March	8.66	95.1	m	78.8	4	73.8	S	m	m	ო	36.3	m	ო	m	m	m	m	m	m	28.2	28.2	27.7	27.1	27.0	26.7	26.3	26.2	26.2	26.0
	į	score	1505	1434.5	1255	1188	1119.5	1112.5	688.5	583	570.5	569.5	547	546	546	545	543	495	493.5	485.5	453	425.5	425	417	408.5	407	402	96	395.5	4	C.
	Result	021	ч	7	m	4	Ŋ	9	7	6 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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trypsin (EC 3.4.21 chymotrypsin (EC 3 hepsin (EC 3.4.21. plasma kallikrein plasmin (EC 3.4.21 chymotrypsin (EC 3 pancreatic elastas trypsin (EC 3.4.21 chymotrypsin (EC 3.4.21	(EC 3.4.2) kallikrein fe growth fatic elasta	Eactor (EC. 33.4.2] (EC. 33.4.2] (EC. 33.4.2] (EC. 21.2] (EC. 21.2) (EC. 21.2	tryptase (EC 3.4.2 tryptase (EC 3.4.2 tryptase (EC 3.4.2 trypsin (EC 3.4.2 mast cell proteina protein (EC 3.4.21 membrane-bound arg plasmin (EC 3.4.21 trypsin (EC 3.4.21 tissue kallikrein tissue kallikrein tissue kallikrein plasmin (EC 3.4.21 tissue kallikrein plasmin (EC 3.4.21 polyprotein (EC 3.4.21 polyprotein (EC 3.4.21
\$13813 \$21195 \$33777 \$23777 \$2777 \$2777 \$26823 \$3496 \$33496 \$31363	A21859 PLMS PLMS ELRT2 TRDG A25606 NGMSG PLG823	KYHUJ PLHU PLHU KYBOB TRKTI S31779 TREGTR A35871 A3368	SS5067 A32410 A32410 A38654 A38654 KCHU B50848 B508494 KCRTP A44284 A44284 TR42 S01971 A61545 TRDGC
00000000000000000000000000000000000000	44444444		244444444444444444444444444444444444444
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ALIGNMENTS

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aminog gen a u-plasminogen activator (BC 3.4.21.73) precursor [validated] - human N,Alternate names: cellular plasminogen activator; urokinase; urokinase-type plasminogen activator chain A; urokinase-type plasminogen ac

64; A C; Species: Homo sapiens (man)
C; Date: 17-Dec-1982 #sequence_revision 04-Dec-1986 #text_change 15-Sep-2000
C; Date: 17-Dec-1982 #sequence_revision 04-Dec-1986 #text_change 15-Sep-2000
C; Accession: A00911; I55209; JT0102; A7561; I38102; 865783; A37662; A37562; A3760; R; Ritcrio, A.; Grimaldi, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.
Nucleic Acids Res. 13, 2759-2771, 1985
A; Title: The human urckinase-plasminogen activator gene and its promoter.
A; Accession: A00931; MUID:85215647; PMID:2987867
A; Accession: A00931
A; Molecule type: DNA
A; Residues: 1-431 extraA; Accession: A00931
A; Note: the authors translated the codon ATG for residue 214 as Ile
R; Nagamine, Y.; Pearson, D.; Grattan, M.
Biochem. Biophys. Res. Commun. 13, 563-569, 1985
A; Title: Exon-intron boundary sliding in the generation of two mRNAs coding fo lorc
A; Reference number: 152209; MUID:86050639; PMID:3933505

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Ajkolociule Kype: process

Ajkolociule Kype: process

Rjil, X.; Bokanan, A.W.; Lilnas, W.; Smith, R.A.G.; Dobson, C.M.

Submitted to the Brookhaven Protein Data Bank, July 1993

Ajkolecine two mubber: AS1255, PDB:LEDU

Bjochemistry 11, 9562-9571, 1903100, PMID:1327118

Ajkolecine two mubber: A44375; WUID:9903110, PMID:1327118

Ajkolecine two mubber: A44375; WUID:9903110, PMID:1327118

Ajkolecine two mubber: A44375; WUID:9903110, PMID:1327118

Ajkolecine two mubber: A6682; PDB:LING

Rjamaen, A.P.; Petrosa, A.M.; Neaddows, R.P.; Nettenbarm, D.G.; Mazar, A.P.; Oli .iczz

Ajkolecine two mubber: A6682; PDB:LING

Rjamaen, A.B.; Si. Phillips, C.; Nowak, U.K.; Pontingo, C.P.; Saunders, D.; Dobs. C.B.

Rjamaen, A.B.; Si. Phillips, C.; Nowak, U.K.; Pontingo, C.P.; Saunders, D.; Dobs. C.B.

Ajkolecine two mubber: A6683; PDB:LING

Rjamaen, A.B.; Si. Phillips, C.; Nowak, U.K.; Pontingo, C.P.; Saunders, D.; Dobs. C.B.

Ajkolecine: annotation; X-ray crystally malecular mass form. consis g of C.Coment: This enzyme is found in urine in a high molecular mass form. consis g of C.Coment: This enzyme is found in urine in a high molecular mass form. Consis g of C.Coment: This enzyme is found in urine in a high molecular mass form. Ajkolecine to the Brookhaven Protein Day and Ajkolecine two mubber: A6683; PDB:LIMM

Ajkolecine: Jokalecine; Alkolecine; Alkolecine; Akap position: 10024-10024

Ajkolecine: Jokalecine; Alkolecine; Alkolecine; Akap position: 10024-10024

Ajkolecine: Jokalecine; Alkolecine; Akap position: 10024-10024

Ajkolecine: 1931; 2317, 1631, 1332, 1541; 237/1; 334/1; 333/3; Alkolecine: 1931; Alkolecine: 10024-10024

Ajkolecine: 1931; 2317, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511, 6511,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 KPSSPPEELKEQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGGSLMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
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Pred. No. 4.2e-123;
1; Mismatches 0;
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Best Local Similarity 99.6%;
Matches 275; Conservative
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A; Cross-references: GB:K03226; NID:G340155; PIDN:AAC97138.1; PID:G340158; GB:D00244; NID A; Cross-references: GB:K03226; NID:G340155; PIDN:AAC97138.1; PID:G340158; GB:D00244; NID Proc. Natl. Acad. Sci. U.S.A. 81, 4727-4731, 1984
A; Title: Identification and primary sequence of an unspliced human urokinase poly(A) + RN A; Reference number: A37561; MUID:84272706; PMID:6589620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of human prep
A;Reference number: 138102; MUID:85203359; PMID:3888571
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A; Residues: 1-150, W', 152-213, 'I', 215-385, 'C', 387-429, 'V', 431 < JAC>
A; Residues: 1-150, W', 152-213, 'I', 215-385, 'C', 387-429, 'V', 431 < JAC>
A; Cross-references: EMBL: K02766; NID: g35297; PIDN: CAAA6535.1; PID: g35298
R; Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki,
Biochim. Biophys. Acta 1293, 83-89, 1996
A; Title: Characterization of single chain urokinase-type plasminogen activator with a nc
A; Reference number: 865783; MUID: 96186279; PMID: 8652631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.; van Elsen
                                                                                                                         NID:g340174; PIDN:AAA61257.1; PID:g340175
neda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 66-431 <VER>
A;Recisares: GB:D00244; NID:g220138
A;Across-references: GB:D00244; NID:g220138
B;Jacobs, P.; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana, DNA 4; 139-146, 1988
A,Accession: 152209
A,Atcutus: preliminary; translated from GB/EMBL/DDBJ
B,Molecule type: DNA
A,Rolecule toloning of cDNA coding for human preprourokinase.
A,Reference number: JT0102; MUID:86056954; PMID:2415429
                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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A; Status: preliminary
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- yellow baboon

u-plasminogen activator (EC 3.4.21.73) precursor

RESULT 2

61

121 287 181 347

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U.D. Saminogen activator (EC 3.4.21.73) precursor - bovine
N.Alternate names: u.P.A
C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Accession: JN0560
R.Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
G.Accession: JN0560
R.Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
G.Accession: JN0560
A.M.Lile: Bovine urokinase-type plasminogen activator and its receptor: cloning
A.Accession: JN0560
A.Molecule type: mRNA
A.Reference number: JN0560; MUID:916180; PIDN:AAA51419.1; PID:9163801
C.Superfamily: urokinase-type plasminogen activator; EGF homology; kringle home activator chain A #status predicted AMA1>
F.21-179/Product: plasminogen activator chain A #status predicted AMA2>
F.21-179/Product: plasminogen activator chain A #status predicted AMA2>
F.13-64/Domain: kringle homology ARR3>
F.131-431/Product: plasminogen activator chain B #status predicted AMA2>
F.181-431/Pomain: kringle homology ARR3>
F.181-431/Domain: trypsin homology ARR3>
F.1826,277,378/Active site: His, Asp, Ser #status predicted
                                                                            F:190-442/Product: urokinase-type plasminogen activator chain B #status predic: F:190-430/Domain: trypsin homology <TRY>
F:152/Binding site: carbohydrate (Asn) (covalent) #status predicted (F:152/Binding site: carbohydrate (Asn) (covalent) #status predicted (F:179-310, 220-236, 228-299, 324-399, 356-372, 383-411/Disnifide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSW 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                PSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDI
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                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                          Length 442;
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                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                      tch 83.2%; Score 1255; DB 1; 1 al Similarity 82.1%; Pred. No. 2.4e-101; 225; Conservative 23; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA
                 33-64/Domain: EGF homology <EGF>,72-153/Domain: kringle homology <KRG>
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Best Local S:
Matches 225
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C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; tr
C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status pradicted <81G>
F;21-188/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
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A; Molecule type: mRNA
A; Molecule type: mRNE: X51935; NID:938130; PIDN:CAA36200.1; PID:938131
C; Superfamily: urokinase-type plasminogen activator; EGF homology; Kringle; berine proteinase
F; 1-20, Domain: signal sequence #status predicted <SIG> F; 1-10, Forduct: plasminogen activator chain A #status predicted <ACH>
F; 20-61/Domain: Erypein homology <ACRG>
F; 60-150/Domain: trypein homology <ACRG>
F; 60-150/Domain: trypein homology <ARNA
F; 7178-421/Domain: trypein homology <ARNA
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F; 718-421/Domain: trypein homology <ARNA
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C; Accession: A00032
R; Magamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 9525-9541, 1984
A; Title: CDNA and gene nucleotide sequence of porcine plasminogen activator.
A; Reference number: A00932; MUID:85087954; PMID:6096832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 07-Aug-1998
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; Pred. No. 5.8e-117; 
13; Mismatches 4; Indels 3;
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C;Date: 04-Dec.1986 #sequence_revision 17-Mar-1987
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A,Molecule type: DNA
A,Residues: 1-240,'H',242-442 <NAG1>
A,Exerimental source: kidney cell line LLC-PK1
R,Nagamine, Y.
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92.8%;
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GOZAQPSKSIQTICLPPEHEDAHSRTRCEITGFG GOZAQPSKSIQTICLPPEHEDAHSRTRCEITGFG GOZAQPSKSIQTICLPPEHEDAHSRTRCEITGFG GOZAGPSKSIQTICLPPEHEDAHSRTRCEITGFG GOZAGPSKSIQTICLPPEHEDAHSRTRCEITGFG GOZAGPSTAGE GOZAGE CONTRIBENTANT CALL 236 GOZAGPSGGPP GOZAGE GOZA	338 Db 276 241 Cy 180 398 Cy 240 Db 396	en activator	R.F. Plasminogen act	Deregulated in Francisco CC	edicted <ach> OY 1 redicted <ach> Db 157 redicted <bch> OY 60 217</bch></ach></ach>	275 Db 397
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                                  Accessive treatments (SH KONZOL) MONIBAGA (SH) FINE ADA98809.1; PID 9339818

Altcose-terences (SH KONZOL) MONIBAGA (S) Higher (S) Higher (S) Higher (S) (A) (Dem. 25, 125-125) 1911

Afficie: Purification and Characterization of tissue plasminogen activator sec .ed 1

Afficie: Purification and Characterization of tissue plasminogen activator sec .ed 1

Afficies: Dirification and Characterization of tissue plasminogen activator sec .ed 1

Afficies: Dirification and Characterization of tissue plasminogen activator protein, a corn with the second of the mature protein, a corn Ripenica, D.; Helmes, W. E.; Kohr, W. J.; Harkhan, R. N.; Wahar, G. A.; Ward, C.A. Bent Mitter 201, 214-211, 1933

Afficies: Dirification and expression of human tissue-type plasminogen activator cDN in Es Repenica (Coning and expression of human tissue-type plasminogen activator CDN in Es Arcession: A3233 MONID: 8315262; PMID: 8339343

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J. Biol. Chem. 261, 14214-14218, 1986
A) Reference number: A37567; MUID:87033611; PMID:3021732
A) Contents: annotation; fibrin binding site
B,Verineijen, J. H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P. BMBO J. 5, 352-3530, 1986
A,Title: Involvement of finger domain and kringle 2 domain of tissue-type plase A; Contents: annotation; fibrin binding site
B;Dodd, I.; Nunn, B.; Robinson, J.H.
Thromb. Haemost. 59, 523-528, 1988
A;Title: Isolation, identification and pharmacokinetic properties of human tis
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A;Contents: annotation; melanoma cells, partial sequence of residues 36-562, R;Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H. FEBS Lett. 168, 29-32, 1984
A;Title: Differences between uterine and melanoma forms of tissue plasminoge: A;Reference number: A91322; MUID:84158956; PMID:6538514
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A, Molecule type: protein
A, Residues: 33-45,311-320 <POH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Cross-references: GB:005187; NID:9212858; PIDN:AAA49131.1; PID:9212859
C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C; Asywords: glycoprotein; heard sequence #status predicted calg.
F; 1-2-17/ Product: urokinase-type plasminogen activator chain A #status predicted calg.
F; 3-15 Momain: Kringle homology calg.
F; 173-428/ Product: urokinase-type plasminogen activator chain B #status predicted calg.
F; 173-416/ Domain: trypsin homology calg.
F; 173-217, 272, 373/ Active site: His, Asp, Ser #status predicted
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u-plasminogen activator (EC 3.4.21.73) precursor - chicken
NyAlternate names: upA
CiSpecies: Gallus gallus (chicken)
CiSpecies: Callus gallus (chicken)
CiSpecies: 20-Uul-1990 #sequence_revision 20-Uul-1990 #text_change 16-Jul-1999
CiAccession: A35008
CiAccession: A35008
N. Intle: The Chicken unckinase-type plasminogen activator gene.
A;Reference number: A35005; MUID:90110185; PMID:2295632
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GNYI>
A;Cross-references: GNION141
A;Note: the codon given for residue 93 (ACC) is inconsisten
R;Friezerac Degen, S.J.; Rajbut, B.; Reich, E.
R;Friezerac Degen, S.J.; Rajbut, B.; Reich, E.
A;Title: The human tissue plasminogen activator gene.
A;Reference number: A23529; MUID:86196143; PMID:3009482
A;Accession: A23529
A;Molecule type: DNA
A;Residues: 1-562 < DEG>
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A:Reference number: A60902; MUID:89044681; PMID:3142086 A:Contents: annotation; novel forms of expressed recombinant t-PA R:Harris, T.J.R.; Patel, T.; Marston, F.A.O.: Little, S.: Emtage, J.S.: Ondenakker, G.:	Db 477 TSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLG 536	
lits	Qy 245 CALKDKPGVYTRVSHFLPWIRSHTK 269	
A; Molecule type: mRNA A; Residues: 1-562 < HAR> A; Cross-references: GB: MID:g190031; PIDN: AAA60111.1; PID:g190032 A; Note: narts of this semisance ware confirmed by nantial sommania.	(0) 10 / 0 / 0	
;	(EC 5.3.21.80) precursor gicus (Norway rat) quence_revision 10-Sep-199	
Ajille: Expression of numan uterine tissue-type plasminogen activator in mouse cells ug Ajreference number: 160110; MUID:88054470; PMID:2824147 Ajrocession: 160110	C;Accession: A35029; A31597 R;Peng, P.; Ohlsson, M.; Ny, T. T Biol Chem 265 2020-2027 1990	
	A; Tille: The structure of the TATA-less rat tissue-type plasminogen activator A; Tille: The property of MUID:90130448; PMID:2105315	ie. Sp
	A; Accession: A35029 A; Status: preliminary	
b. tivato	A;NOSCALLE LYBE: LNA A;Residues: 1-559 «FEN» A;Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431; GB:J	.26
	RiNy, T.; Leonardsson, G.; Hsueh, A.J.W. DNA 7, 671-677, 1988 A.H.H.B. Clondar and characterization of a chara	, t
	A; Reference number: A31597; MUID:89170114; PMID:3148445)
a sing	A; Molecule type: mRNA A; Residues: 1-379, KY, 381-559 < NYT> The A; Residues: 1-379, KY, 381-559 < NYT > A; Residues: 1-379,	
repea	Trickobs relected of Markey, Albridge of Trickobs of Arbridge of Trickobs of Arbridge of Trickobs of T	seat E
	F;1-17/Domain: signal sequence #status predicted <sig>F;18-29/Domain: propeptide #status predicted <pro></pro></sig>	
155/3;	F;30-559/Product: t-plasminogen activator #status predicted <mat> F;30-589/Product: t-plasminogen activator chain A #status predicted <ach> F;0-76/Activator in the control of the control</ach></mat>	
einase	F;30-7-7-0usain: Introductur Type 1 repeat nomology viris F;80-116/Domain: EGF homology <egf> F;124-205/Domain: Kringle homology <kr1></kr1></egf>	
	F;213-294/Domain: kringle homology <kr2> F;309-555/Product: t-plasminogen activator chain B #status predicted <bch></bch></kr2>	
	F:349-553/Johnann: Erypsin nomology <tky> F:38-68-66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265 F:144 481/Rinding site: carbohodrate (Apr) (covalent) #status predicted</tky>	19,297
F;127-208/Domain: kringle homology <kr1> F;215-226/Domain: kringle homology <kr2></kr2></kr1>	F;308-309/Cleavage site: Arg-11e (plasmin, trypsin) #status predicted F;355,404,510/Active site: His, Asp, Ser #status predicted	
Fill-562/Product: t-plasminogen activator chain B #status experimental <bch> Fill-562/Domain: trypsin homology <try></try></bch>	Query Match 37.8%; Score 570.5; DB 1; Length 559;	
F:14-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296,236-278,267-291,299-4 F:152,483,91ainding site: carbohydrate (asn) (covalent) #status experimental F:219/81nding site: carbohydrate (asn) (covalent) #status experimental		
F.310-311/Cleavage site: Valoupurate (ASM) (Covatent) (Partial) #Status experimental F.310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental F.357,466/Active site: His. Asp #status predicted	Qy 13 CGQKTLR-PRFKIIGGEFTTIENQPWFAAIY-RRHRGGSVTYVVCGGSLISPCWVISATHC 70	
F;513/Active site: Ser #status experimental	ikggletditshewqaaifvrnkapgerf	
Query Match 38.7%; Score 583; DB 1; Length 562; Best Local Similarity 44.9%; Pred. No. 8.5e-43; Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;	Qy 71 FIDYPKKEDYIVYLGRSRLNSNTQGENKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130 :	
OY 13 CG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHC 70	QY 131 GRCAQPSRTIQTICLPSMYNDDQFGTSCEITGFGKENSTDYLYPBQLKMTVVKLIS 186	
71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFBVENLILHKDYSADTLAHHNDIALLKIRSKE 1	187 HRECOOPHYYGSEVTTKMLCAADPOWKTDSCOGDSGGPLVCSLOGRWTLTGIVSW	
n n		
QY 131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREC 190	Cy 242 GRGCALKDKPGVYTRVSHFLFWIRSHTKE 270 Db 531 GLGCGOKDVPGTYTKVTHYTHVIODNKKO 559	
QQPHYYGSEVTTKMLCAADPQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRG 2		

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C; Species: Desmodus rotundus (common vampire bat)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C; Accession: J60599
R; Kraetzachmar, J; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alago: R.; Kraetzachmar, J; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alago: A; Title: The plasminogen activator family from the salivary gland of the vampi bat A; Reference number: J50597; MUID: 92039036; PMID: 1937019
A; Accession: J50599
A; Accession: J50599
A; Accession: J50599; MUID: 9166076; PIDN: AAA31594.1; PID: 9166077
A; Residues: 1-431 < kRA>
A; Residues: GB: M63989; NID: 9166076; PIDN: AAA31594.1; PID: 9166077
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I C; Keyworda: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase F; 1-21/Domain: signal sequence #status predicted < kRO>
F; 2-36/Domain: propeptide #status predicted < kRO>
F; 32-36/Domain: trypsin homology < kRO>
F; 31-74/Domain: trypsin homology < kRO>
F; 41-74/Domain: trypsin homology < kRO>
F; 41-52, 46-63, 65-74, 82-163, 103-145, 134-158, 168-299, 211-227, 219-288, 313-388/Dis: %ide F; 19-180/Cleavage site: His-Ser (plasmin) #status predicted
F; 226, 275, 382/Active site: His-Ser (plasmin) #status predicted
F; 226, 275, 382/Active site: His-Ser (plasmin) #status predicted
F; 350-351, 378-406/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: JS0600
A,Molecule type: mRNA
A,Residues: 1-34 «KRA
A,Residues: 1-34 «KRA
A,Cross-references: GB:M63990; NID:gl66078; PIDN:AAA31595.1; PID:gl66079
A,Note: the authors translated the codon ATC for residue 75 as Thr
C,Superfamily: tissue plasminogen activator; pGF homology; fibronectin type I
C,Keywords: fibrinolysis; glycoprotein; hydrolase; Kringle; serine proteinase
F;22-36/Domain: signal sequence #status predicted «SIG»
F;22-36/Domain: propeptide #status predicted «PRO»
F;37-394/Product: plasminogen activator gamma #status predicted «PLA»
F;45-126/Domain: kringle homology «TRY»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IALLKIRSKEGRÇAÇPSRTIQTIÇLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSGGPLVCSLQGRMT 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t-plasminogen activator (BC 3.4.21.68) gamma precursor - common vampire bat N;Alternate names: tissue plasminogen activator C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar.1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 SPPEELKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VTYVCGGSLISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.3%; Score 547; DB 2; Length 431; 42.9%; Pred. No. 8.4e-40; Live 43; Mismatches 102; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 LLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNWR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 LTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 42.9
Matches 118; Conservative
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A; Rosidues: 33-37, X', 39-40 cLIW>
A; Rosidues: 33-37, X', 39-40 cLIW>
C; Ruperfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C; Keywords: fibrinolysis; glycoprotein; hydrolase, kringle; serine proteinase
C; Keywords: fibrinolysis; glycoprotein; hydrolase, kringle; serine proteinase
E; 1-17/Domain: signal sequence #status predicted <RRO>
F; 30-559/Product: t-plasminogen activator factuus predicted <NAT>
F; 30-559/Product: t-plasminogen activator chain A #status predicted <ACH>
F; 31-559/Product: t-plasminogen activator chain B #status predicted <ACH>
F; 31-264/Domain: kringle homology <RRI>
F; 31-264/Domain: kringle homology <RRI>
F; 31-264/Domain: kringle homology <RRI>
F; 31-264/Domain: tryingle homology <RRI>
F;
                                                                                                 L-plasminogen activator (EC 3.4.21.68) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29941; S48205; S48206
R;Rickles, R.J.; Darrow, A.L.; Strickland, S.
A;Biol. Chem. 263, 1563-1569, 1988
A;Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mR
A;Reference number: A29941; MUID:88087303; PMID:2826484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: mENA
A,Residues: 1-559 «RIC»
A,Cross-references: B. Seelen, V.; Collen, D.
R,Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Sur. J. Biochem. 224, 863-871, 1994
A,Title: Characterization of the murine plasma fibrinolytic system.
A,Ritle: Characterization of the murine plasma fibrinolytic system.
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37.8%; Score 569.5; DB 1; Length 559;
Best Local Similarity 42.8%; Pred. No. 1.3e-41;
Matches 115; Conservative 47; Mismatches 90; Indels 17
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A,Molecule type: protein
A,Residues: 33-37,'X',39-40 <LIJ>A,Accession: S48207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 309-316 <LI2> A; Accession: S48206
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A34369
L-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderm: yra) C.Species: Megaderma lyra lycasion: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C.Accession: A34369
C.Accession: A34369
B.Gardell, S.J.; Duong L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.; J. J. Biol. Chem. 264, 17947-17952, 1989
A.fitle: Isolation, characterization, and cDNA cloning of a vampire bat saliva plas A; Reference number: A34369, MUD:90036867; PMID:2509450
A; Retaus: predliminary
A; Releatus: predliminary
A; Releatus: predliminary
A; Releatus: predliminary
A; Residues: 1-477 CGAR>
A; Residues: 1-477 CGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 SVPVCSKATGGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGRFFLGGGILISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
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IALLQLKSGSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEG
                                                                        VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSGGPLVCSLQGRMT
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                                                                                                                                                                                                                                                   LIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK
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Best Local Similarity 42.9°
Matches 118; Conservative
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Cispecies: Desmodus rotundus (common vampira bat)

Cispecies: Desmodus rotundus (common vampira bat)

Cistae: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

Cistaession: Uso598

Rixtaetzschamar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 229-237, 1991

A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des A;Reference number: Uso597; MuID:92039036; PMID:1937019

A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des A;Reference number: Uso597; MuID:92039036; PMID:1937019

A;Accession: Uso598

A;Molecule type: MRNA

A;Residues: 1.477 ckRA>

A;Cross-references: GB:MG3988; NID:g166074; PIDN:AA31593.1; PID:g166075

C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C;Keyordes: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C;Keyordes: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted colors
F;2-16/Domain: EGF homology ckRG>
F;22-16/Domain: EGF homology ckRG>
F;22-17/Domain: EGF homology ckRG>
F;22-17/Domain: EGF homology ckRG>
F;22-17/Domain: trypes in homology ckRG>
F;22-17/Domain: trypes in homology ckRG>
F;22-27/Domain: trypes in homology ckRG>
F;22-37/Domain: trypes in his-Ser (plasmin) #status predicted
F;28-296/Cleavage site: His-Ser (plasmin) #status predicted
F;22-321,428/Active site: His-Ser (plasmin) #status predicted
       F;45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:
F;142-143/Cleavage site: His-Ser (plasmin) #status predicted
F;189,238,345/Active site: His, Asp, Ser #status predicted
F;315/Binding site: carbohydrate (Asn) (covalent) #status predicted
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IAILQLKSGSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEG 298
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                                                                                                                                                                                      Query Match 36.2%; Score 546; DB 2; Length 394; Best Local Similarity 42.9%; Pred. No. 9.2e-40; Matches 118; Conservative 43; Mismatches 102; Indels ::
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42.9%; Pred. No. 1.2e-39;
ive 43; Mismatches 102; Indels
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Argethmay: blood coagulation, fibrinolysis

C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat moll (K;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat mollogy capulation; fibrinolysis; glycoprotein; hydrolase; kringle, asmm C;Keywords: blood coagulation; fibratus predicted cSIG>
F;20-372,373-615/Product: coagulation factor XIIa, alpha form #status experime II c F;47-88/Domain: fibronectin type II repeat homology cFB2>
F;217-200main: fibronectin type II repeat homology cFB2>
F;217-200main: EGF homology cEG2>
F;217-200main: Kringle homology cEG2>
F;217-205/Domain: Kringle homology cKRG>
F;238-356/Region: profiler erich
F;238-366/Product: coagulation factor XIIa, beta form #status experime; II c F;373-609/Domain: trypsin homology cTRY>
F;333-109/Domain: trypsin homology cTRY>
F;333-109/Domain: trypsin homology cTRY>
F;349-433/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;249,433/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;312,412,461,563/Active site: His, Asp, Ser #status predicted
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A;Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 4:
C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound t
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                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 146-378, 'G', 380-615 <QUE>
A; Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361
A; McMullen, B.A.; Fujikawa, K.
J. Biol. Chem. 260, 5328-5341, 1985
A; Tille: Amino acid sequence of the heavy chain of human alpha-factor XIIa (A; Reference number: A22248; MUID:85182674; PMID:3886654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 GGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADT
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A, Residues: 354-362;373-615 <FUJ>
R; Harris, R.J.; Ling, V.T.; Spellman, M.W.
Biol. Chem. 267, 5102-5107, 1992
A,Tille: O-linked fucose is present in the first epidermal growth factor A, Reference number: A44606; MUID: 92184750; PMID:1544894
A, Contents: annotation; carbohydrate binding site
                                                                                                                                                                                                                           (Hageman
                                                                               PID:9180359
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Local Similarity 38.5%; Pred. No. 4.2e-35;
es 107; Conservative 44; Mismatches 109; Indels
A;Residues: 14-332,'S',334-615 <CO2>
A;Cross-references: GB:M11723; NID:g180358; PIDN:AAA51986.1;
R;Que, B.G.; Davie, E.W.
Biochemistry 25, 1525-1528, 1986
A;Title: Characterization of a cDNA coding for human factor X:A;Reference number: A25191; MUID:86216049; PMID:3011063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 20-379 <MCM>
R; Fujikawa, K.; McMullen, B.A.
J; Biol. Chem. 258, 10954-10933, 1983
A; Title: Amino acid sequence of human beta-factor XIIa.
A; Reference number: A21037; MUID:83291041; PMID:6604055
A; Accession: A21037
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                                                                                                                            A Molecule type: mRNA
A; Residues: 1-47° cKRA>
A; Cross-references: GB: M63997; NID: g166070; FIDN: AAA31591.1; FID: g166071
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 1-21/Domain: stopaptide #status predicted <PRO>
F; 23-45/Domain: propeptide #status predicted <PRO>
F; 27-95/Domain: EGF homology <EGF>
F; 27-95/Domain: Kringle homology <EGF>
F; 27-70-79; B7-98; 92-109; 111-120, 129-209, 149-191, 180-204, 214-345, 257-273, 265-334, 359-48; 153, 398 Binding site: arabohydrate (Ann) (covalent) #status predicted
F; 22-226/Cleavage site: His-Ser (plasmin) #status predicted
F; 222, 321, 428/Active site: His, Asp, Ser #status predicted
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;Residues: 4-615 <TRI>
;Cross-references: GB-M11315; NID:g182291; PIDN:AAA70225.1; PID:g182292;
;Cross-references: GB-M11315; NID:g182291; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.T.
;Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.T.
Biol. Chem. 260, 1366-13676, 1985
;Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the
;Reference number: A00930; MUID:86033830; PMID:3877053
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Cibace: 27-Nov-1985 Hequence revision 30-Jun-1991 #text_change 08-Dec-2000
Cibacesion: A29411; A26814; A00930; A25191; A22248; A21037
Riccol, D.E.; MacGillivray, R.T.A.
J. Biol, Chem. 262, 13662-13873, 1987
A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon A;Reference number: A29411; MUID:88007593; PMID:2888762
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Molecule type: DNA

Sesidues: 1-615 - COO>

Sesidues: 1-615 - COO>

Sesidues: 1-615 - COO>

Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.

Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CWVLTAAHCF----QESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDT-- 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 LKWITVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSGGPLVCSLQ 230
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N;Alternate names: Hageman factor (activated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98; Indels
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                                                 A; Reference number: JS0597; MUID: 92039036; PMID: 1937019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.0%; Score 543; DB 2; 42.2%; Pred. No. 2.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
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Matches 117; Conserv
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                                                                                                   A; Accession: JS0597
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coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
NAlternate names: Hageman factor
Cippecies: Cavia porcellus (guinea pig)
Cipate: 25-Fbb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
CiAccession: S28941
Risemba, U1; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; cabe Risemba, U1; Yamamoto, T.; Xunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; cabe Biochim: Biophys. Acta 1159, 113-121, 1939
A;Title: Primary structure of guinea-pig Hageman factor: sequence around the c avaganterion: S28941; MUID:93003367; PMID:1390917
A;Accession: S28941
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-603 <SEM>A;Cross-references: EMBL:X68615; NID:q49578; PIDN:CAA48600.1; PID:q49579
C;Superfamily: coagulation factor XII; EGF homology, fibronectin type I repeat homology cipcase F;46-87/Domain: Eibronectin type I repeat homology <FB17-208/Domain: Eibronectin type I repeat homology <FB2-597/Domain: EdF homology <EGF>F;216-294/Domain: trypsin homology <FR7>F;359-597/Domain: trypsin homology <FR7>F;359-597/Domain: trypsin homology <FRY>
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N,Alternate names: Hageman factor (activated)
C;Species: Bos primigenius taurus (cattle)
C;Species: Lo.Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
C;Accession: 845281; A61329
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biophys. Acta 1206, 63-70, 1994
A;Title: Primary structure of bovine Hageman factor (blood coagulation factor A;Reference number: 845281; MUID:94242782; PMID:8186251
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A, Residues: 1-593 <SHI>
A, Coss-references: GB:S70164
A, Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 247 as Leu, CCG for residue 26 as Phe, GTG for residue 505 as Leu
is, and ATC for residue 505 as Leu
K; Fujikawa, K.; Walsh, K.A.; Davie, B.W.
Biochemistry 16, 2270-2278, 1977
A; Thille: Isolation and characterization of bovine factor XII (Hageman factor).
A; Reference number: A61329; MUID:77182112; PMID:861210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 PETSSLICCOR-LRKKLSSLSKIVGGLVALPGAHPYIAALY----WGS--NFCSGSLIAP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ALLKI-RSKEGRÇAQPSRTIQTICLPSMYNDPQFG--TSCEITGFGKENSTDYLYPEQLK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 ALLRIQKSADGSCAQLSPYVQTVCLPSGPAPPSESETTCCEVAGWGHQFEGAEEYSSFLQ 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 EAQVPLISSERCSSPEVHGDAFLSGMLCAGFLEGGTDACQGDSGGBLVCEDEAAEHRLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PEELKFOCGOKTLRPRF----KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISP
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Best Local Similarity
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Matches 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A) Description: activates hepatocyte growth factor by specific proteolytic cleavage A) Pethway: tissue repair and regeneration
C) Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C) Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C) Reywords glycoprotein; by divolase; krindje; liver; plasma; serine proteinase
F) 108-148 Domain: Edpronectin type II repeat homology <1F2>
F) 108-129 Domain: EGF homology <2G1>
F) 245-279 Domain: EGF homology <EG2>
F) 286-367 Domain: kringle homology <EG2>
F) 286-367 Domain: kringle homology <EG2>
F) 373-407 Product: hepatocyte growth factor activator heavy chain #status experimental 

F) 408-655 Product: hepatocyte growth factor activator heavy chain #status predicted

F) 40, 49, 290, 468, 492, 546 Minding site: carbohydrate (Asn) (covalent) #status predicted

F) 40, 49, 290, 468, 492, 546 Minding site: carbohydrate (Asn) (covalent) #status predicted

F) 447, 497, 598 Active site: His, Asp, Ser #status predicted

                                                                                                                                                                                                                                                                                                                          hepatocyte growth factor activator (EC 3.4.21.-) precursor [validated] - human C;Species: Homo sapiens (man) C;Date: 21-Sep-1993 #sequence_revision 25-Aug-1995 #text_change 08-Dec-2000 C;Accession: A46688 R;Miyazawa, K.; Shimomura, T.; Kitamura, A.; Kondo, J.; Morimoto, Y.; Kitamura, N. Biol. (fmem. 2568, 10024-10028, 1993 A;Title: Molecular cloning and sequence analysis of the cDNA for a human serine proteased coagulation factor XII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: DDBJ:D14012; NID:g219680; PIDN:BAA03113.1; PID:g219681
A;Experimental source: liver (mRNA); serum (protein)
A;Note: sequence extracted from NCB1 backbone (NCB1R:131227, NCBIP:131228)
A;Note: parts of the sequence, including the amino ends of the heavy and light chains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 AHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 QLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQG-- 231
                                                          516 ASFLOBAQVPFLSLERCSAPDVHGSSILPGMLCAGFLEGGTDACOGOSGGPLVCEDOAAE 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KPSSPPEELKFQCGQK----TLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 655;
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                                                                                                                            268
                                                                                                                                                                                          613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A46688; MUID:93252878; PMID:7683665
A;Accession: A46688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.7%; Score 493.5; DB 1;
llarity 38.3%; Pred. No. 6.2e-35;
Conservative 43; Mismatches 109;
                                                                                                                                                              -RMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: GDB:HGFAC; HGFA; HGFAP
Cross-references: GDB:954514
Map position: 4p16-4p16
Punction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-655 <MIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
174
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plasma hyaluronan-binding protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Accession: JC5878
C;Accession: JC5878
R;Hashimoto, K.; Tobe, T.; Sumiya, J.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi saiol. Pharm. Bull. 20, 1127-1130, 1997
A;Fitle: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyal saiol. Pharm. Bull. 20, 1127-1130, 1997
A;Fitle: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyal saidle the cDNA for a mouse homologue of human PHBP: A novel hyal saidles: JC588 cHAS
A;Fesidues: JC588 cHAS
C;Comment: This protein acts as serine protein; EGF homology; Kringle homolo; trf; C;Comment: This protein acts as serine protein; EGF homology; EGG>
C;Cupperfamily: plasma hyaluronan-binding protein large chain #status predic: 1 c/F;1-13/Domain: EGF homology eEG3>
F;1-23/Domain: EGF homology eEG3>
F;113-145/Domain: EGF homology eEG3>
F;113-145/Domain: Kringle homology eEG3>
F;112-158/Domain: kringle homology eEG3>
F;122-158/Domain: kringle homology eRE3>
F;122-588/Product: plasma hyaluronan-binding protein small chain #status predic if cF;112-558/Product: plasma hyaluronan-binding protein small chain #status predic if cF;112-558/Product: plasma hyaluronan-binding protein small chain #status predic if cF;112-558/Product: plasma hyaluronan-binding protein small chain #status predic if cF;112-558/Product: plasma hyaluronan-binding protein small chain #status predic if cF;112-558/Product: plasma hyaluronan-binding protein small chain #status predic id cA; F;112-558/Product: plasma hyaluronan-binding protein small chain #status predic id cA; F;112-558/Product: plasma hyaluronan-binding protein small chain #status predic id cA; F;112-558/Product: plasma hyaluronan-binding protein small chain #status predic id cA; F;112-558/Product: plasma hyaluronan-binding protein small chain #status predic id cA; F;112-558/Product: plasma hyaluronan-binding protein small chain #status predic id cA; F;112-113-1145/Product id cA; F;112-1145/Product id cA; F;112-1145/Product id cA; F;112-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 TKHLKVV-LGDQDLKKTESHEQTFRVEKILKYSQYNERDEIPHNDÍALLKLKFVGGHCAL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 ESRYVKTVCLPS---DPPFSGTECHISGWGVTETGE--GSRQLLDAKVKLIANPLCNSRQ 479
                                                                                                                                                                                                    180 TVVKLISHRECQQPHYYGSEVTTKMLCAADPQW--KTDSCQGDSGGPLVCSLQGR-MTLT 236
                                                                                                                                                                                                                                                  136 PSRTIQTICLPSMYNDP-QFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasma hyaluronan-binding protein precursor - human
NyAlternate names: hopatocyte growth factor activator-like protein; PHBP
NyAlternate names: hopatocyte growth factor activator-like protein; PHBP
N;Contains: serine proteinase (EC 3.4.21.-)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 15-Oct.1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
C;Accession: JC4795
C;Accession: JC4795
JC Biochem. 119, 1157-1165, 1996
                                                                                                        480 LYDHTIDDSMICAGNLQKPGSDTCQGDSGGPLTCEKDGTYYVYGIVSWGQECG--KKPGV
                                                         IALLKIRSKEGRÇAQPSRTIQTICLPSMYNDPQ-FGTSCEITGFGKENSTDYLYPEQLKM
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                                                                                                                                                                                                                                                                                                                                                                                         728 GVTSWGYGCGVKDTPGVYTRVPAFVPWIKSVT
                                                                                                                                                                                                                                                                                                                                               GIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 YTRVSHFLPWIRSHTKEENGL 274
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A.Residues: 1-761 <YAM>
A.Across-references: DB9971
A.Experimental source: brain
C.Superfamily: brain-specific serine proteinase; scavenger receptor cysteine-rich domain
C.Superfamily: brain-specific serine proteinase
C.Superfamily: brain-specific serine proteinase
C.Superfamily: ringle-like #status predicted <RIS
F.165-266,Domain: kringle-like #status predicted <RIS
F.165-266,273-372_386-486/Domain: scavenger receptor cysteine-rich domain homology <SRC7>
F.151-516-266,273-372_386-486/Domain: scavenger receptor cysteine-rich #status predicted <SR
F.513-516/Domain: furin binding #status predicted <RRB>
F.513-516/Domain: trype:n homology <TRV>
F.513-516/Domain: trype:n homology <TRV>
F.513-517/Domain: trype:n homology <TRV>
F.521,569/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.522,512,711/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drain-specific serine proteinase (EC 3.4.21.-) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 31-Mar-2000
C;Accession: JC5759
R;Yamamura, Y:; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.; Tsujimura, A.; Yamaguchi, N.
Biochem: Biophys. Res. Commun. 239, 386-392, 1997
A;Title: Molecular cloning of a novel brain-specific serine protease with a kringle-like
A;Reference number: JC5759, MUID:98008848; PMID:9344839
A;Accession: JC5759.
A,Accession: A61329
A,Molecule type: protein
A,Molecule type: protein
A,Residues: 10-16,'X',18-19;525-550 <FUJ>
A,Residues: 10-16,'X',18-19;525-550 <FUJ>
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma; e7;88-120/Domain: fibronectin type II repeat homology <1F2>
F;88-120/Domain: fibronectin type II repeat homology <FEI>
F;207-287/Domain: kringle homology <FRC>
F;207-287/Domain: kringle homology <FRC>
F;5507-287/Domain: krypain homology <FRC>
F;551/Active site: Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-S 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQRCSAPDVHGAAFTQGMLCAGFLEGGTDACQGDSGGPLVCEDETPERQLILRGIVSWGS 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEGRCAQPSRTIQTICLPSMYNDPQFGTS--CEITGFGKENSTDYLYPEQLKMTVVKLIS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONRPAPKELTVVLGQDRHNQSCEQCQTLAVRDYRLHEAFSPITYOH--DLALVRLQES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.0%; Score 453; DB 2; Length 59: 38.5%; Pred. No. 1.8e-31; tive 44; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCALKDKPGVYTRVSHFLPWIRSHT 268
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GCGNRLKPGVYTDVANYLAWIREHT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 38.5
Matches 102; Conservative
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Plasma Atllikrein (BC 3 4.21.34) precursor - mouse
C'Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C'Species: Musculus (house mouse)
C'Species: Muscap-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C'Accession: A56557
R'Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.
DNA Cell Biol. 9, 737-748, 1990
A;Title: Mouse plasma kallikrein: CDNA structure, enzyme characterization, and A;Title: Mouse plasma kallikrein: CDNA structure, enzyme characterization, and A;Title: Mouse plasma kallikrein: CDNA structure, enzyme characterization, ampa A;Reference: Maka
A;Reference: Maka
A;Reference: GB:MSBSB; NUD:91090844; PMID:2264928
A;Molecule type: maka
A;Residues: 1-638 <8EI
A;Note: part of this sequence, including the amino ends of both the heavy and A;Note: part of this sequence, including the amino ends of both the heavy and C;Comment: This protein, synthesized in the liver, circulates as a noncovalent c;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule c;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule c;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule c;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule c;Cysuperfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; diplication; fibrinolysis; glycoprotein; hydrol F;1.19/Domain: apple repeat <APP>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <LCH>
F;20-289/Domain: apple repeat <APP>
F;20-289/Domain: apple repeat <APP>
F;20-289/Domain: apple repeat <APP>
F;20-589/Domain: apple repeat <APP>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;31-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;21-104/A7-77;51-57;11-196;141-147;201-286;231-237;237;292-375;3 347
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                                                                                                                                                                                                       A,Gene: GDB:PRSS8
A,Cross-references: GDB:676446; OMIM:600823
A,Cross-references: GDB:676446; OMIM:600823
A,Cross-references: GDB:676446; OMIM:600823
A,Map position: 16p11.2-16p11.2
C,Superfamily: trypsin; trypsin homology
C,Reywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F,13.2-44,Domain: aignal sequence #status predicted <MAT>
F,33.44,Ab-343/Product: prostasin #status predicted <MAT>
F,33.44/Domain: prostasin light chain #status predicted <CHI>F,53.3-41/Domain: transmembrane #status predicted <CHI>F,53.3-341/Domain: transmembrane #status predicted <CHI>F,53.3-341/Domain: transmembrane #status predicted <CHI>F,53.3-341/Domain: transmembrane #status predicted <CHI>F,53.3-341/Domain: transmembrane #status predicted <CHI>F,55.134,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted
F,55.134,238/Active site: His, Asp, Ser #status predicted
F,55,134,238/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK-ENSTDYLYPEQLKWTVVKLISH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SRPITFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---OOPHYYGSEVITIONLCAADPOWKIDSCOGDSGGPLVCSLOGRMILIG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTY----VCGGSLISPCWVISAT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 CG---VAPQARITGGSSAVAGOWPWQV-----SITYEGVHVCGGSLVSEQWVLSAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.1%; Score 408.5; DB 1; Length 343; 36.6%; Pred. No. 7.1e-28; ...
ive 36; Mismatches 100; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 IVSWGDACGARNRPGVYTLASSYASWIQSKVTE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 36.6
les 100; Conservative
                                                                         protein
                                                                                                                        A;Residues: 45-64 <YUA>
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                                                                                                                                                                                  A Rolecule type: MRNA
A Residues: 1-560 < CHO>
A; Experimental source: plasma
A; Note: parts of this sequence, including the amino ends of the mature chains, were dete
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: disulfide-bonded beterodimer of chains produced from the same precursor; th
A; Cross-references: OBB: 4573962
C; Complex: a disulfide-bonded heterodimer of chains produced from the same precursor; th
C; Superfamily: plasma hyaluronan-binding protein; EGF homology; Kringle homology; tryps;
C; Reywords: chondroit in sulfate proteins glycoprotein; hyaluronic acid; hydrolase;
C; Complex: a gisulfide-bonded heterodimer of chains gredicted < SIG>
C; Complex: a gisulfide-bonded heterodimer of chains produced from the same precursor; th
C; Superfamily: plasma hyaluronan-binding protein, 50K chain #status predicted < SIG>
F; 24-13/Pormain: EGF homology < EG2>
F; 115-147/Domain: EGF homology < EG2>
F; 115-147/Domain: kingle homology < EG3>
F; 115-147/Domain: kingle homology < EG3>
F; 115-147/Domain: trypsin homology < EG3>
F; 115-147/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hud
A, Title: Purification and characterization of a novel hyaluronan-binding protein (PHBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and cellular localization of
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C;Species: Homo sapiens (man)
C;Deccies: 44-May-1996 #text_change 21-Apr-2003
C;Accession: A57014; A54866
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 1343-13489, 1995
A;Fitle: Molecular cloning, tissue-specific expression, and cellular localization
A;Reference number: A57014; MUID:9528644; PMID:7768952
A;Fitle: Molecular cloning, tissue-specific expression, and cellular localization
A;Reference number: A57014
Millian (MID:9528644; PMID:7768952
A;Reference number: A57014
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-343 -RES>
A;Rossidues: 1-343 -RES>
A;Rossidues: L343 -RES
A;Rossidues: L34343 -RES
A;Ross
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWK-TDSCQGDSGGPLV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 PTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQ----SSLPLTISMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --YVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PSSPPEELK--FOCGOKTLRPR--FKIIGGEFTTIENOPWFAAIYRRHRGGSVT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 CSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENG
                                                                                                         A;Reference number: JC4795; MUID:96425001; PMID:8827452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 36.2%; Pr. 104; Conservative 40;
                                                                                                                                                             JC4795
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Kasuli 20

S00845

C,Species Homo sapiens (man)

C;Species Homo sapiens (man)

C;Accession: S00845

R;Leytus, S.P.; Lobb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.

Biochemistry 27, 1067-1074, 1986

A;Title: A novel trypsin-like serine protease (hepsin) with a putative transmerance number: S00845

A;Reference number: S00845, MUID:88209431; PMID:2835076

A;Reference 1-417 «LEY»

A;Residues: 1-417 «LEY»

A;Residues: 1-417 «LEY»

A;Gene: 1-417 «LEY»

A;Gene: GDB:HPW; TMPRSS1; hepsin

A;Gene: GDB:HPW; TMPRSS1; hepsin

A;Cross-references: GDB:135685; OMIM:142440

A;Map postition: 19911-19943.2

C;Superfamily: hepsin; trypsin homology

C;Keywords: Hydrolase; liver; serine proteinase; transmembrane protein

F;23-45/Domain: trypsin homology «TRX»

F;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted

F;203,257,353/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 VHLSSP----LPLTEYIQPVCLPAAGQALVDGKICTVTGWG---NTQY-YGQQAGVLQEA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVC----SLQGRWTLT 236
F;127,308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status expe
F;318-347,340-345/Disublifide bonds: #status predicted
F;390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted
F;434,463,578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                               DYPKKEDYIVYLGRSRLNSNTQGE-----MKFEVENLILHKDY----SADTLAHHNDIAL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 DGLPLQDVWRIYSGILNLSDITKDTPFSQIKEIIIHQNYKVSEGNH--DIALIKLQAP-- 492
                                                                                                                                                                                                                                                                                                                                                                                                                     72 IDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 COK-RYODYKITORMVCAGYKEGGKDACKGDSGGPLVCKHNGMWRLVGITSWGEGCARRE 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LNYTEROKPICLPSKGDTSTIYTNCWVTGWGFSKEKGE---IQNILOKVNIPLVTNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 LKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQ---LKMT
                                                                                                                                                                                                                                                                                          17 TLRPRFKIIGGEFTTIENQPWFAAIY-----RRHRGGSVTYVCGGSLISPCWVISATHCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 RCAQPSRTIQTICLPSMYNDPQFGTSCEITGFG--KENSTDYLYPEQLKMTVVKLISHRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COOPHYYGSEVITIKMLCAADPOWKIDSCOGDSGGPLVCSLOGRWTLIGIVSWGRGCALKD
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35.8%; Pred. No. 9.8e-27;
ive 51; Mismatches 89; Indels
                                                                                                                                                               26.7%; Score 402; DB 1; 33.1%; Pred. No. 5.4e-27;
                                                                                                                                                                                                                             56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 KPGVYTRVSHFLPWIRSHTKEENGLA 275
                                                                                                                                                                                                                                Conservative
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101; Conservative
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88; Conserv
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Best Local &
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A, Gene: GDB:KLK3
A, Cross-references: GDB:127575; OMIM:229000
A, Cross-references: GDB:127575; OMIM:229000
A, Cross-references: GDB:127575; OMIM:229000
C, Superfamily: coagulation factor XI; trypsin homology
C, Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F):10, Pomain: signal sequence #status predicted <ASIC>
F):20-390/Domain: apple repeat <APIS-
F):20-390/Domain: apple repeat <APIS-
F):20-289/Domain: apple repeat <APIS-
F):20-289/Domain: apple repeat <APIS-
F):20-380/Domain: apple repeat <APIS-
F):391-638/Domain: apple repeat <APIS-
F):391-638/Domain: apple repeat <APIS-
F):391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F):391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F):391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F):31-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F):31-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F):31-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F):31-631/Domain: plasma kallikrein light chain #status predicted <LCH>
F):31-631/Bomain: plasma kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasma kallikrein (EC 3.4.21.34) precursor - human NiAlternate names: Kininogenin; plasma prekallikrein Cispecias: Homo Sapians (man) Cispecias: Homo sapians (man) Cispecias: Homo sapians (man) Cispate: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999 CiAccession: A00921; A37939 R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W. Biochemistry 25, 2410-2417, 1986 A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four A;Reference number: A00921; MUID:86243359; PMID:3521732
F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted F;434,483,578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                          441
                                                                                                                                                                                                                                                                                                                                                    KEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRTIQTICLPSMYNDPQFGTSCEITGFG---KENSTDYLYPEQLKMTVVKLISHRECQQP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIKINARIVGGINASLGEWPWQVSL--QVKLVSQTHLCGGSIIGRQWVLTAAHCFDGIPY
                                                                                                                                                                                                                                                                                                                                                                                                PDVWRIYGGILSLSEITKETPSSRIKELIHQEYKVS--EGNYDIALIKLQTP----LNY
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                                                                                                                                                                   16;
                                                                                                  DB 1; Length 638;
                                                                                                                                                               Indels
                                                                                           Query Match 27.0%; Score 407; DB 1; L
Best Local Similarity 33.8%; Pred. No. 2e-27;
Matches 89; Conservative 55; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611 YTKVSEYMDWILEKTQSSDVRAL 633
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Ribartley, B. S.

Philos. Trans. R. Soc. Lond. B257, 77-87, 1970

A)Reference number: A93755

A)Contents: annotation; revisions

R)Titani, K.; Ericason, L.H.; Neurath, H.; Walsh, K.A.

Biochemistry 14, 1358-1366, 1975

Biochemistry 14, 1358-1366, 1975

Biochemistry 14, 1358-1366, 1975

Biochemistry 14, 1358-1366, 1975

A)Title: Amino acid sequence of degish trypein.

A)Reference number: A00950; MUDI-75146445; PMID:1092332

A)Contents: annotation; revisions

A)Reference number: A00950; MUDI-75146445; PMID:1092332

A)Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom

A)Reference number: A92954; MUID:76072097; PMID:512

A)Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom

A)Reference number: A92954; MUID:76072097; PMID:512

A)Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom

A)Reference number: A92954; MUID:76072097; PMID:512

C)Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.

C)Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasi

C)Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasi

C)Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasi

C)Comment: Arypsin bomology

C)Reywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F)1-6/Domain: activation peptide #status experimental charpers

F)1-131,132-229/Product: alpha-trypsin #status experimental

F)1-131,132-229/Product: alpha-trypsin #status experimental

F)1-131,132-229/Product: alpha-trypsin #status experimental

F)1-131,132-229/Product: alpha-trypsin #status experimental

F)1-131,132-239/Product: alpha-trypsin #status experimental

F)1-131,132-239/Product: alpha-trypsin #status experimental

F)1-131,132-239/Product: alpha-trypsin #status experimental

F)1-131,132-239/Product: Also,184-184,178-203/Disualitade bonds: #status experimental

F)1-131-132-131-131-143,11-143,11-143,11-143,11-132/Cleavage site: Lys-184-184-184,178-203/Disualitade bonds: #status experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 ICLESMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 KMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 NWFCAGYLEGGKDSCQGDSGGPVVCS--GK--LQGIVSWGSGCAQKNKFGVYTKVCNYVS 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 RLGEDNINVVEGNEQFISASKSIVHPSYNSNTL--NNDIMLIKLKS----AASLMSRVAS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWISATHCFIDYPKKEDYIV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmin (EC 3.4.21.7) precursor - sheep (fragments)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
N;Contains: miniplasminogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
C;Accession: B61545; S28200
R;Schaller, U; Rickli, E.E.
Enzyme 40, 63-69, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 KIVGGYTCGANTVPYQVSL-----KSGIQV
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                      -57, 'Q', 59-67,'Q',69-150,'N',152-176,'N',178-229 <MIK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 26.2%; Score 394.5; DB 1; Length 2 Local Similarity 37.4%; Pred. No. 7.2e-27; nes 91; Conservative 41; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Title: Structural aspects of the plasminogen of various A,Reference number: A61545; MUID:89005015; PMID:3168975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residuse: 1-37;38-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli,
A, Molecule type: protein
A, Residues: 1-57, 'Q', 59-6
R, Hartley, B.S.
Philos. Trans. R. Soc. Lo
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221 WIK 223
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Best Local S
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N;Contains: trypsingen
N;Contains: trypsingen
C;Species: Bos primigenius (cattle)
C;Date: 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 18-Jul-1997
C;Date: 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 18-Jul-1997
C;Date: 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 18-Jul-1997
R;Mikes, O.; Holleysovsky, V.; Tomasek, V.; Sorm, F.
Biochem: Biophys. Res. Commun. 24, 346-352, 1966
A;Aitle: Covalent structure of bovine trypsinogen. The position of the remaining amides.
A;Reference number: A90164; MUID:67168848; PMID:5967094
                                                                                                                                                                                                                                                                                                                                                             Journal (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken sylveriate names: trypsinogen II C. Species: Gallus gallus (chicken) (c.) Species: Gallus gallus (chicken) (c.) Species: Gallus gallus (chicken) (c.) Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999 (c.) Cacession: S55066; S72347 (c.) Gallus (c.) L.; Lee, I.; Hood, L. Biochem J. 307, All-479, 1995 A;Title: Isolation and characterization of the chicken trypsinogen gene family. A, Reference number: S55065; MUD:95251611; PMID:7733885 A;Accession: S55066 A;Molecule type: mRNA A;Residues: 1-248 (wANL) A;Residues: 1-248 (wANL) A;Accession: S72047 A;A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: DNA
A, Residues: 1-248 (WAN2)
A, Residues: 1-248 (WAN2)
A, Experimental source: clone 2-29
C, Superfamily: trypsin, trypsin homology
C, Reywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F, 1-16/Domain: signal sequence #status predicted <SIG>
F, 25-25/Domain: activation peptide #status predicted <AIT>
F, 26-248/Product: trypsin II #status predicted <ANT>
F, 26-248/Product: trypsin II #status predicted <ANT>
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313 RVPIISNDVCNGADFYGNQIKPKMFCAGYPEGGIDACQGDSGGPFVCEDSISRTPRWRLC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.2%; Score 395.5; DB 2; Length 248; 38.7%; Pred. No. 6.5e-27; ive 40; Mismatches 84; Indels 25
                                                                                                                                    373 GIVSWGTGCALAQKPGVYTKVSDFREWIFQAIKTHS-EASGM 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;26-241/Domain: trypsin homology <rxi>F;55,109,202/Active site: His, Asp, Ser #status predicted
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Matches 9
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                                                                                                                                                                                                                                                                                    71 VRLGBYNIDVLEGGEQFIDASKIIRHPKYSSWTL--DNDILLIKLSTP----AVINARVS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 FGCGVPAIQPVLSGLSRIVNGEDAVPGSWPWQVSL---QDSTGFHFCGGSLISEDWVT 72
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Dacession: S33777, S32013
R;Farley, D.; Reymond, F.; Nick, H.
R;Farler, Cloning and sequence analysis of rat hepsin, a cell surface serine
A;Reference number: S33777; MUID:93305733; PMID:8318546
A;Status: Dreliminary
A;Nolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chymotrypsin (EC 3.4.21.1) 2 precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C;Accession: A21195
                                                                                                                                11 FQCGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
                                                                                                                                                                                                                                               202 TKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFL
                                                                                          TICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECOOPHYYGSEVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.9%; Score 390; DB 2; Length 263;
33.2%; Pred. No. 2.1e-26;
vative 51; Mismatches 100; Indels 22; Car-KIIGGEFTTIENQPWFA...
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Best Local Similarity 33.2%
Matches 86; Conservative
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A/Rolecule type: protein;
B/Rolecule type: plasmin, kringle homology; plasminogen-related protein precursor homolog
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase;
F;1-37,38-117,118-460/Product: plasminogen (fragment) #status experimental cAPT>
F;1-118/Domain: kringle homology (KRZ)
F;118-460/Product: miniplasminogen #RT4>
F;118-460/Product: miniplasminogen #RT4>
F;132-211/Domain: kringle homology cKRS>
F;231-450/Domain: prypsin homology cKRS>
F;231-450/Domain: prypsin homology cRXP>
F;202-3150/Domain: prypsin homology cRXP>
F;202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 VYLGRSRLNSNTOGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAOPSRTIQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTSCEITGFGKENSTDYLYPEQL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 KIVGG-YTCAENSVPYQVSLNAGY-----FFCGGSLINDQWVVSAAHCY-----QYHIQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 KIIGGEPTTIENO-PWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQCESSFDCGKPKVEPKKCPARVVGGCVATPHSWPWQVSLRRRSR----EHFCGGTLISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 EWVLTAAHCLDSILGPSFYTVILGAHYEMAREASVQEIPVSRLFLEPSRA-----DI
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A/Status: preliminary
A/Aolecule type: mary
A/Coss-references: EMBL:X54703; NID:g829; PIDN:CAA38513.1; PID:g830
C/Superfamily: trypsin; trypsin tryp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.0%; Score 392.5; DB 2; Length 460; 36.0%; Pred. No. 2.5e-26; ive 35; Mismatches 107; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Indels
                                                                  ovine miniplasminogen; PMID:1492092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.9%; Score 390.5; DB 2
llarity 38.1%; Pred. No. 1.8e-26;
Conservative 41; Mismatches 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 IVSWGRGCALKDKPGVYTRVSHFLPWI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ||| || || || || || || || || || || || VTSWGLGCARPNKPGVYVRVSTYVPWI 453
Arritle: Complete amino acid sequence of ov ArReference number: S28200; MUD:93149995; is ArAccession; S28200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trypsin (EC 3.4.21.4) - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Matches 96; Conserv
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Best Local Simil
Matches 93; C
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NAPETER ABILIKTEIN (EC 3.4.21.34) precursor - rat
NAPETER ABILIKTEIN (EC 3.4.21.34) precursor - rat
NAPETER ABILIKTEIN ONVOGICUS (NOTWAY rat)
NAPETER ABILIKTEIN ONVOGICUS (NOTWAY rat)
C. Species: Rattus norvogicus (Notway rat)
C. Species: Rattus norvogicus (Notway rat)
C. Species: 30.58p.1932 #sequence_revision 30.58p.1922 #text_change 18-Jun-1999
C. Accession: A39180; A33320; 50681; ISSO41; S06852 bbizel ability (Notway N.; Chretien, M.; Seidah, N.G.
R. Rederence number: A39180; MUDD:91129236; PMID:1993180
A. Title: Gene structure and chromosomal localization of plasma kallikrein.
A. A. Reference number: A39180; MUD:91129236; PMID:1993180
A. Residues: 1-638 cB2.
A. Cross references: GB:05515
A. Cross references: GB:05515
A. Cross references: GB:0515
A. Reference number: A33320; MUD:90091743; PMID:2598771
A. Reference number: A33320; MUD:90091743; PMID:2598771
A. A. Reference number: A33320
A. Status not compared with conceptual translation
A. Reference number: A33320
A. Status and Compared with conceptual translation
A. Reference number: A33320
A. Status and Compared with Conceptual translation
A. Reference number: A33320
A. Reference number: A33320
A. Reference number: A58 cBI.
A. A. Reference number: Bobyle: A5 Sawayer, N.; Lazure, C.; Chretien, M.; Seidah, N.G.
B. B. B. Dayle: Acta 999, 100-110, 1989
A. A. Cross references: GB:M01282; MUD:9008457; PMID:2597701
A. Reference number: S06851; MUD:9008457; PMID:2597701
A. Reference number: Bobyle: Acta 999, 100-110, 1980
A. Reference number: Bob
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                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQ---LKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYPKKEDYI - - - - VYLGRSRLNSNTQGEMKFEVENLILH-----KDYSADTLAHHNDIA
                                                                                                                                                                                                                                                                                                                                                                                           CGOKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
                                                                                                                                                                                                                                                                                                                               Gaps
A,Residues: 1-416 <FAR>
A;Cross-references: ENGL:X70900, NID:G57928, PIDN:CAA50256.1; PID:G57929
C;Superfamily: hepsin; trypsin homology cs. transmembrane protein C;Reywords: hydrolase; liver; serine proteinase; transmembrane #status predicted <TMN>
F;22-44/Domain: transmembrane #status predicted <TMN>
F;162-399/Domain: trypsin homology <TRY>
F;187-203,290-358,321-337,348-380/Disulfide bonds: #status predicted
F;202,256,352/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                               90; Indels
                                                                                                                                                                                                                                                                   Ouery Match 25.6%; Score 386.5; DB 1; Length Best Local Similarity 35.0%; Pred. No. 7.3e-26; Matches 99; Conservative 51; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGIVSWGRGCALKDKPGVYTRVSHFLPW----IRSHTKEENGL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGIVSWGTGCALARKPGVYTKVIDFREWIFQAIKTHS-BATGM 412
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Status: translated from GB/EMBL/DDBJ

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NyAlternate names: plasminogen
NyAlternate names: plasminogen
NyContains: miniplasminogen
NyContains: miniplasminogen
CySpecies: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S03733; S03737; A25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison ith A;Residues: 1550 <SCHA
A;Accession: S03733
A;Molecule type: protein
A;Residues: 1-560 <SCHA
B;Residues: 1-560 <SCHA
B;Residues: 1-560 <SCHA
B;Residues: 1-560 <SCHA
B;Residues: 1-560 SCHA
B;Residues: 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-102, 1-10
A; Molecule type: mRNA
A; Residues: 1-638 < RES>
A; Cross = references: GB: MSSS90; NID:9206721; PIDN:AAA42069.1; PID:9206722
A; Cross = references: GB: MSSS90; NID:9206721; PIDN:AAA42069.1; PID:9206722
C; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule c; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule c; Genetics:
C; Genetics: C; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule c; Genetics: S; Genetics: A; Gene: PS: C; Superfamily: coagulation; duplication; fibrinolysis; glycoprotein; hydrol, C; Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrol, F; 1.19/Domain: signal sequence #status predicted 'sIG'
C; Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrol, F; 1.19/Domain: apple repeat AP2>
F; 20-109/Domain: apple repeat AP2>
F; 21-104, 47-77; 51-57; 11-1944, 137-166, 141-147, 201-284, 227-256, 231-237, 292-375, 3 347
F; 31-621/Domain: trypsin homology afRY>
F; 21-104, 47-77; 51-57; 11-1944, 137-166, 141-147, 201-284, 227-256, 231-237, 292-375, 3 347
F; 127, 215, 308 453, 459, 494/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 434, 483, 578/Active site: His, Asp, Ser #status predicted
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A,Residues: 1-57 4BRU>
R,Marti, T.; Schaller. J.; Rickli, B.E.
B. J. Biochem. 149, 279-285, 1985
A,Title: Determination of the complete amino-acid sequence of porcine miniplas:
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1 Similarity 32.3%; Pred. No. 1.6e-25;
85; Conservative 56; Mismatches 106; Indels 1
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72 IDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 RCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 --VSLÍDKÍQLGČEPAAGTILPNNYVČYVTGWGR-LQTNGASPDILQQGQLLVVDYATCS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 OPHYYGSEVTTKALCAADPQWKTDSCOGDSGGPLVC-SLOGRATLTGIVSWGR--GCALK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 ATP----AQFSETVSAVCLFNVDDDFPPGTVCATTGWGKTKYNALKTPEKLQQAALPIVS 182
                                                                                                                                                                                                                                                                                                                                                                   67 ATHOFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                 73 AAHCGV----KTSDVVVAGEFDQGSDEENIQVLKIAQVFKNPKFNMFTV--RNDITLLKL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 RSKEGRCAQPSKTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMTVVKLIS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 HRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCESSON: A26823
R; Kawashima, 1.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA, 6, 163-172, 1987
A; Title: Characterization of pancreatic elastase II CDNAs: two elastase II mR
A; Reference number: A90958; MUID:87217962; PMID:3646943
A; Accession: A26623
A; Molecule type: mRNA
A; Residues: 1-269 «KANA»
A; Cross-references: GB M16651; NID:g164441; PIDN:AAA31027.1; PID:g164442
C; Superfamily: trypsin; trypsin homology
C; Koywords: hydrolase; seriane proteinase
F;1-16/Domain: signal sequence #status predicted «SIG»
F;17-28/Domain: propeptide #status predicted «FNO»
F;29-269/Froduct: elastase II #status predicted «MAT»
F;29-269/Product: elastase II #status predicted
F;73,121,216/Domain: trypsin homology «TRY»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic elastase II (EC 3.4.21.71) precursor - pig
N'Alternate names: pancreatopeptidase E
C'Species: Sus scrofa domestica (domestic pig)
C'Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elastase II
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                                                                                                                                                                                                                                    11 FQCGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
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25.2%; Score 380; DB 2; Length 269;
Best Local Similarity 34.1%; Pred. No. 1.6e-25;
Matches 88; Conservative 50; Mismatches 106; Indels 14; Gaps
                                                                                                                                                                   22;
                                                                                          ch 25.3%; Score 382; DB 1; Length 263; I Similarity 33.6%; Pred. No. 1e-25; 87; Conservative 47; Mismatches 103; Indels 2
   F;34-256/Domain: trypsin homology <TRY>
F;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 LKDKPGVYTRVSHFLPWIR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 STSTPAVYSRVTALMPWVQ 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 DKPGVYTRVSHFLPWIRS 266
                                                                                                     Query Match
Best Local S:
Matches 87
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                                                                                                                                                               A; peacription: dissolves the fibrin of blood clots; acts as a proteolytic factor in a value the walls of the graafian follicle; also activates the urckinase-type plasminogen act A; peathway: fibrinolysis can follicle; also activates the urckinase-type plasminogen act A; pathway: fibrinolysis glycoprotein; hydrolase; kidney; kringle; plasma; serine prote C; Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote F; 1-77/Domain: plasminogen-related protein precursor homology (fragment) < F; 1-77/Domain: plasminogen-related protein precursor homology (fragment) < F; 1-77/Domain: plasminogen-related protein precursor homology (fragment) < F; 1-77/Domain: kringle homology < KRA:
F; 1-77/Domain: kringle homology < KRA:
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F; 1-77/Domain: kringle homology < KRA:
F; 1-77/Domain: kringle homology < KRA:
F; 1-77/Dom
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Chymotrypsin (EC 3.4.21.1) B precursor - rat
NyAlternate names: chymotrypsinogen B
C.Speciaes: Rattus norvegicus (Norway rat)
C.Speciaes: Rattus norvegicus (Norway rat)
C.Accession: A2258
R.Bell, G.I.; Quinto, C.; Quintoga, M.; Valenzuela, P.; Craik, C.S.; Rutter, W.J.
J. Biol. Chem. 259, 14265-14270, 1984
A;Reference number: A22658; MUID:85054881; PMID:6209274
A;Reference number: A22658; MUID:85054881; PMID:6209274
A;Residues: 1-263 < BEL>
A;Residues: 1-263 < BEL>
A;Residues: 1-263 < BEL>
A;Coss-references: GB;K02298; NID:9203653; PIDN:AAA98732.1; PID:g203654
C;Genetics: 18/1; 52/3; 79/2; Ins/3; 166/1; 210/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.; Craik, C.S.; Rutter, W.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKEGRCAQPSRTIQTICLPSMYNDPQF----GTSCEITGFGKENSTDYLYPEQLKMTVVK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SP----AVITDKVIPACLPT----PNYVVADRTACYITGWGETKGT--YGAGLLKEARLP 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 PQCGQKTLRPR---FKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISA
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C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-33/Domain: propeptide #status predicted <PRO>
F;34-263/Product: chymotrypsin B #status predicted <PAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 25.4%; Score 383.5; DB 1; Length 7 1 Similarity 36.0%; Pred. No. 2.8e-25; 94; Conservative 39; Mismatches 99; Indels
A;Reference number: A25834; MUID:85203907; PMID:3846533
A;Accession: A25834
A;Molecule Lype: protein
A;Residues: 450-790 <MAR>
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 GCALKDKPGVYTRVSHFLPWI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCALPNKPGVYVRVSRFVTWI 783
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Best Local S:
Matches 94
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143 ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 202
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R;Wiegand, U.; Corbach, S.; Minn, A.; Kang, J.; Muller-Hill, B.
Gene 136, 167-175, 1993
A;Title: Cloning of the cDNA encoding human brain trypsinogen and characteriza A;Reference number: 138363; MUID:94123994; PMID:8294000
A;Accession: 138363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 HCNVS-PGR--HFVVLGEYDRSSNAEPLQVLSVSRAITHPSWNSTTW--NNDVTLLKLAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 ECOOPHYYGSEVITIKMLCAADPOWKTDSCOGDSGGPLYCSLOGRMTLIGIVSWG-RGCAL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rypsin (EC 3.4.21.4) IV form b precursor - human (fragment)
;Species: Homo sapiens (man)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 SMFCVGFLEGGKDSCQRDSGGFVVCNGQ----LQGVVSWGHGCAWKONFBGVYTKVYNYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 KIVGG-YTCENSLPYQVSL-----KTRIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 KMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 ISLPTA--PPAAGTECLISGWGNTLSFGADYPDELKCLDAPVLTQAECKAS--YPGKITN
                                                                                                                                                                                                                                                                                                                                                13 CGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISAT
                                                                                                                                                                                                                                                                                                                                                                                                   19 CGIPAIKPALSFSQRIVNGENAVLGSWPWQVSL----QDSSGFHFCGGSLISQSWVTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR
                                                                                                                                                                            Length 264;
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                                                                                                                                                                        Query Match 25.1%; Score 378.5; DB 2; Length Best Local Similarity 35.0%; Pred. No. 2.1e-25; Matches 90; Conservative 43; Mismatches 101; Indels
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-259 **RESI-X71345; NID:g405755
A; Cross-references: ENEBL:X71345; NID:g405755
G; Genetics: 25/3; 78/1; 162/3; 208/2
G; Superfamily: trypsin; trypsin homology
G; Superfamily: trypsin; trypsin homology
F; 37-25/10omain: trypsin homology **TRY*
F; 75/119,212/Active Bite: His, Asp, Ser #status predicted
C;Keywords: hydrolase; serine proteinase
F;34-257/Domain: trypsin homology <TRY>
F;75,121,214,Active site: His, Asp, Ser #status predicted
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R; Wiegand, U.; Corbach, S.; Minn, A.; Kang, J.; Mueller-Hill, B.
submitted to the EMBL Data Library, March 1993
A; Description: Identification, cloning and characterization of a cDNA encoding a human A; Reference number: $33496
A; Accession: $33496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 VYLGRSRLNSNTQGEMKPEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cjaccession: I38136
Rjarsen, F.; Solheim, J.; Kristensen, T.; Kolsto, A.B.; Prydz, H.
Hum. Mol. Genet. 2, 1589-1595, 1989-1595, A. Title: A tight cluster of five unrelated human genes on chromosome 16q22.1.
A; Fitle: A tight cluster of five unrelated human genes on chromosome 16q22.1.
A; Reference number: I38135; MUID:94093544; PMID:8268911
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C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                  trypsin (EC 3.4.21.4) IV form a - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 15-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 VRLGEHNIKVLEGNEQFINAAKIIRHPKYNRDTL--DNDIMLIKLSSP----AVINARVS
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A,Map position: 7q35-7q35
C,Superfamally: trypsin, trypsin homology
C,Superfamally: trypsin, trypsin homology
C;Keywords: hydrolase, serine proteinase
F;81-296/bomain: trypsin homology <TRX>
F;120,164,257/Active site: His, Asp, Ser #status predicted
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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A.Map posttuon: 16622.1-16622.1
A:Introns: 18/1; 52/3; 72/2; 106/3; 167/1; 211/3
C;Superfamily: trypsin; trypsin homology
         247 HKPSVFTRVSNYIDWINS
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-304 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: PRSS4; TRY4
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plasmin (EC 3.4.21.7) precursor - mouse
N'Contains: angiostatin; plasminogen
C'Species: Was musculus (house mouse)
C'Date: 20-8ep-1991 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
C'Date: 20-8ep-1991 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
C'Accession: A38514; 848202; 848203
R'Pittle: Characterization of the cDNA coding for mouse plasminogen and localize the Affitle: Characterization of the cDNA coding for mouse plasminogen and localize the Affitle: Characterization of the cDNA coding for mouse plasminogen and localize the Affitle: Characterization of the CDNA coding for mouse plasminogen and localize the Affitle: The State of the Third of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Musch of the Mu
     A; Residues: 16-43 < KIM>
*Kixolvunen, B.; Huhtala, M.L.; Stenman, U.H.

J. Siol. Chem. 264, 14095-14099, 1989
A; Title: Human ovarian tumor-associated trypsin. Its purification and characte.
A; Reference number: A43988; MUD:89340515; PMID:2503510
A; Accession: A43988
A; Molecule type: protein
A; Residues: 16-54 < KOI>
A; Residues: 16-54 < KOI>
A; Experimental source: mucinous ovarian tumor cyst fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:RSS1; TRY1
A;Cross-references: GDB:119620; OMIM:276000
A;Cross-references: GDB:119620; OMIM:276000
A;Cross-references: GDB:119620; OMIM:276000
A;Map position: 7q35-7q35
A;Map position: 7q35-7q35
A;Mote: The human genome contains at least ten trypsin genes or pseudogenes, as C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancras; phosphoprotein; protein digestion; serine pro: F;1-15,Domain: signal sequence #status experimental <2YM>F;1-15,Domain: activation peptide #status experimental <APT>F;24-246/Product: trypsin I #status predicted <ENZ>F;24-246/Product: trypsin | Momology <TRX>F;24-246/Product: trypsin homology <TRX>F;30-160,48-64,139-206,171-185,196-220/Disulfide bonds: #status predicted F;30,107,200/Active site: His, Asp, Ser #status predicted F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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WIKN 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Tomita, N.; Izumoto, Y.; Horii, A.; Doi, S.; Yokouchi, H.; Ogawa, M.; Mori, T.; Matsub Biochem. Biophys. Res. Commun. 158, 569-575, 1989
A;Title: Molecular cloning and nucleotide sequence of human pancreatic prechymotrypsinog A;Reference number: A31299; MUID:89134264; PMID:2917002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trypsin (EC 3.4.21.4) I precursor [validated] - human N.Alternate names: trypsin, cationic; trypsinogen I C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) A25612; B61066; A43988 C; Accession: A25622; B61066; A43988 R; Emi, M.; Nakamura, Y.; Ogawa, M.; Yamamoto, T.; Nishide, T.; Mori, T.; Matsubara, K. A; Ellis, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Cario, Ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 AAHCGV----RTSDVVVAGEFDQGSDEENIQVLKIAKVFKNPKFSILTV---NNDITLLKL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 RSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLIS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                               chymotrypsin (EC 3.4.21.1) precursor - human
C;Species: Homo sapiens (man)
C;Date: 08-Jun.1989 #sequence_revision 08-Jun-1989 #text_change 22-Jun-1999
C;Accession: A31299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ATP----ARFSQTVSAVCLPSADDDFPAGILCATTGWGKTKYNANKTPDKIQQAALPLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 FOCGOKTLRPRF----KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Residues: 1-247 <EMI>
A;Residues: 1-247 <EMI>
A;Cross-references: GB/M22612; NID:9521215; PIDN:AAA61231.1; PID:9521216
R;Ximland, M.; Russick, C.; Marks, W.H.; Borgetroem, A.
Clin. Chim. Acta 184, 31-46, 1989
A;Title: Immunoreactive anionic and cationic trypsin in human serum.
A;Reference number: A61066; MUID:90091010; PMID:2598466
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A31299
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-263 <TOM>
A;Residues: 1-263 <TOM>
Cross-references: GB:M24400; NID:g181189; PIDN:AAA52128.1; PID:g181190
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.0%; Score 377; DB 2; Length 263; Best Local Similarity 33.2%; Pred. No. 2.8e-25; Matches 86; Conservative 46; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Cenes: GDB::CTRB
A; Crsp sosition: 16q23.1-16q23.1
C; Superfamily: trypsin; trypsin homology
C; Reywords: hydrolase; protein digestion; serine proteinase
F; 4-256/Domain: trypsin homology < TRX>
F; 75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 LKDKPGVYTRVSHFLPWIR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 STSSPGVYARVTKLIPWVQ 257
          WIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
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В
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GB:J00731; NID:g204019; PIDN:AAA98780.1; PID:g2 COOPHYYGSEVITIXALCAADPOWKIDSCOGDSGGPLVC-SLOGRWTLIGIVSWGR--GCA 246 CFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSK 129 CI---SNSRTYRVLLGRHSLSTSESGSLAVQVSKLVVHEKWNAQKLSNGNDIALVKLASP 132 130 EGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRE 189 | | :::||:: | | :::||: | | 17 CGYPTYEVQHDVSRVVGGQEASPNSWPWDVSL-QYLSSGKWHHTCGGSLVANNWVLTAAH 13 CGOKTLRPRF---KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATH / Match
24.8%; Score 374; DB 1; Length 271;
Local Similarity 33.5%; Pred. No. 5.3e-25;
les 87; Conservative 52; Mismatches 105; Indels 1 A;Residues: 1-271 <MAC>
A;Cross-references: GB:L00124; GB:J00731; NID:g204019; PIDN CS:Superfamily: trypsin, trypsin homology
C;Superfamily: trypsin, trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymoger
F;1-16/Domain: activation peptide #status predicted <AIG>
F;17-30/Domain: activation peptide #status predicted <APT>
F;31-271/Product: elastase II #status predicted <MPT>
F;31-264/Domain: trypsin homology <TRX>
F;75,123,218/Active Bite: His, Asp, Ser #status predicted 247 YPRKPSVFTRVSNYIDWINS 266 247 LKDKPGVYTRVSHFLPWIRS 82 20 94 190 188 g ઠ δ g 셤 ઠે 셤 ઢ Š g à ò ద C.Function:
A.Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variable solution of the graafian follicle; also activates the urckinase-type plasminogen act be the walls of the graafian follicle; also activates the urckinase-type plasminogen act be the walls of the graafian follicle; also activates the urckinase-type plasminogen act be also because the act of the graafian follicle; also activates the urckinase-type plasminogen act because the angiogenesis inhibitor; blood, duplication; fibrinolysis; glycoprotein; hydr Fil-19/Domain: plasminogen-related protein precursor homology closed angiogenesis inhibitor; blood, duplication; fibrinolysis; glycoprotein; hydr Fil-19/Domain: plasminogen #status predicted cand cand cand peptide #status predicted cand.
Fig. 9-45/Domain: activation peptide #status predicted cand.
Fig. 9-56/Domain: chain A #status predicted cand.
Fig. 9-51/Domain: kringle homology cand.
Fig. 9-51/Domain: kringle homology cand.
Fig. 9-51/Domain: kringle homology cand.
Fig. 9-51/Domain: chain B #status predicted cand.
Fig. 9-75/Domain: Molecule type: protein A, Residues: 22-37 <LIS-37 calis-37 cali pancreatic elastase II (EC 3.4.21.71) precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 18-Aug-1962 #sequence_revision 18-Aug-1982 #text_change 24-Sep-1999 C;Date: 18-Aug-1961 C;Accession: A00961 R;MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Rutte Biochemistry 21, 1453-1463, 1982 A;Title: Primary structure of two distinct rat pancreatic preproelastases determined by A;Reference number: A00960; MUID:82182967; PMID:6918221 A;Accession: A00961 622 127 673 724 SKEGRCAQPSRTIQTICLPSMYNDPQF----GTSCEITGFGKENSTDYLYPEQLKMTVVK 183 LISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGR 243 67 ---SRPATITDKVIPACLPS----PNYMVADRTICYITGWGETQGT--FGAGRLKEAQLP THCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR AHCLEKSSRPEFYKVILGAHEEYIRGLDVQEISVAKLILE-----PNNRDIALLKL-FOCGOKTLRPR----PKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISA Gaps 28; Query Match 24.9%; Score 375; DB 1; Length 812; Best Local Similarity 34.9%; Pred. No. 1.6e-24; Matches 91; Conservative 38; Mismatches 104; Indels GCARPNKPGVYVRVSRFVDWI 805 GCALKDKPGVYTRVSHFLPWI 264 1 999 68 623 184 RESULT 43 ELRT2 g g ò a 8 임 ò a ò ò

TYPSIN (EC 3.4.21.4) precursor, anionic - dog
TYPSIN (EC 3.4.21.4) precursor, anionic - dog
NyAlternate names: cationic trypsinogen
C;Becies: Canis lupus familiaris (dog)
C;Date: 30-Sep-1997 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A2673
R;Finsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length r :A Reference number: A26773; MUID:86284628; PMID:3841794
A;Reference number: A26773; MUID:86284628; PMID:3841794
A;Reference number: A26773; MUID:86284628; PMID:3841794
A;Residues: 1-247 <PIN>
A;Residues: 1-247 <PIN>
A;Residues: 1-247 <PIN>
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A;Residues: 1-247 <PIN>
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A;Residues: 1-247 <PIN>
A;Residues: 1-247 <PIN>
A;Residues: 1-247 <PIN>
A;Residues: 1-247 <PIN Display trypsin, poptide #status predicted <AND:
F;16-23/Domain: signal sequence #status predicted <AND:
F;24-247/Product: trypsin, anionic #status predicted <AND:
F;24-239/Domain: trypsin, anionic #status predicted <AND:
F;24-239/Domain: trypsin, anionic #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted VYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ 141 23 XIVGG-YTCEENSVPYQVSLNAGY-----HFCGGSLISDQWVVSAAHCY-----KSRIQ 70 142 TICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVT 201 23 KIIGGEFTTIENO-PWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDVI 27; DB 1; Length 247; Query Match

24.8%; Score 373.5; DB 1; Length 2
Best Local Similarity 38.0%; Pred. No. 5.3e-25;
Matches 93; Conservative 40; Mismatches 85; Indels g

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nerve growth factor a

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A, Introns: 16/1; 69/2; 165/1; 210/3
C, Superfamily: trypsin; trypsin homology
C, Superfamily: trypsin; trypsin homology
C, Superfamily: trypsin; trypsin homology
T, 1-18/Domain: signal sequence #status predicted <SIG>
F, 1-25.00main: signal sequence #status predicted <SIG>
F, 25-107/Domain: segment B1 <GB1>
F, 25-107/Domain: segment B1 <GB1>
F, 25-107/Domain: segment C <GCC>
F, 112-261/Domain: segment C <GCC>
F, 112-261/Domain: segment C <GCC>
F, 112-164/Domain: segment C <GCCO
F, 112-164/Domain: segment C <GCCO
F, 112-164/Domain: segment C <GCCO
F, 112-164/Domain: segment C <GCCO
F, 112-164/Domain: seg
                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Realdues: 1-261 cEVA>
A,Realdues: 1-261 cEVA>
B,VIlrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.:
DNA 3; 387-392, 1984
A,FILIE: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve
A,Reference number: A90949; WUID:85076169; PMID:6548955
A,Accession: A90949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residudes: 1.261 cULL.
A; Cross-references: GB:X01389; NID:g53373; PIDN:CAA25645.1; PID:g53374
A; Cross-references: GB:X01389; NID:g53373; PIDN:CAA25645.1; PID:g53374
R; Howles, P.N.; Dickinson, D.P.; Dicaprio, L.L.; Woodworth-Gutai, M.; Gross, K
Nucleic Acids Res. 12, 2791-2805, 1984
A; Title: Use of a CDNA recombinant for the gamma-subunit of mouse nerve growth
A; Ritle: Use of a CDNA recombinant for the gamma-subunit of mouse nerve growth
A; Reference number: A93510; MUID:84169573; PMID:6200835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 25-107,112-261 «THO>
A)Exerimental source: outbred strain Swiss Webster
C;Comment: 75 nerve growth factor is composed of two alpha chains, a beta dimes
C;Comment: The active form of the gamma chain occurs naturally as combinations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHH...----NDIALLKIRSKEGRC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 WIGKNNILFKDEPSAQHRFVSKAIPHPGFNMSLMRKHIRFLEXDYSNDLMLLRL----SKP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 KIIGGEFTTIENOPWFAALYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV 82
7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: As Dec. 1981 # #sequence_revision 17-May-1985 #text_change 18-Jun-1999
C; Accession: As1005; A90949; A33510; A92341; A00942; A21093; A22705
R; Evans, B.A.; Richards, R.I.
EMBO J. 4, 138-138, 1985
A; Title: Genes for the alpha and gamma subunits of mouse nerve growth factor A; Reference number: A91005; MUID:85257431; PMID:3848399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYYGSBVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGR-GCALKDKPG
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24.7%; Score 372; DB 1; Length 261;
Best Local Similarity 32.4%; Pred. No. 7.6e-25;
Matches 82; Conservative 48; Mismatches 91; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A93510
A;Molecule type: mRNA
A;Residues: 127-202, 'E',204-261 <HOW>
A;Residues: 127-202, 'E',204-261 <HOW>
A;Residues: 127-202, 'E',204-261 <HOWS
A;Cross-references: GB:X00472; NID:G54260; PIDN:CAA25154.1; PID:G54261
A;Experimental source: inbred strain DBA/2J
R;Thomas, K.A.; Baglan, N.C.; Bradehaw, R.A.
Biol. Chem. 256, 9156-9166, 1981 
A;Title: The amino acid sequence of the gamma-subunit of mouse submaxil
A;Title: The amino acid sequence of the gamma-subunit of mouse submaxil
                                                                                                                                                                                                                                                                                                                                  A; Accession: A91005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue kallikrein (EC 3.4.21.35) submandibular precursor - mouse
NiAlternate names: glandular kallikrein; kininogenin
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1088 Hesquence_revision 30-Jun-1991 #text_change 13-Nov-1998
C;Accession: A25606; S06661
R;van Leeuwen, B.H.; Evans, B.A.; Tregear, G.W.; Richards, R.I.
A;Title: Mouse glandular kallikrein genes. Identification, structure, and expression (A;Reference number: A25606; MuID:86168299; PMID:3007510
A;Accession: A25606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as Ala, CTC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-261 <VAN.>
A; Cross-references: GB:M13498
A; Experimental source: renal
A; Note: the authors translated the codon GTC for residue 57 as Ala, CTC for resi
B; Murakami, K; Tikigai, H.; Nagumo, N.; Tomita, M.; Shimamura, T.
FEBS Lett. 257, 400-402, 1989
A; Title: A cytocidal tissue Kallikrein isolated from mouse submandibular glands.
A; Reference number: S06660; MUID:90060365; PMID:2593286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 YLGRSRLNSNTOGEMKFEVENLILHKDYSADTLAHH------NDIALLKIRSKEGRC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 AQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQP 193
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                    202 TKWLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV
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24.8%; Score 373.5; DB 2; Length 261;
Best Local Similarity 33.8%; Pred. No. 5.7e-25;
Matches 88; Conservative 43; Mismatches 96; Indels 33
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NALecrate names: plasminogen

NAAlecrate names: plasminogen

Cipbecias: Bos primigenius tautus (cattle)

Cipbecias: Bos primigenius tautus (cattle)

Cipbecias: Bos primigenius tautus (cattle)

Cipbecias: Bos primigenius tautus (cattle)

Cipbecias: Bos primigenius tautus (cattle)

Cipbecias: Bos Bos 1997 # Heaquence revision 28-Apr-1995 #text_change 18-Jun-1999

Cipcession: 845046

Albertition: Cioning and Library May 1994

Alpecition: Cioning and Caracterizatin of the bovine plasminogen CDNA.

Alpecition: Cioning and Caracterizatin of the bovine plasminogen CDNA.

Alpeciale type: MRNA

Alpeciale type: MRNA

Alpeciale type: May 1994

Alpeciale type: Diposer, PW.; Danneggar-Muller, G.A.K.; Rosselet, S.J.; Kampfer J.; R.

Alpeciale type: Diposer, PW.; Danneggar-Muller, G.A.K.; Rosselet, S.J.; Kampfer J.; R.

Alpecale anno acid sequence of bovine plasminogen. Comparison with h. m pla

Alpecale anno acid sequence of bovine plasminogen. Comparison with h. m pla

Alpecale type: Diposen

Alpecale type: Diposen

Alpecale type: Diposen

Alpecale type: Diposen

Alpecale type: Diposen

Alpecale type: May 10-133-15, HV.; 517-554, LV.; 556-812 cach-

Alpecale type: Mail-1986 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 and 1980 an
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A;Description: dissolves the fibrin of blood clots; acts as a proteolytic fact;
ns the walls of the graafian follicle; also activates the urokinase-type plasm. nger.
A;Bathway: fibrinolysis
A;Bathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precurso come C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle
F;1-26/Domain: signal sequence #status precursor homology <PLPH>
F;27-812/Product: plasminogen-related protein precursor homology <PLPH>
F;27-812/Product: plasmin #status experimental <APP>
F;27-812/Product: plasmin #status experimental <APP>
F;10-188/Domain: plasmin chain A #status experimental <ACH>
F;10-188/Domain: kringle homology <KR1>
F;282-269/Domain: kringle homology <KR2>
F;282-355/Domain: kringle homology <KR4>
F;384-461/Domain: plasmin chain B #status experimental <BCH>
F;584-812/Domain: crypsin homology <KR3>
F;584-812/Domain: trypsin homology <KR3>
F;584-805/Domain: trypsin homology <KR3
bonds: #status predicted
P;315/Binding site: carbohydrate (Asn) (covalent) #status experimental
P;365/Binding site: carbohydrate (Ser) (covalent) #status experimental
P;624,667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                            240 RLGCNYYHKPSVFTRVSNYIDWINS
                                                                                                                                                                             244 --GCALKDKPGVYTRVSHFLPWIRS
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                                                                                                                                                                                                                                                                                                                                                                                                                               parcreatic elastase II (EC 3.4.21.71) A precursor - human c) parcreatic elastase II (EC 3.4.21.71) A precursor - human c) pancreatic elastase II (EC 3.4.21.71) A precursor - human c) Species: Homo sapiens (man) (c) Pate: 16-Aug-1988 #text_change 20-Jun-2000 (c) Pate: 16-Aug-1988 #text_change 20-Jun-2000 (c) Pate: 16-3.172, Pat/31; A24431, S34491 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) Pat/31.71 (c) 
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A;Rolecule type: mRNA
A;Rolecule type: mRNA
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A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Cossion: 1-268 < FLED
A;Cross-creferences: GB:M1631; NID:g182022; PIDN:AAA52374.1; PID:g182023
B;Chirasu, Y.; Yoshida, H.; Mateuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, T
J. Biochem. 102, 155-1563, 1997
A;Teference number: A41431; MUD:88198076; PMID:2834346
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: Tanslated the Codon GTG for residue 202 as Cys
B;Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C.
FEBS Lett. 261, 179-183, 1990
A;Title: Purther studies on the human pancreatic binary complexes involving procarboxypp
A;Rolecule number: S08253; MUD:90169111; PMID:2307232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 IDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSK-- 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVC-SLQGRMTLTGIVSWGR 243
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A, Rolecule type: protein
C, Ganetics:
C, Ganetics:
A, Gene: GDB:L124
A, Cross-references: GDB:119866, OMIM:130120
A, Map position: 12pter-12qter
C, Superfamily: trypsin, trypsin, homology
C, Koywords: hydrolase; pancreas; serine proteinase
F; 11-28/Domain: propeptide #status predicted <SIG>F; 11-28/Domain: propeptide #status predicted <PRO>F; 29-269/Product: pancreatic elastase IIA #status predicted <MAT>F; 29-262/Domain: trypsin homology <ARY>F; 73, 121, 216/Active site: His, Asp, Ser #status predicted
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24.7%; Score 372; DB 2; Length 269
Best Local Similarity 34.0%; Pred. No. 7.9e-25;
Matches 90; Conservative 46; Mismatches 101; Indels
                                                                                                                                                           VYTRVSHFLPWIR
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writtul coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human coagulation factor XIa (EC 3.4.21.27) precursor [validated] - human NiAlternate names: antihemophilic factor C; plasma thromboplastin antecedent C; Species: Howo spatiens (man) C; Date: 13-Aug-1986 #sequence revision 26-May-1994 #text_change 08-Dec-2000 C; Accession: A27431; A00920; Ā37940

R; Askala, R; Parvie, E. W; chung, D. W.
Biochemistry 26, 721-7228, 1987

A; Reference number: A27431; MUID:88107663; PMID:2827746

A; Residues: 1-625 48A>
A; Residues: 1-625 48A>
A; Residues: 1-625 48A>
A; Cross-references: GB:M18295

A; Note: the sequence shown follows the authors' translation
B; Phylkawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2444, 1986
A; Title: Amino acid sequence of human factor XI, a blood coagulation factor wil foun A; Reference number: A00920; MUID:86243360; PMID:3636155
A; Accession: A00920; MUID:86243360; PMID:3636155
A; Reference number: A00920; MUID:91152017; PMID:1998667
A; Molecule type: mRNA
A; Residues: 1-625 < PUIX A; Fullkawa, K.; Davie, E.W.
B; Accession: A00920
A; Molecule type: mRNA
A; Residues: 1-625 < PUIX A; Fullkawa, K.; Davie, E.W.
B; Accession: A00920
A; Molecule type: mRNA
A; Residues: 1-625 < PUIX A; Fullkawa, K.; Davie, E.W.
B; R; Mochullen, B.A.; Fullkawa, K.; Davie, E.W.
A; Title: Location of the disulfide bonds in human coagulation factor XI: the pp. sence A; Reference number: A37940; MUID:91152017; PMID:1998667
A; Title: Location of the disulfide bonds in human coagulation factor XI: the pp. A; Title: Location of the disulfide bonds in human coagulation factor XI: the pp. sence A; Reference number: A37940; MUID:91152017; PMID:1998667
A; Residues: 28-13;39-49; X: 51-85, X: 57-63;70-75, X: 777-79;107-109; X: 711-11: 32-7500-75, X: 777-79;107-109; X: 711-11: 32-7500-75, X: 777-79;107-109; X: 711-11: 32-7500-75, X: 777-79;107-109; V: 777-79;107-109; V: 777-79;107-109; V: 777-79;107-109; V: 777-79;107-109; V: 777-79;107-109; V: 777-79;107-109; V: 777-79;107-109; V: 777-79;
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A;Cross-references: GDB:119891; OMIM:264900
A;Map position: 4q35-4q35
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2;
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 ECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: trypsin; trypsin homology
C;Keywords: hydroleas; parctass; protein digestion; serine proteinase; zymoge
C;Keywords: hydroleas; parctass; protein experimental <2YM>
F;1.245/Product: chymotrypsinogen #status experimental <APT>
F;1.13,16-146,149-245/Product: alpha-chymotrypsin #status experimental <APT>
F;1-123,42-58,136-201,168-182,191-220/Disulfide bonds: #status experimental
F;57,102,195/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | :: | : | : | : | : : | | :: | CGVPAIQPVLSGLSRIVNGEEAVPGSWPWQVSLQDK----TGFHFCGGSLINENWVVTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 HCGV----TTSDVVVAGEFDQGSSSEXIQKLKIAKVFKNSKYNSLTI---NNDITLLKLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 CGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISAT
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                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                      24.6%; Score 371; DB 1; Length 245; 32.3%; Pred. No. 8.7e-25; ive 52; Mismatches 100; Indels 2
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223 STPGVYARVTALVNWVQ 239
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A/Accession: A901-245 <br/>
A/Accession: A901-245 <br/>
A/Accession: A901-245 <br/>
A/Accession: Birkhoft, J.J.; Hartley, B.S.<br/>
A/Accession: A913-340, 1969<br/>
A/Accession: Birkhoft, J.J.; Morava, V.; Morava, L.; Pursik, Z.; Vanacek, J.; Kell, B.; Sorm A/Accession: Blophys. Actallo; 543-56, 1966<br/>
A/Accession: Blophys. Actallo; J.S. 543-56, 1966<br/>
A/Accession: A93158<br/>
A/ACCESSION: A93159<br/>
A/ACCESSION: A041161, 201-208, 1993<br/>
A/ACCESSION: A05150<br/>
A/ACCESSION: A05
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                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NiAlternate names: chymotrypsinogen A
C;Species: Bos primigenius taurus (cattle)
C;Dacte: 07-May-1991 #sequence_revision 07-May-1991 #text_change 07-May-1999
C;Accession: A90235; A93158; $29650; A00952
R;Brown, J.R.; Hartley, B.S.
Biochem. J. 101, 214-228, 1966
A;Title: Location of disulphide bridges by diagonal paper electrophoresis. T
A;Reference number: A90235; MUID:67181721; PMID:5971783
                                                                                                                                                                                                                    181 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
                                                                                                                                                               5 PPEELKFQCGQKTLRPR---FKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISP
                                                                                                                                                                                                                                                                                                                      CWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDI
                                                                                             Gaps
        24.7%; Score 372; DB 1; Length 812; 35.2%; Pred. No. 2.9e-24; ive 34; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chymotrypsin (EC 3.4.21.1) A precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WGLGCARPNKFGVYVRVSPYVPWI 805
                                                                                         93; Conservative
                                                 Similarity
            Query Match
Best Local S:
Matches 93,
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C; Superfamily: coagulation factor XI; trypsin homology
C; Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro
C; Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-18/Domain: apple repeat <AP1>
F; 10-108/Domain: apple repeat <AP2>
F; 10-108/Domain: apple repeat <AP2>
F; 10-108/Domain: apple repeat <AP2>
F; 290-379/Domain: apple repeat <AP4>
F; 280-1379/Domain: apple repeat <AP4
F; 280-1379/Dislified bonds: interfact arbohydrate (Asn) (covalent) #status experimental
F; 431, 480, 575/Active site: Arg-II (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| | ::|| |:|| | |:|| 379 ECTTK-IKPR--IVGGTASVRGEWPWQVTLHTTSPTQRH------LCGGSIIGNQWILT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 ATHCF -- IDYPK-KEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIAL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 LKLET----TVNYTDSQRPICLPSKGDRNVIYTDCWVTGWGYRKLRDKI-QNTLQKAKIP 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 QCGQKTLRPRFKIIGGEFTTIENQPWFAAIY-----RRHRGGSVTYVCGGSLISPCWVIS 66
A;Description: catalyzes the proteolytic activation of coagulation factor IX A;Pathway: blood coagulation intrinsic pathway C;Superfamily: coagulation factor XI; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

24.6%; Score 370.5; DB 1; Length 6;
Best Local Similarity 33.5%; Pred. No. 2.9e-24;
Matches 89; Conservative 49; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAQRERPGVYTNVVEYVDWILEKTQ 623
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Job time : 17.9649 secs
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May 25, 2004, 14:43:40 ; Search time 10.6433 Seconds (without alignments) 1350.274 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
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Title:
Perfect score: 1508
Sequence: 1 KPSSPPEELKFQCGQKTLRP......VSHFLPWIRSHTKEENGLAL 276
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	מן מ		UROK HUMAN P00749	UROK_PAPCY	UROK_PIG P04185	UROK_BOVIN Q05589	UROK_RAT	UROK_MOUSE P06869	UROK_CHICK P15120	TPA HUMAN	TPA_RAT P19637	TPA_BOVIN Q28198 bos	TPA_MOUSE P11214	URTB_DESRO	DESRO	URT2_DESRO	URT1_DESRO	Q9r098 mus r	P00748 homo	Q04756 homo	FA12 CAVPO Q04962 cavi	FA12_BOVIN P98140	1 NETR_HUMAN P56730 homo sapien	NETR_MOUSE 008762 mus m	HATT_HUMAN O60235 homo	Q16651 homo	KAL_MOUSE P26262 mus r	TMS6_MOUSE	KLKD HUMAN Q9ukr3 homo	TMS6_HUMAN Q8iu80 homo	HEPS_MOUSE 035453 mus m	KAL HUMAN	TMS5 MOUSE	HEPS HUMAN
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ALIGNMENTS

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MEDITALE 9737920; PubMed=9194591;

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-!- FUNCTION: Potent plasminogen activator and is clinically used for
therapy of thrombolytic disorders.

-!- FUNCTION: Potent plasminogen activator and is clinically used for
--- CARTALTITE Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.

-!- SUBUNIT: Found in high and low molecular mass forms. Each consists
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MEDLINE=9721851; PubMed=9065988;
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EMBL; X02419; CAA26268.1; ...

EMBL; X02419; CAA26268.1; ...

EMBL; X02760; CAA2623.1; ...

EMBL; X0226; AA461382.1; ...

EMBL; X0226; AA461382.1; ...

EMBL; X0226; AA461382.1; ...

EMBL; X0226; AA461382.1; ...

EMBL; X0226; AA461390.1; ...

EMBL; A1837; CAA01559.1; ...

EMBL; A1837; CAA01559.1; ...

EMBL; A00931; UMHU.

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of two chains, A and B. The high molecular mass form contains a long chain A. Cleavage occurs after residue 155 in the low molecular mass form to yield a short Al chain.

-!- PHARMACEUTICAL: Available under the name Abbokinase (Abbott). Used in Pulmonary Embolism (PE) to initiates fibrinolysis.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 BGF-like domain.
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01-APR-1990 (Rel. 14, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
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99.6%; Pred. No. 9e-129;
iive 1; Mismatches 0;
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                                                                                                                                                                                                                                   PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
                                                                                                                                                                                                                                                                                                     121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQ---FGTSCEITGFGKENSTDYLYPEQL 177
                                                                                                                                                                                                                                                                                                                                                                                               335 KMIVVIKLVSHQKCQQPHYYGSEVTTKMLCAADPQWETDSCQGDSGGPLVCSIQGHMTLIG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Kidney;
MEDLINE=85087954; PubMed=6096832;
Nagamine Y., Pearson D., Altus M.S., Reich E.;
Nagamine Y., Pearson D., Altus M.S., Reich E.;
Nagamine Y., Pearson D., Altus B.S.,
Nagamine Y., Pearson D., Altus B.S.,
Nucleic Acids Res. 12:9525-9541(1984).
                                                                                                                                                                                                                                                                                                                                                                            178 KMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTG
                                                                                                                                                                               155 KPSSPPBELQFQCGQRTLRPRFKIVGGEFTTIENQPWFAAIYRRHRGGSUTYVCGGSLIS
                                                                                                                                                                                                                                                                                                                         275 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPNPPFGTSCEITGFGKENSTDYLYPEQL
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                                                                                                                                                            1 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRHRGGSVTYVCGGSLIS
                                                                                                                          Gaps
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P041E5;
P041E5;
13-0MR-1987 (Rel. 04, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . .) (BY SIMILARITY)
816D12DFEDDC8792 CRC64;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NOSI_TaxID=9823,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISION TO 241.

Nagamine Y.;

Nagamine Y.;

Submitted (DEC-1986) to the PIR data bank.

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-!- SIMILARITY: Belongs to peptidase family 81.

-!- SIMILARITY: Contains 1 EGF-like domain.

-!- SIMILARITY: Contains 1 kringle domain.
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                                                                                       DB 1; Length 433;
                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 IVSWGRGCALKDKPGVYTRVSRFLPWIHSHTREQNGLAL 433
                                                                                                        .2e-122;
                                                                                   'Match 95.1%; Score 1434.5; Local Similarity 92.8%; Pred. No. 2.2e es 259; Conservative 13; Mismatches
                                                     48595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X01648; CAA25806.1; -. EMBL; X02724; CAA26511.1; -. PIR; A00932; UKPG. HSSP; P00749; IKDU.
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324 3
433 AA;
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ACT_SITE
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 ALLKIRTDKGOCAQPSKSIQTICLPPVNGDAHFGASCEIVGFGKBDPSDYLYPBQLKMTV
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                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (RC 3.4.21.73) (uPA)
(U-plasminogen activator).
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WM; 4DE1BBD4DA47027A CRC64;
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS001014; TRYPSIN_HIS; 1.
PROSITE; PS001015; TRYPSIN_SE; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-like domain; Signal; Zymogen.
1 20
CHAIN 21 433 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                           h Similarity 76.4%; Pred. No. 4.7e-100; Similarity 76.4%; Pred. No. 4.7e-100; Conservative 32; Mismatches 33; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Fischer 344;
MEDLINE=92233409; PubMed=1568219;
Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
Kefford R.F.;
                                                                            CHAIN A (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 GRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                      48730 MW;
                                                                                                                                                                                                                                                                                                                                                   Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UROK RAT
P29598;
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DISULFID
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CONFLICT
SEQUENCE
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Best Local 8
                                                                                                                                                                                                                      DISULFID
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UROK RAT
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Transcriptional and pestranscriptional activation of urchinase

Plasminogen activator gene expression in metastatic tumor cells.",

Calcor Res. 22:2489-2496(1992).

E. Calcor Res. 22:2489-2496(1992).

E. Calcor Res. 22:2489-2496(1992).

E. Calcor Res. 22:2489-2496(1992).

E. Calcor Res. 26:2489-2496(1992).

E. Calcor Res. 26:2489-2498.

E. Calcor Res. 26:2489-2498.

E. Calcor Res. 27:2489-2498.

E. Calcor Res. 27:2489-2498.

E. Calcor Res. 26:2489-2498.

E. Calcor Res. 27:2489-2498.

E. Calcor Res. 27:2489-2499.

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215
 DIALLKIRSKEGRCAOPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKM 179
 TVVKLISHRECQQPHYYGSEVTTKALCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIV 239
 5
 SPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHN
 1 KPSSPPEELKFOCGOXTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGS-VTYVCGGSLI
 Gaps
 01-07N-1988 (Rel. 06, Created)
01-07N-1988 (Rel. 06, Last sequence update)
01-07N-1988 (Rel. 41, Last annotation update)
UzekrBe-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 SEQUENCE FROM N.A.
MEDILINE=85179474; PubMed=2985383;
MEDILINE=81187474; PubMed=2985383;
MEDILINE=8118747; PubMed=2985383;
Reich E., Kocher H.P., Duvoisin R.M.;
Reich E., Kocher H.P., Duvoisin R.M.;
"Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase-type plasminogen activator.";

Eur. J. Biochem. 148:225-232(1985).
 11,
 DB 1; Length 432;
 39; Indels
362 BY SIMILARITY.
401 BY SIMILARITY.
225 CHARGE RELAY SYSTEM.
276 CHARGE RELAY SYSTEM.
377 CHARGE RELAY SYSTEM.
16 N -> H (IN REF. 2).
24 G (IN REF. 2).
332 D -> N (IN REF. 2).
34 47957 MM, 4BB1B96C716244C8 CRC64;
 240 SWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA 275
 SWGSGCAEKNKPGVYTRVSYFLNWIQSHIGEENGLA 431
 74.2%; Score 1119.5; DB 71.4%; Pred. No. 7.5e-94 cive 39; Mismatches 3:
 Matches 197; Conservative
 STANDARD;
 346
373
273
276
276
377
16
28
332
432 AA;
 SEQUENCE FROM N.A.
 Similarity
 UROK MOUSE
P06869;
 DISULFID
DISULFID
ACT SITE
ACT SITE
ACT SITE
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 120
 9
 180
 Query Match
 Local
 RESULT 6
UROK MOUSE
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 DIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKM 179
 217 SPCWVASAAHCFIQLPKKENYVVYLGQSKESSYNPGEMKFEVEQLILHEYYREDSLAYHN 276
 01-APR-1990 (Rel. 14, Last sequence update)
28-PRB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (BC 3.4.21.73) (uPA)
(U-plasminogen activator).
(Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianiae;
 P SEQUENCE FROM N.A.

MEDLINE=90110185; PubMed=2295632;

AA Leslie N.D., Kessler C.A., Bell S.M., Degen J.L.;

RT "The chicken urokinase-type plasminogen activator gene.";

RI "The chicken urokinase-type plasminogen activator gene.";

RI "The chicken urokinase-type plasminogen activator gene.";

RI "The chicken urokinase-type plasminogen of Arg-|-Val bond in glasminogen to form plasmin.

CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

CC -!- SIMILARITY: Contains 1 EGF-like domain.

CC -!- SIMILARITY: Contains 1 kringle domain.

CC -!- SIMILARITY: Contains 1 kringle domain.

CC -!- SIMILARITY: Contains 1 kringle domain.

CC -!- SIMILARITY: Contains 1 kringle domain.

CC -!- SIMILARITY: Contains 1 kringle domain.
 SWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA 275
 397 SWGRGCAEKUKPGVYTRVSHFLDWIQSHIGEEKGLA 432
 434 AA
 FERM; PP000E1; Kringle; 1.

Pfam; PP000E1; Kringle; 1.

Pfam; PP000E9; trypsin; 1.

PRINF; PRSPO0144; Urk plasm_act; 1.

PRINTS; PR00018; KRINGLE.

PRODOM; PD000195; Kringle; 1.

SMART; SM00181; EGP; 1.

SMART; SM00181; EGP; 1.

SMART; SM00181; EGP; 1.

PROSITE; PS01186; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.
 InterPro; IRR009003; Cys Ser trypsin.
InterPro; IRR006210; EGF_like.
InterPro; IRR006210; IRGF.
InterPro; IRR008203; Pept SIA uPA.
InterPro; IRR008203; Pept Idase_SI.
InterPro; IRR001254; PeptIdase_SI.
 01-APR-1990 (Rel. 14, Created)
 EMBL; JOS187; AAA49131.1; -.
EMBL; JOS188; AAA49130.1; -.
PIR; A35005; A35005.
HSSP; P00763; 1DPO.
MEROPS; S01.231; -.
 STANDARD;
 Gallus.
NCBI_TaxID=9031;
 CHICK
 120
 277
 240
 RESULT 7
UROK CHICK
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstands. Liberther the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 216
 60 SPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHN 119
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VTYVCGGSLI 59
 1; Gaps
 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A (BY SIMILARITY).
SHORT A CHAIN (A1).
CHAIN B (BY SIMILARITY).
 73.8%; Score 1112.5; DB 1; Length 433; 71.0%; Pred. No. 3.2e-93; cive 39; Mismatches 40; Indels 1;
 KRINGLE.
CONNECTING PEPTIDE.
SERING PROFIDE.
SERING PROFIDE.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
 A99C35F6250443F9 CRC64;
 EGF-LIKE.
 48268 MW;
 EMBL, X02389; CAA26211.1; ---
EMBL, MI7922; AAA40539.1; ---
PIR; A29420; UKWB.
HSSP, P00749; IKUU.
MEROPS; S01.231; ---
 Best Local Similarity 71.0%
Matches 196; Conservative
 433 AA;
 ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
 CHAIN
CHAIN
CHAIN
CHAIN
DOMAIN
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Tue May

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SEQUENCE FROM N.A. (ISOFORM SHORT).
 mouse cells using BPV vectors.";
DNA 6:461-472(1987).
 structural domains.
 QUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Haiung N.;
 209
 269
 177
 237
 330 MSATVNLISODDCKNKYYDSTRVTDNNVCAGDPLWETDACKGDSGGPMVCEHNGRMTLYG 389
 CWVISATHCFID----YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAH 117
 61
 178 KMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTG
 CWVLTAAHCFYNPTKKQPNKSVYKVFLGKSILNTNDEHEQVFMVDEIISHPDFTDHTGGN
 270 DNDIALIRIRTASGQCAVESNYVRTVCLPEKNLNLYDNTWCEIAGYGKQNSYDIYYAQRL
 118 HNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQL
 PSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISP
 Gaps
 COUNCIL IN STATE STATE SERVING PROTESSE.

BY SIMILARITY.

CHARGE RELAY SYSTEM (BY SIMILARITY).

 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
No.N. TaxID=9606;
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS502440; TRYPSIN_BOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
20 POTENTIAL.
 UROKINASE-TYPE PLASMINOGEN ACTIVATOR
 TPA HUMAN STANDARD; PRT; 562 AA.
P00750; Q15103;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 03, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
(L-Plasminogen activator) (Alteplase) (Reteplase).
PLAT.
 'n
 45.7%; Score 688.5; DB 1; Length 434;
llarity 47.4%; Pred. No. 8.2e-55;
Conservative 48; Mismatches 89; Indels 5;
 49400 MW; BD881048DD666A55 CRC64;
 CHAIN A (BY SIMILARITY)
CHAIN B (BY SIMILARITY)
 KRINGLE.
CONNECTING PEPTIDE.
 390 IVSWGDGCAKKNKPGVYTRVTRYLNWIDSN 419
 IVSWGRGCALKDKPGVYTRVSHFLPWIRSH 267
 EGF-LIKE
 SEQUENCE FROM N.A.
TISSUE-Melanoma;
MEDLINE-83115262; PubMed-6337343;
 210
310
342
369
217
272
372
373
434 AA;
 Similarity
 Best Local Simi
Matches 128;
 DISULFID
DISULFID
DISULFID
DISULFID
 ACT_SITE
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ACT_SITE
CARBOHYD
 238
 DOMAIN
DISULFID
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 62
 210
 Query Match
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 RESULT 8
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WEDLINE=2238857; PubMed=12477932;

REDLINE=2238857; PubMed=12477932;

REDLINE=2238857; PubMed=12477932;

REDLINE=2238857; PubMed=12477932;

RALGEBER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Blat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Diatchenko L., Marusian K.H., Rubin G.M., Hong L.,

A Diatchenko L., Marusian K.J., Maley J.J., Scheefer T.E.,

Brownstein M.J. Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nilalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rahiting W., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., SEQUENCE FROM N.A. MEDLINE-88054470; PubMed-2824147; Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J., TISSUE=Umbilical vein;
MEDLINE=90192129; PubMed=2107528;
Siebbert P.D., Fong K.;
"Variant tissue-type lassminogen activator (FLAT) cDNA obtained from human endothelial cells.";
Numan endothelial cells.";
Nucleic Acids Res. 18:1086-1086 (1990). MEDIINE-86284200; PubMed=3090401;
Harris T.J., Patel T., Marston F.A., Little S., Emtage J.S.;
Copdenakker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
"Cloning of CDNA coding for human tissue-type plasminogen activator and its expression in Escherichia coll.";
Mol. Biol. Med. 3:279-292(1986). Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A., Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L., Goeddal D.V., Collen D.; "Cloning and expression of human tissue-type plasminogen activator CDNA in E. coli."; "Asture 301:214-221(1983). SEQUENCE FROM N.A.
MEDLINE=84291137; PubMed=6089198;
MPDLINE=84291137; PubMed=6089198;
MPT., Elgh F., Lund B.;
"The structure of the human tissue-type plasminogen activator gene: correlation of intron and exon structures to functional and TISSUE=Petal lung;
MEDLINE=88265579; PubMed=3133640;
Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
"Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fetal lung cells.";
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MEDLINE=86196143; PubMed=3009482;
Priezner Degen S.J., Rajput B., Reich E.;
"The human tissue plasminogen activator gene.";
J. Biol. Chem. 261:6972-6985(1986).

'Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA seguences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

plasminogen activator.

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Josephson

STRUCTURE BY NMR OF KRINGLE 2.
MEDLINE-90122799; PubMed=2558718;
Byeon I.-J., Kelley R.F., Llinas M.;
"IH NMR structural characterization of a recombinant kringle 2 domain from human tissue-type plasminogen activator.";
Biochemistry 28:9350-9360(1989). 359 FQERPPPHHLTVILGRIYRVVPGEBEGKFEVEKYIVHKEFDDDT--YDNDIALLQLKSDS ||||| | ::|:||| 417 SRCAQESSVVRIVCLPPADLQLPDWTECELSGYGKHRALSPFYSERLKRAHVRLYPSSRC 13 CG-QXTLRPRFKIIGGEFTTIENOPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHC 71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKE GRCAOPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREC X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN. MEDLINE=97449126; PubMed=9305622; Renatus M., Engh R.A., Stubbs M.I., Huber R., Fischer S., Kohnert U., MEDINE=92106329; PubMed=1762144; Byeon I.-J.L., Llinas M.; "Solution structure of the tissue-type plasminogen activator kringle 2 domain complexed to 6-aminohexanoic acid an antifibrinolytic 10; Gaps of tPA: X-ray 1H-NMR Ā X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2. MEDLINES 292118803; PubMed=1310033; MEDLINES 292118803; PubMed=1310033; Med Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Tulinskly A. Westbrook M.L., Kossiakof A.A.; Westbrook M.L., Kossiakof A.A.; Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4-A resolution."; Biochemistry 31:270-279(1992). MEDLINE=91200042; PubMed=1901789;
Byeon I.-J.L., Kelley R.F., Llinas M.;
"Kringle-2 domain of the tiseue-type plasminogen activator...
sasignments and secondary structure.";
Eur. J. Biochem. 197:155-165(1991). Length 562; 38.7%; Score 583; DB 1; Length 562 44.9%; Pred. No. 4.1e-45; tive 39; Mismatches 97; Indels "Lysine 156 promotes the anomalous proenzyme activity crystal structure of single-chain human tPA."; EMBO J. 16:4797-4805(1997). Mol. Biol. 222:1035-1051(1991). STRUCTURE BY NMR OF KRINGLE 2. STRUCTURE BY NMR OF KRINGLE Best Local Similarity 44.9 Matches 119; Conservative Query Match drug ઠ 셤 셤 ઠ

SEQUENCE OF 36-562.

RESULT 9 ઠ ሯ TISSUE-Melanoma;
MEDINDE-BSGOOG468;
PubMed=6433976;
MININDE-BSGOOG468;
Pobl G., Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.;
Tissue plasminogen activator: peptide analyses confirm an indirectly derived amino acid sequence, identify the active site serine residue, establish glycosylation sites, and localize variant differences.";
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MEDLINE-91291340; PubMed-1368681;
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
"Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
Agric. Biol. Chem. 55:1225-1232(1991). Schleuning W.-D.;
"Isolation and characterization of the human tissue-type plasminogen activator structural gene including its 5' flanking region.";
J. Biol. Chem. 260:11223-11230(1985). X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
MEDLINE=86200985; Pubmed=86119982;
Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
Bode W.;
The 2.3 A crystal structure of the catalytic domain of recombinant
two-chain human tissue-type plasminogen activator.";
J. Mol. Biol. 258:117-135(1996). MEDLINE-83209620; PubMed-6682760; Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.; "Purification and characterization of a melanowa cell plasminogen t C MEDLINE-91244765; Pubmed-164536; Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.; Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.; Distriction parting of the recombinant kringle-2 domain of tissue plasminogen activator produced in Escherichia coli."; Jaiol. Chem. 266:10070-10072(1991). (15)
CARBOHYDRATE-LINKAGE SITE THR-96.
MEDLINE-9159408; Pubmed=1900431;
Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
"Itsene plasminogen activator has an O-linked fucose attached threonine-61 in the epidermal growth factor domain.";
Blochemistry 30:2311-2314(1991). Isolation of cDNA sequences coding for a part of human tissue STRUCTURE OF CAREOHYDRATES.
MEDLINE=90092112; PubMed=2513186;
Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
"Carbohydrate structure of recombinant human uterine tissue plasminogen activator expressed in mouse epithelial cells.";
Eur. J. Blochem. 186:273-286(1989). SEQUENCE OF 212-361 FROM N.A. MEDLINE-83169656; PubMed=6572897; Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren SEQUENCE OF 1-36 FROM N.A.
BIDILINES 82289338; PubMed=3161893;
Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
Schleuning W.-D.; ). | Natalinogen activator:"; | Natalinogen Acad. Sci. U.S.A. 80:349-352(1983). J. Biochem. 132:681-686(1983). SEQUENCE OF 33-52 AND 311-330. DISULFIDE BONDS IN KRINGLE 2

TISSUE=Melanoma;

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activator

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191 QQPHYYGSEVTTXALCAAD-----PQWKT-DSCQGDSGGPLVCSLQGRATLTGIVSWGRG

477 TSQHLIARTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRWTLVGIISWGLG

CGOKDVPGVYTKVTNYLDWIRDNMR 561 245 CALKDKPGVYTRVSHFLPWIRSHTK 269

TPA\_RAT P19637; TPA RAT

1D TPA

AC P19

DT 01DT 01DT 10DT 10DB Ti8

559 AA

01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (t-PA)
(t-PA) (t-plasminogen activator).

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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=90130448; PubMed=2105315;

MEDLINE=90130448; PubMed=2105315;

The structure of the TATA-less rat tissue-type plasminogen activator gene. Species specific sequence divergences in the promoter predict differences in regulation of gene expression.";

J. Biol. Chem. 265:2022-2027(1990).

J. Biol. Chem. 265:2022-2027(1990).

L. FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important controlling plasmin-mediated proteolysis, it plays an important controlling plasminogen single Arg-val bond in magration and many other physiopathological events.

CC -:- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in CC -:- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
 -!- SUBCELULLAR LOCATION: Secreted, extracellular.
-!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG.-108 CATALYZED BY PLASHIN, TISSUE KALLIKERIN OR FACTOR XA.
-!- MISCELLANEOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 Eibronectin type I domain.
-!- SIMILARITY: Contains 2 kringle domains.
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 SECTION N.A.
MEDLINE=89170114; PubMed=3148445;
NY T., Leonardsson G., Heneh A.J.W.;
Cloning and characterization of a cDNA for rat tissue-type plasminogen activator.";
 Cys Ser trypsin.
EGF_like.
Fibrnctn1.
IEGF.
 EMBL; M21697; AAA41812 11; EMBL; M31197; AAA42261.1; OINED EMBL; M311897; AAA42261.1; OINED EMBL; M311897; AAA42261.1; OINED EMBL; M311897; AAA42261.1; OINED EMBL; M311897; AAA42261.1; OINED EMBL; M311997; EMPROGESO; EGF like. InterPro; IPROGGSO9; EGF like. InterPro; IPROGGSO9; EGF like. InterPro; IPROGGSO9; EGF. IME. InterPro; IPROGGSO9; EGF.
 Kringle.
Peptidase S1.
Peptidase_S1A.
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71 FIDYPKKEDYIVYLGRSRLNSNTOGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
 131 GRCAQPERTIQTICLPSMYNDPQF----GTSCEITGFGKENSTDYLYPEQLKMTVVKLIS 186
 13 CGOXTLR-PRFKIIGGEFTTIENOPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHC
 Pfam; PF00008; EGF; 1.

Pfam; PF00008; EGF; 1.

Pfam; PF00018; Kingle; 2.

Pfam; PF00018; Kingle; 2.

PRINTS; PR0018; Kingle; 2.

PRINTS; PR0018; Kingle; 2.

PRODOM; PR0018; Kingle; 2.

PROSTE; SM0018; EGF; 1.

PROSTE; PS00020; EGF 2; 1.

PROSTE; PS00022; EGF 2; 1.

PROSTE; PS00022; EGF 2; 1.

PROSTE; PS00021; EGF 2; 1.

PROSTE; PS00021; EGF 2; 1.

PROSTE; PS00021; EGF 2; 1.

PROSTE; PS00021; FIREOMECTIN 1; 1.

PROSTE; PS00018; FIREOMECTIN 1; 1.

PROSTE; PS00018; FIREOMECTIN 1; 1.

PROSTE; PS00135; FIREOMECTIN 1; 1.

PROSTE; PS00135; TRYPSIN HIS; 1.

PROSTE; PS00135; TRYPSIN HIS; 1.

PROSTE; PS00135; TRYPSIN HIS; 1.

PROSTE; PS00135; TRYPSIN HIS; 1.

PROSTE; PS00135; TRYPSIN HIS; 1.

PROSTE; PS00135; TRYPSIN SER; 1.

PROSTE; PS00135; TRYPSIN SER; 1.

PROPER 1: PS00135; TRYPSIN SER; 1.

PROPER 2: TISSUE-TYPE PLASMINOGEN ACTIVATOR.

THEAN 30 SS9 TISSUE-TYPE PLASMINOGEN ACTIVATOR.

THEAN
 Query Match

37.8%; Score 570.5; DB 1; Length 559;

Best Local Similarity 42.4%; Pred. No. 5.5e-44;

Matches 114; Conservative 47; Mismatches 91; Indels 17; Gaps
 TISSUE-TYPE PLASMINOGEN ACTIVATOR A CHAIN.
TISSUE-TYPE PLASMINOGEN ACTIVATOR B CHAIN.
TISSUE-TYPE PLASMINOGEN ACTIVATOR B CHAIN.
FIBRONECTIN TYPE-I.
EGF-LIKE.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
 241
 530
415 SQCAQESSSVGTACLP----DPDVQLPDWTECELSGYGKHEASSPFFSDRLKEAHVRLYP 470
 TISSUE=Kidney;
Ravn P., Berglund L., Petersen T.E.;
"Cloning and characterization of the bovine plasminogen activators upA and tpA."; and characterization of the bovine plasminogen activators upA and tpA."; close 17(1995).

Int. Dalry J. 5:605-617(1995).

To plasmin by hydrolyzing a single Arg-Val bond in plasminogen remodelating and degradation, in cell migration and many other physiopathological events.

Int. Dalry Marcol Activity: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

Int. Subunit: Heterodimer of chain A and chain B held by a disulfide
 BONG.
SUBCELLUIAR LOCATION: Secreted, extracellular.
SUBCELLUIAR LOCATION: Secreted, extracellular.
FINSTER SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-314 CATALYZED BY FLASMIN, TISSUE KALLIKKEIN OR FACTOR XA.
MISCELLANBOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
SIMILARITY: Belongs to peptidase family $1.
SIMILARITY: Contains I EGF-like domain.
SIMILARITY: Contains I fibronectin type I domain.
SIMILARITY: Contains 2 kringle domains.
 HRECOOPHYYGSEVITIMICAADP----QWKIDSCOGDSGGPLYCSLOGRMILIGIVSW
 TPA BOVIN STANDARD, PRT, 566 AA. 028198, 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 15-MAR-2014 (Rel. 43, Last annotation update) 15-MAR-2014 (Rel. 43, Last annotation update) 15-MAR-2014 (Rel. 43, Last annotation update) 15-MAR-2014 (Rel. 43, Last annotation update) 15-MAR-2014 (Rel. 43, Last annotation update) 15-MAR-2014 (Rel. 43, Last annotation) 15-MAR-2014 (Rel
 EMBL; X65800; CAA59795.1; -. HSSP; P00750; IRTF. MEROPS; S01.222; -. InterPro; IPR009003; Cys_Ser_trypsin. InterPro; IPR006209; EGF_like. InterPro; IPR006209; EGF_like. InterPro; IPR006210; IEGF. InterPro; IPR001254; Peptidase_S1. InterPro; IPR001254; Peptidase_S1. Pfam; PF00039; EGF; 1. Pfam; PF00039; EGF; 1.
 Bos taurus (Bovine).
 SEQUENCE FROM N.A.
 187
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 RESULT 10
TPA_BOVIN
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362
 130
 420
 QQPHYYGSEVTTKMLCAADPQW-----KTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRG 244
 71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE
 13 CG-QKTLRPRFKIIGGEFTTIENQPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHC
 131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKOTTVVKLISHREC
Gaps
 FIGURE 1.

KRINGLE 1.

KRINGLE 1.

KRINGLE 2.

KRINGLE 2.

KRINGLE 2.

KRINGLE 2.

KRINGLE 3.

KRINGLE
 Ouery Match
37.5%; Score 565; DB 1; Length 566;
Best Local Similarity 43.4%; Pred. No. 1.8e-43;
Matches 115; Conservative 41; Mismatches 99; Indels 10;
 FIBRONECTIN TYPE-I.
 40 82 FIII RGG 219 300 KR2 219 300 KR2 315 566 SEE 317 CH4 410
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RC TISSUE-Mammary gland;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeeberg B. B., Buetow K.H., Schemen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bark N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Habeh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Habeh F.,

RA Bopatchenck L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brachenck L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brakesley M., Dedin T.B., Toofilyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulky S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Hold D. K., Munny D.M., Sodergren B.J., Lu X., Glibs R.A.,

RA Hothig M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hakesley R.M., Touchaan M., Machan A., Rodrigues S., Sanchez A.,

RA Hothig M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.M., Touchaan M., Green B.D., Dickson M.C.,

RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RY Generation by hydrolyzing a single Arg-Val bond in plasminogen to Dlasmin by hydrolyzing a single Arg-Val bond in migration and controlling plasminediated proteolysie, it plays an important role in tissue remodeling and degradation, in cell migration and plasminogen to Carlarytic Activity: Specific cleavage of Arg-|-Val bond in plasminogen to Carlarytic Activity: Specific cleavage of Arg-|-Val bond in plasminogen because the control beautile of C. -- Carlarytic Activity: Specific cleavage of Arg-|-Val bond in plasminogen beautile beautil
481 TSQHLFNRTVTNNMLCAGDTRSGGDHTNLHDACQGDSGGPLVCMKDNHMTLVGIISWGLG·540
 -!- SUBCELLULAR LOCATION: Secreted; extracellular.
-!- FUR: THE SINGLE CHAIN, ALMOST FULLY ACTIVE BIXEME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE PORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-!- MISCELLANDOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
-!- SIMILARITY: Conteains 1 EgF-like domain.
-!- SIMILARITY: Conteains 1 EdF-like domain.
-!- SIMILARITY: Conteains 2 kringle domains.
 SEQUENCE FROM N.A.

MEDLINE-BROBG7303; PubMed=2826484;

Rickles R.J., Darrow A.L., Strickland S.;

"Molecular cloning of complementary DNA to mouse tissue plasminogen
"Molecular cloning of semplementary DNA to mouse tissue plasminogen
activator mRNA and its expression during F9 teratocarcinoma cell
differentiation.";
J. Biol. Chem. 263:1563-1569(1988).
 Mus musculus (Mouse).
Eukaryota, Mecazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 | TPA_MOUSE | STANDARD; | PRT; | 559 AA. |
| 1011214; | Q91VP2; | Q91VP2; | Q91VP2; | G91VP2; |
 CALKDKPGVYTRVSHFLPWIRSHTK 269
 541 CGRKDVPGVYTKVINYLDWIRDNTR 565
 245
 RESULT 11
TPA_MOUSE
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 297 CGLRQYKRPQFRIKGGLYTDITSHPWQAPIFVKNKRSPGERFLCGGVLISSCWVLSAAHC 356
 414
 241
 GRCAQPSRTIQTICLPSMYNDPQF----GTSCEITGFGKENSTDYLYPEQLKMTVVKLIS 186
 70
 FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Probable potent thrombolytic
 71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE
 FLERFPPNHLKVVLGRIYRVVPGEEEQTFEIEKYIVHEEFDDDT--YDNDIALLQLRSQS
 HRECQQPHYYGSEVTTKMLCAADP----QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSW
 471 SSRCTSQHLFNKTVTNNMLCAGDTRSGGNQDLHDACQGDSGGPLVCMINKQMTLTGIISW
 CG-OKTLRPRFKIIGGEFTTIENQPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHC
 Gaps
 "Plasminogen activators from the saliva of Desmodus rotundus (common vample bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403[1922].
--- FUNCTION: Probably essential to support the feeding habits of thi
 URTB DESRO STANDAKU;
P98121;
01-FBS-1996 (Rel. 33, Created)
01-FBS-1996 (Rel. 33, Last sequence update)
01-FBS-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
 SEQUENCE FROM N.A.

MEDLINE-9213/92, PubMed=1937019;

Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;

The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";

Gene 105:229-237(1991).
 37.4%; Score 564.5; DB 1; Length 559;
42.4%; Pred. No. 1.9e-43;
ive 47; Mismatches 91; Indels 17;
 (POTENTIAL) (POTENTIAL)
 CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
SUBUNIT: Monomer.
 CHARACTERIZATION.
MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 8CCEE2BDB94514D9 CRC64;
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (1
G -> A (IN REF. 1)
P -> A (IN REF. 1)
 SIMILARITY: Belongs to peptidase family S1
 GRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
 63122 MW;
 Matches 114; Conservative
 442
474
506
149
481
260
325
559 AA;
 Similarity
 NCBI_TaxID=9430;
 Donner P.;
 DISULFID
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
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 CWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 4 SPPEELKFOCG-OKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGS-VTYVCGGSLISP 61
 R PRINTS; PRO0722; CHYMOTRYPEIN; I.

R PRINTS; PRO0722; CHYMOTRYPEIN; I.

R PROMOTS; CHYMOTRYPEIN; I.

R PROMOTS; CHYMOTRYPEIN.

R PROMOTS; SMO018; KR:11

R SMART; SM00180; KR:2

R SMART; SM00180; KR:2

R PROSTTE; PS0002; EGF 1; I.

R PROSTTE; PS0002; EGF 3; I.

R PROSTTE; PS0002; KRINGLE 1; I.

R PROSTTE; PS00014; TRYPEIN LDM; I.

R PROSTTE; PS00134; TRYPEIN LM; I.

R PROSTTE; PS00135; TRYPEIN HIS; I.

R PROSTTE; PS00135; TRYPEIN HIS; I.

R PROSTTE; PS00136; TRYPEIN SER; I.

R PROSTTE; PS00136; TRYPEIN SER; I.

R PROSTTE; PS00136; TRYPEIN HIS; I.

R PROSTTE; PS00136; TRYPEIN HIS; I.

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R PROSTTE; PS00136; TRYPEIN HIS; I.

R PROSTTE; PS00136; TRYPEIN HIS; I.
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 SALIVARY PLASMINOGEN ACTIVATOR BETA
 12;
 36.3%; Score 547; DB 1; Length 431; 42.9%; Pred. No. 5.4e-42; ive 43; Mismatches 102; Indels
 699BSE675B162CBF CRC64;
SIMILARITY: Contains 1 EGF-like domain. SIMILARITY: Contains 1 kringle domain.
 InterPro; IPR009003; Cye_Ser_trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; ISGF_.
InterPro; IPR000011; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 1.
Pfam; PF00008; trypsin; 1.
 EGF-LIKE.
 KRINGLE
 48221 MW;
 EMBL; M63989; AAA31594.1; -.
 Best Local Similaricy Antiches 118; Conservative
 PIR; JS0599; JS0599.
HSSP; P98119; 1A5I.
 352
431 AA;
 MEROPS; S01.239
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 181 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSGGPLVCSLQGRMT
 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator gamma precursor (SC 3.4.21.68) (DSPA gamma).
 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Salivary gland;
MEDLINE-92039036; PubMed-1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Kraetzschmar J., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
 Desmodus rotundus (Vampire bat).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodua
 CHARACTERIZATION.
MEDLINE=93393059; PubWed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 -:- CATALTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-:- SUBUNIT: Monomer.
-:- SIMILARITY: Bellongs to peptidase family S1.
-:- SIMILARITY: Contains 1 kringle domain.
 LIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 269
 396 LLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNMR 430
 PRT; 394 AA
 HSSP, P98119; 1A51.
MEROPS; S01.239; -.
InterPro; IPR0090013; Cye_Ser_trypsin.
InterPro; IPR0010013; Kingle.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
 EMBL, M63990; AAA31595.1; -.
PIR; JS0600; JS0600.
 STANDARD;
 NCBI_TaxID=9430;
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238
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 01-APR-1990 (Rel. 14, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-Ivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA alpha-2) (BAT-PA) (T-plasminogen activator).
Desmodus rotundus (Vampire bat).
Bukaryota; Matzaoa; Chordata; Chordata; Caniata; Vertebrata; Euteleostomi;
Desmodontinae; Desmodus.
 4 SPPEELKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VTYVCGGSLISP
 62 CWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 181 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSGGPLVCSLQGRMT
 Gaps
 126 AALINE PROTEASE.
189 CHARGE RELAY SYSTEM (BY SIMILARITY).
238 CHARGE RELAY SYSTEM (BY SIMILARITY).
345 CHARGE RELAY SYSTEM (BY SIMILARITY).
126 BY SIMILARITY.
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262 BY SIMILARITY.
263 BY SIMILARITY.
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 SALIVARY PLASMINOGEN ACTIVATOR GAMMA
 SIMILARITY).
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SIMILARITY).
 Serine protease; Glycoprotein;
 Ouery Match 36.2%; Score 546; DB 1; Length 394; Best Local Similarity 42.9%; Pred. No. 5.9e-42; Matches 118; Conservative 43; Mismatches 102; Indels 12;
 235 LIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 269
 359 LLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNMR 393
Pfam; PF00051; kringle; 1.
PFfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00021; KRINGLE 2; 1.
PROSITE; PS00021; KRINGLE 2; 1.
PROSITE; PS000134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00136; TRYPSIN SER; 1.
PROSITE; PS00136; TRYPSIN SER; 1.
PROSITE; PS00136; TRYPSIN SER; 1.
 KRINGLE
 STANDARD;
 341 3
315 3
394 AA;
 NCBI TaxID=9430;
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Tue May 25 15:05:09 2004

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this Donner P.;
"Plasminogen activators from the saliva of Desmodus rotundus (common "Plasminogen activators from the selicity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!-FUNCTION: Probably essential to support the feeding habits of th:
exclusively haematophagous animal. Probable potent thrombolytic

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- BUZYME REGULATION: Activity toward plasminogen is stimulated in the presence of fibrin I.
-!- SUBUNIT: Monomer.
-!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin, and the kringle domain apparently mediates fibrin-induced stimulation of activity.
-!- SIMILARITY: Belongs to peptidase family SI.
-!- SIMILARITY: Contains I fibronectin type I domain.
-!- SIMILARITY: Contains I fibronectin type I domain.

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INEACES JOILEAN JOILEAN JOILEAN JOILEAN JOILEAN JOILEAN JOINEAN MBL, M62988; AAA31593.1; -.
EMBL, U65082; AAA31596.1; -.
PIR; A34369; A34369.
PIR; A3699; A34369.
HSSP; P98119; 1A51.
MEROPS; S01\_232; -.

A SMART; SMO0020; Tryp\_SPC; 1.

B PROSITE; PS01021; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; 1.

DR PROSITE; PS0125; FIBROMECTIN 1; 1.

DR PROSITE; PS0125; FIBROMECTIN 1; 1.

DR PROSITE; PS00121; KRINGLE\_1; 1.

DR PROSITE; PS00134; TRYPSIN DOM; 1.

DR PROSITE; PS00134; TRYPSIN DOM; 1.

DR PROSITE; PS00135; TRYPSIN DOM; 1.

DR PROSITE; PS00135; TRYPSIN JSR; 1.

RW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; KW kringle; EGF-like domain; Signal; Multigene family.

A 77 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 2.

FIRBNOMECTIN TYPE-I.

EGF-LIKE.

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102, Indels 12, Gaps

36.2%; Score 546; DB 1; Length 477; 42.9%; Pred. No. 7.5e-42; tive 43; Mismatches 102; Indels 12;

llarity 42.9%; Conservative 4

Best Local Similarity Matches 118; Conserv

Query Match

LIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 269 442 LLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNWR 476 Ź 477 STANDARD; RESULT 15
URT1\_DESRO
AC P98119;
DT 01-FEB-1996 ( 235 ઠે

(Rel. 33, Created) (Rel. 33, Last sequence update)

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| Pfam; PF00051; kringle; 1. |
| R PRINTS; PR0072; chrydin; 1. |
| R PRINTS; PR00102; chrydin; 1. |
| R RINTS; PR00018; KRINGLE. |
| R SMART; SM0018; KRINGLE; 1. |
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 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1. FIBRONECTIN TYPE-I. EGF-LIKE.
 N-LINKED (GLCNAC. .).
/FTIG=CAR 000027.
N-LINKED (GLCNAC. .).
/FTIG=CAR_000028.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
15-WAR-2004 (Rel. 43, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (BC 3.4.21.68) (DSPA
alpha-1).
 Donner P.;
"Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
 Desmodus rotundus (Vampire bat).

Bukaryota, Metazota, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae;
Desmodontinae, Desmodus.
 SEQUENCE FROM N.A.
TISSUB-Salivary gland;
MEDLINE-29039036; PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.; the plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
 CHARACTERIZATION.
MEDLINE-93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 EMBL, M3987, AAA31591.1; --
EMBL, M3986; AAA31591.1; --
PIR, JS0597; JS0597.
PIR, JS0597; JS0597.
PIR, JS0597; JS0597.
PIR, JS0597; JS0597.
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PIR, JS0597; JS0597.
IncerPro; IPR0005003; Cys Ser Lrypsin.
IncerPro; IPR0005003; Pibricin.
IncerPro; IPR000510; BEGF like.
IncerPro; IPR000510; REF.
IncerPro; IPR0001314; Peptidase_S1.
IncerPro; IPR001344; Peptidase_S1.
Pfam; PF00008; EGF; 1.
 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
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318 YNNDIALLQLKSDSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQ 377
 177 LKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKT-----DSCQGDSGGPLVCSLQ 230
 205 SVPVCSKATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISS 264
 117 HHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQ 176
 61
 SPPEELKFOCG-OKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGS-VTYVCGGSLISP
 vitro.";
J. Biol. Chem. 276:15099-15106(2001).
-!- FUNCTION: Activates hepatocyte growth factor (HGF) by converting
 Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
NCBI_TaxID=10090;
 HGFA_MOUSE STANDARD; PRT; 653 AA.
09R098, Q9STCV4;
16-OCT-2001 (Rel. 40, Last sequence update)
15-ORT-2004 (Rel. 43, Last annocation update)
Heparocyte growth factor activator precursor (EC 3.4.21.-) (HGF
 SEQUENCE FROM N.A.
MEDLINE=21226753; PubMed=11032833;
van Adelsberg J.S., Sehgal S., Kukes A., Brady C., Barasch J.,
Yang J., Huan Y.;
"Activation of hepatocyte growth factor (HGF) by endogenous HGF
activator is required for metanephric kidney morphogenesis in
 20;
 Query Match 36.0%; Score 543; DB 1; Length 477; Best Local Similarity 42.2%; Pred. No. 1.4e-41; Matches 117; Conservative 42; Mismatches 98; Indels
 SEQUENCE FROM N.A.
STRAIN=BALB/C;
Itoh H., Kataoka H., Koono H.;
"Mouse hepatocyte growth factor activator.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 53616 MW; AA06FD1739C10E5E CRC64;
 231 GRMTLIGIVSWGRGCALKDKPGVYTRVSHFLPWIRSH 267
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property and as the activated to state the ac
 HEPATOCYTE GROWTH FACTOR ACTIVATOR LONG
from a single chain to a heterodimeric form (By similarity). WINIT: Dimer of a short chain and a long chain linked by a
 EGF-LIKE 1.
FIBRONECTIN TYPE-I.
EGF-LIKE 2.
KRINGLE.
SERINB PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
 SUBUNIT: Dimer of a short chain and a long chain linked by a disulfide bond (By similarity).
SUBCELLUMA LOCATION: Secreted as an inactive single-chain precursor and is then activated to a heterodimeric form (By
 CHAIN.
FIBRONECTIN TYPE-II.
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432
 SLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLA 116
 2 PSSPPEELKFOCGOK----TLRPRPKIIGGEFTTIENOPWFAALYRRHRGGSVTYVCGG 56
 117 HHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQ
 LKMTVVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLT
 Gaps
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 FA12 HUMAN STANDARD; PRT; 615 AA.
P00748; P78339;
21-UUL-1986 (Rel. 12, Last sequence update)
01-OCT-1989 (Rel. 12, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
SIMILARITY)
SIMILARITY)
 (POTENTIAL)
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(POTENTIAL)
 33.0%; Score 497.5; DB 1; Length 653; 38.5%; Pred. No. 2.7e-37; tive 44; Mismatches 109; Indels 15;
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 SEQUENCE FROM N.A.
MEDLINE-88007593; PubMed=2888762;
Cool D.E., McGillivray R.T.A.;
 70567 MW;
 Similarity 38.5'
05; Conservative
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163 AA;
 Best Local Sim
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Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B.; Engel W.; "The novel acceptor splice site mutation 11396(G-->A) in the factor XII gene causes a truncated transcript in cross-reacting material megative patients.";
 SEQUENCE OF 4-615 FROM N.A.
MEDLINE=86176794; PubMed=3754331;
Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
Cortese R.;
"CDNA sequence coding for human coagulation factor XII (Hageman).";
Nucleic Acids Res. 14:3146-3146(1986).
 "Coagulation factor XII (Hageman factor) Washington D.C.: inactive factor XIIa results from Cys-571-->Ser substitution."; Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
 VARIANT LOCARNO PRO-372.
MEDLINE-94325559; PubMed-8049433;
Hovinga J.K., Schaller J., Stricker H., Wuillemin W.A., Furlan M.,
 MEDLINE=85182674; PubMed=3886654; MEDLINE=85182674; PubMed=3886654; McMullen B.A., Fujikawa K.; Fubmed K.; Fujikawa K.; Fujikawa K.; Fujikawa K.; Fujikawa K.; Fujikawa K.; Fujikawa K.; Fujikawa K.; Fujikawa K.; Fujikawa Factori, "; Fujikawa Factori,"; Fujikawa Factori, "; Fujikawa Factori,"; Fujikawa Factori, 260:5328-5341(1985).
 "Characterization of human blood coagulation factor XII cDNA. Prediction of the primary structure of factor XII and the tertiary structure of beta-factor XIIa.";
J. Biol. Chem. 260:13666-13676(1985).
 S.A.,
 CARBOHYDRATE-LINKAGE SITE THR-109.
MEDLINE-92184750; PubMed=1544894;
Harris R.J., Ling V.T., Spellman M.W.;
"O-linked fuccose is present in the first epidermal growth factor
domain of factor XII but not protein C.";
J Biol. Chem. 267:5102-5107(1992).
 SEQUENCE OF 146-615 FROM N.A. MEDLINES-86216049; PubMed=3011063; Que B.G., Davie E.W., a cDNA coding for human factor XII (Hägeman "Characterization of a cDNA coding for human factor XII (Hägeman
 MEDLINE-86033830; PubMed=3877053;
Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.
McGillivray R.T.A.;
 SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605. Rieder M.U., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek Frajkumar N., Toth E.J., Yi Q., Nickerson D.A.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
"Characterization of the human blood coagulation factor XII gr
Intron/exon gene organization and analysis of the 5'-flanking
 VARIANT WASHINGTON D.C. SER-590.
MEDLINE-90046788; PubMed=2510163;
Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving
 SEQUENCE OF 354-362 AND 373-615.
MEDLINE-83291041; PubMed-6604055;
Fulikawa K., McMullen B.N.;
"Amino acid sequence of human beta-factor XIIa.";
Jaiol. Chem. 258:10924-10933(1983).
 region.";
J. Biol. Chem. 262:13662-13673(1987).
 Hum. Mol. Genet. 4:1235-1237(1995).
 IISSUE=Blood;
MEDLINE=96133302; PubMed=8528215;
 Biochemistry 25:1525-1528(1986)
 SEQUENCE OF 561-615 FROM N.A.
 SEQUENCE OF 14-615 FROM N.A.
 SEQUENCE OF 20-379.
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WELLINE=99290785; PubMed=10361128;

MEDLINE=99290785; PubMed=10361128;

MEDLINE=99290785; PubMed=10361128;

MEDLINE=99290785; PubMed=10361128;

MEDLINE=99290785; PubMed=10361128;

MEDLINE=99290785; PubMed=10361128;

MEDLINE=87300783 F. Amano S., Koide T.;

MEDLINES AND 4330014391 A proteasome-mediated degradation.";

Lancod 93:4300-4308 (1999) .

MEDLINES AND 11 is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and amplotenals.

C. I- FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the complex bonds in factor XII to form factor XII to form factor XII.

C. I- PTM: O- AND M-GLYCOXIATED.

C. I- DISEASE: Defects in that whole-blood clotting time is prolonged.

C. I- MISCELANEROUS: Factor XII, prekallikrein, is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to an anionic surface. Prekallikrein is cleaved by factor XII to factor XII.

C. I- SIMILARITY: Contains 1 fibronectin type II domain.

C. I- SIMILARITY: Contains 1 fibronectin type II domain.

C. I- SIMILARITY: Contains 1 kringle domain. Liaemmle B.; "Coagulation factor XII Locarno: the functional defect is caused } "Coagulation acid substitution Arg-353-->Pro leading to loss of a kallikrein cleavage site."; Blood 84:1173-1181(1994). 

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MIM, 234000, 2300 F12.

R GO; GO:0003805; F:blood coagulation factor XI activity; TAS.

GO; GO:0003805; F:blood coagulation factor XI activity; TAS.

GO; GO:0003806; F:blood coagulation factor XII activity; TAS.

R GO; GO:0007596; F:blood coagulation; TAS.

R InterPro; IPR0000303; Cys.er\_trypsin.

R InterPro; IPR000083; Fibrnctnl.

R InterPro; IPR000083; Fibrnctnl.

R InterPro; IPR00001554; Peptidase S1.

R InterPro; IPR001254; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R Ffam; PF00009; EGB; 2.

R Ffam; PF00009; EGB; 2.

R Ffam; PF00009; Kingle.

R Ffam; PF0001314; Peptidase S1A.

R Ffam; PF00009; Kingle: 1.

R Ffam; PF0001314; Peptidase S1A.

R Ffam; PF00009; Kingle: 1.

PRINTS; PRO0722; CHYMOTRIPSIN.
PRINTS; PRO0013; PRYPEII.
PRINTS; PRO0018; KRINGIE.
PRODOM; PO000995; FN\_TYPE\_II;

Prodom, PD000395; Kringle; 1.

SMART; SM00181; EGF; 2.

RMART; SM000181; EGF; 2.

RMART; SM000181; EGF; 2.

RMART; SM00029; FN1; 1.

RMART; SM00020; Tryp\_SPC; 1.

RMART; SM00020; Tryp\_SPC; 1.

RMART; SM00020; Tryp\_SPC; 1.

RMART; SM00020; Tryp\_SPC; 1.

RMART; SM00020; Tryp\_SPC; 1.

RMART; SM00020; Tryp\_SPC; 1.

RMOSITE; PS00020; FIBRONECTIN.1; 1.

RMOSITE; PS00002; FIBRONECTIN.2; 1.

RMOSITE; PS00002; FIBRONECTIN.2; 1.

RMOSITE; PS00014; TRYPSIN DM; 1.

RMOSITE; PS00014; TRYPSIN TRYPSIN THS; 1.

RMOSITE; PS001186; EGF; 2.

RMART; BLOOG COAGULATION; Plasma; Kringle; Serine protease; Mydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen; Mydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen; Mydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen; Mydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen; Mydrolase; Fibrinolysis; Signal; EGF-like 1.

RMART 2.

RMART 2.

RMART; SM000202 TRYPSIN TRYPSIN TYPE-I.

RMAIN 373 615 BETA-FACTOR XIIA PART 1.

FT DOMAIN 373 615 RRINGER FORD:

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FT DOMAIN 373 615 RRINGER FORD:

FT DOMAIN 373 615 RRINGER FORD:

FT DOMAIN 373 615 RRINGER FORD:

FT CARBOHYD 296 349 N-LINKED (GICNAC. .)

CARBOHYD 296 349 N-LINKED (POTENTIAL).

FT CARBOHYD 305 305 N-LINKED (POTENTIAL). O-LINKED (FUC).

N-LINKED (GLCNAC...).

O-LINKED (BOTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL).

O-LINKED (POTENTIAL). CARBOHYD CARBOHYD CARBOHYD CARBOHYD 

1 KPSSPPEELK---PQCGQ---KTLRPRFK11GGEFTT1ENQPWFAA1YRRHRGGSVTYVC ; Score 495; DB 1; Length 615; ; Pred. No. 4.3e-37; 44; Mismatches 109; Indels 18; Gaps Query Match Best Local Similarity 38.5%; Matches 107; Conservative 44

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55 GGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADT 114

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RESULT 18 HGFA HUMAN

HGFA HUMAN STANDARD; PRT; 655 AA.

004756, 01470-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF activator) (HGFA).

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A Zhao S., Odell C.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
L Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Activates hepatocyte growth factor (HGF) by converting it from a single chain to a heterodimeric form.
-!- SUBMUT: Dimer of a short chain and a long chain linked by a disulfide bond.
-!- SUBMUT: Dimer of a short chain and a long chain linked by a precursor and is then activated to a heterodimeric form.
-!- SUBCELLULAR LOCATION: Secreted as an inactive single-chain precursor and is then activated to a heterodimeric form.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kingle domain.
-!- SIMILARITY: Contains 1 kingle domain. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; SECUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUE-Liver, and Serum;
MEDLINE=93222878; PubMed=7683665;
Miyazawa K., Shimomura T., Kitamura A., Kondo J., Morimoto Y.,
Kitamura N.;
"Molecular cloning and sequence analysis of the cDNA for a human
serine protease reponsible for activation of hepatocyte growth
factor. Structural similarity of the protease precursor to blood
coagulation factor XII.",
D. Biol. Chem. 268:10024-10028(1993). Genew, Holaristati, Hoffac.

R MM, 604552; -
R GO; GO:0000576; C:extracellular; TAS.

GO; GO:00005576; C:extracellular; TAS.

GO; GO:00005526; F:serine-type endopeptidase activity; TAS.

GO; GO:0000508; F:serine-type endopeptidase activity; TAS.

InterPro; IPR000508; Cys.Ser.trypsin.

R InterPro; IPR000742; EGF.2.

InterPro; IPR000508; Fibrnctn.

R InterPro; IPR000519; Fibrnctn.

R InterPro; IPR000510; Kingle.

R InterPro; IPR001134; Peptidase S1.

R Pfam; PF00089; Edr; 2.

R Pfam; PF00089; Edr; 1.

R Pfam; PF00081; Kingle; 1.

R Pfam; PF00081; Kingle; 1.

R Pfam; PF00081; Kingle; 1.

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R Pfam; PF00081; Kingle; 1.

R PRINTS; PR00012; CHYNOTRYPSIN.

R PRINTS; PR00013; KINGLE. EMBL, D14012; BAA03113.1; -.
EMBL, 569923; -; NOT\_ANNOTATED\_CDS.
PIR; A46688; A46688.
HSSP, P00763; 1DPO.
MERQPS; S01.228; -.
Genew; HGNC:4894; HGFAC. Homo sapiens (Human) 

R SWART; SM00059; FN2; 1.

R SMART; SM00130; KR; 1.

R PROSITE; PS00022; EGF 1; 2.

R PROSITE; PS00026; EGF 2; 1.

R PROSITE; PS01253; FIBRONECTIN 1; 1.

R PROSITE; PS00021; KRINGLE 1; 2.

R PROSITE; PS00021; KRINGLE 1; 1.

R PROSITE; PS500021; KRINGLE 2; 1.

R PROSITE; PS500134; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

372

SIGNAL

56 GSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTL 115 116 AHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPB 175 385 BPASPGRQ---ACGRRHKKRTFLRPR--IIGGSSSLPGSHPWLAAIY---IGDS---FCA 433 SDH-DLVLIRLKKKGDRCATRSQFVQPICLPEPGSTFPAGHKCQIAGWGHLDENVSGYSS 552 1 KPSSPPEBLKFQCGQK----TLRPRFKIIGGEFTTIENQPWFAAIYRHRGGSVTYVCG 55 Query Match
32.7%; Score 493.5; DB 1; Length 655;
Best Local Similarity 38.3%; Pred. No. 6.3e-37;
Matches 105; Conservative 43; Mismatches 109; Indels 17; Gaps CLEAVED IN ACTIVE FORM. HEPATOCYTE GROWTH FACTOR ACTIVATOR SHORT HEPATOCYTE GROWTH FACTOR ACTIVATOR LONG KALNGLAE
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ProDom; PD000995; FN Type\_II; 1. ProDom; PD000395; Kringle; 1. SWART; SWO0181; EGF; 2. SWART; SWO0058; FNI; 1.

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NOTE TO SEQUENCE FROM N.A., AND SEQUENCE OF 19-37; 318-332 AND 359-373.

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NOTE TISSUE TO SEQUENCE OF 19-37; 318-332 AND 359-373.

Rembara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shibuya Y., Tanase S.,

Rambara T., Okabe H.; Kunisada T., Shiba Hat participates in the initiation of blood coagulation, fibrinolysis, and the Generation of bradykinin and anglotensin.

C. -I. CATALIVITIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor

C. -I. CATALIVITY: Cleaves Relocity In the Corm factor XII.

C. -I. CATALIVITY: Contains 1 Section XII.

C. -I. SIMILARITY: Contains 1 Section And HWW kininogen form a coagulation of blood coagulations of the Corm factor XII.

C. -I. SIMILARITY: Contains 1 Sibronectin type II domain.

C. -I. SIMILARITY: Contains 1 Stringle domain.
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 176 QLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTL 235
 Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
NCBI_TaxID=10141;
 0104952.
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Coaquiation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAP) (Fragment).
 236 TGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 269
 603 AA
 InterPro; IPR009003; Cya_Ser_trypsin.
InterPro; IPR0010841; EGF 2.
InterPro; IPR001881; EGF 2.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR000638; Fibrnctn1.
InterPro; IPR00652; FN Type_II.
 nterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase Sl.
InterPro; IPR001314; Peptidase_SlA.
 EMBL; X68615; CAA48600.1; -. PIR; S28941. HSSP; P00763; 1DPO. MEROPS; S01.211; -.
 STANDARD;
 PF00008; EGF; 2.
PF00039; fn1; 1.
PF00040; fn2; 1.
 CAVPO
 FA12 CA
Q04962;
 RESULT 19
FA12_CAVPO
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509 BAQVPLISSERCSSPEVHGDAFLSGMLCAGFLEGGTDACQGDSGGPLVCEDEAAEHRLIL 568
 179 MTVVKLISHRECQOPHYYGSEVTTKMLCAADPOWKTDSCOGDSGGPLVC---SLQGRMTL 235
 MEDINE-54242782, PubMed-8186251,
Shibiya Y., Semba U., Okabe H., Kambara T., Yamamoto T.,
Yamanoto Structure of bovine Hageman factor (blood coagulation factor
XII): comparison with human and quinea pig molecules.",
Biochim. Biophys. Acta 1206:63-70(1994).
 Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidea, Bovinae, Bos.
 FALS BOUIN STANDARD; PRT; 593 AA.
P98140.
01-FPB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Cocquiation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAF) (Fregment).
 SEQUENCE OF 10-21; 350-364 AND 525-550.
MEDIATRE=7132; PubMed=861210;
Fujikawa K., Falsh A.K., Davie W.E.;
"Isolation and characterization of bovine factor XII (Hageman
 236 TGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT 268
 EMBL; S70164; AAB30804.2; -. PIR; S45281; S45281.
HSSP; P00763; 1DPO.
 SEQUENCE FROM N.A.
TISSUE=Liver;
 RESULT 20
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 C. TISSUE=Testis;

MEDLINE=29203523; PubMed=10103056;

MEDLINE=29203523; PubMed=10103056;

MEDLINE=29203523; PubMed=10103056;

Pooraffshar M., Hellman L.;

"Cloning and structural analysis of leydin, a novel human serine

"The protease expressed by the Leydig cells of the testis.";

Bur. J. Blochem. 261:244-250[1999].

-!- FUNCTION: Plays a role in neuronal plasticity and the proteolytic

action may subserve structural reorganizations associated with

learning and memory operations (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCELLULAR LOCATION: Deptidase family S1.

-!- SIMILARITY: Contains 1 kRCR domains.
 447
 129 KEGRCAQPSRTIQTICLPSMYNDPQFGTS--CEITGFGKENSTDYLYPEQLKMTVVKLIS 186
 448 ADGCCAHPSPFVQPVCLPSTAARPAESEAAVCEVAGWGHQFEGGE-YSSFLQEAQVPLID 506
 187 HRECOOPHYYGSEVITIKMLCAADPOWKTDSCOGDSGGPLVC---SLOGRMTLIGIVSWGR 243
 507 PORCSAPDVHGAAFTQGMLCAGFLEGGTDACQGDSGGPLVCEDETPERQLILRGIVSWGS 566
 69
 70 CFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-S
 13 CGQ---KTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATH
 Gaps
 Proba K., Gschwend T.P., Sonderegger P.; "Cloning and sequencing of the cDNA encoding human neurotrypsin."; Biochim. Biophys. Acta 1396:143-147(1998).
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TaxID=9606;
 18;
Length 593;
Query Match
30.0%; Score 453; DB 1; Length 593
Best Local Similarity 38.5%; Pred. No. 2.6e-33;
Matches 102; Conservative 44; Mismatches 101; Indels
 NETR HUMAN STANDARD; PRT; 875 AA.
856730; QOUD16;
80-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
88-FEB-2003 (Rel. 41, Last annotation update)
Neurotrypsin precursor (EC 3.4.21.-) (Motopsin) (Leydin).
 EMBL; AJ001531; CAA04816.1; -.
 SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=98201705; PubMed=9540828;
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 121 IALLKIRSKEGRCAOPSRIIQTICLPSMYNDPQ-FGTSCEITGFGKENSTDYLYPBQLKM 179
 180 TVVKLISHRECQQPHYYGSEVTTKMLCAAD--PQWKTDSCQGDSGGPLVCSLQGR-MTLT 236
 3 SSPPEELKFOCGOXTLRPRFK-IIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISP 61
CWVISATHCFIDYPKK-EDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 29.3%; Score 442.5; DB 1; Length 875; larity 36.6%; Pred. No. 3.8e-32; Conservative 47; Mismatches 113; Indels 13;
 26 N-LINKED (GLCNAC. .) (POTENTIAL)
683 N-LINKED (GLCNAC. .) (POTENTIAL)
663 A -> V (IN REF. 2).
701 E -> V (IN REF. 2).
841 VVY -> AAL (IN REF. 2).
97011 MW; B66EC946DC208DC8 CRC64;
 GIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 269
 POTENTIAL.
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Matches 100; Conserva
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 30-0747-2000 (Rel. 39, Created)
30-0747-2000 (Rel. 39, Last sequence update)
15-MAY-2000 (Rel. 43, Last annotation update)
15-MAY-2004 (Rel. 43, Last annotation update)
brockease 3) (BSSP-3).
PRSS12 OR BSSP3.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 SEQUENCE FROM N.A.
TISSUEBRAIN;
MEDLINE=97401523; PubMed=9245503;
Gschwend T.P., Krueger S.R., Kozlov S.V., Wolfer D.P., Sonderegger P.
"Neutoctrypain, a novel multidomain serine protease expressed in the mervous system."
Mol. Cell. Neurosci. 9:207-219(1997).
 SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

YamaDLINES 98008848; PubMed=9344839;

Yamamura Y., Yamashiro K., Tsuruoka N., Nakazato H., Tsujimura A., Yamaguchi N.;

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 Biochem. Biophys. Res. Commun. 239:386-392(1997).
 and amygdala.
-- SIMTLARITY: Belongs to peptidase family S1.
-- SIMTLARITY: Contains 1 kringle domain.
-- SIMILARITY: Contains 3 SRCR domains.
 761 AA
 STANDARD;
 RESULT 22
NETR MOUSE
ID NETR MOUSE
AC 008762;
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CWVISATHCFIDY-PKKEDYIVYLGRSRLNSNTQCEMKFEVENLILHKDYSADTLAHHND 120
 121 IALLKIRSKEGRÇAQPSRTIQTICLPSMYNDPQ-FGTSCEITGFGKENSTDYLYPEQLKM 179
 180 TVVKLISHRECQQPHYYGSEVTTKMLCAADPQW--KTDSCQGDSGGPLVCSLQGR-MTLT 236
 3 SSPPERLKFQCGQXTLRPRFK-IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISP
 2 761 FOLDATION RELIGION REGION CHARGE RELAY SYSTEM CHARGE CH
 Query Match
28.2%; Score 425.5; DB 1; Length 761;
Best Local Similarity 37.1%; Pred. No. 1.1e-30;
Matches 101; Conservative 42; Mismatches 116; Indels 13;
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 MEDINE-97224034; PubMed-9970615;
MEDINE-97224034; PubMed-9970615;
MEDINE-97224034; PubMed-9970615;
MEDINE-97224034; PubMed-9970615;
Masuda K.-I., Yamanoka K., Takanashi M., Sano T.;
Masuda K.-I., Yamanoka K., Takanashi M., Sano T.;
Thurification, characterization, and localization of a novel
trypsin-like procease found in the human alrway.";
Mm. J. Respir. Cell Mol. Biol. 16:300-3081697).
Mm. J. Respir. Cell Mol. Biol. 16:300-30816997).
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Mm. J. Respir. Cell Mol. Biol. 16:300-30816997.
Mm. J. Respir. Cell Mol. Biol. 16:300-30816997.
Mm. J. Respir. Cell Mol. Biol. Mol. Biol. Certain beptides of criminal side of arginine residues at the PI position of certain peptides, cleaving Boc-Phe-Ser-Arg-4-methyl.commaryl-7-amide most efficiently and sorphosphate, leupeptin, antipain, aprotinin, and soybean trypsin inhibitor, but hardly inhibited by secretory leukocyte procease inhibitor at 10 microm.

- SUBUNIT: Monomer.
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 cleavage and secreted. The formal process of the submucosal serous glands of the bronchi and trachea. SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 1 SEA domain.
 SEQUENCE FROM N.A. MEDLINE=98234382; PubMed=9565616; AmbuliNE=98234382; PubMed=9565616; Yakagi K., Umemoto N., Yasuoka E. Yamaoka K., Masuda K.-I., Ogawa H., Takagi K., Umemoto N., Yasuoka E. "Cloning and characterization of the cDNA for human airway trypsinlike protease."; J. Biol. Chem. 273:11895-11901(1998).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 EMBL; ABO02114; BAA28691.1; -
HSSP; P00750; 1RTF.
MEROPS; S01.301; -
MEROPS; S01.301; -
MEROPS; S01.301; -
MEROPS; S01.301; -
MEROPS; S01.301; -
MEROPS; S01.301; -
MEROPS; S01.301; -
MEROPS; S01.301; -
MEROPS; S01.301; -
GO; GO:0005276; C:integral to plasma membrane; TAS.
GO; GO:000528; F:peptidase activity; TAS.
GO; GO:000588; F:peptidase activity; TAS.
InterPro; IPRO01354; Peptidase S1.
InterPro; IPRO01354; Peptidase S1.
InterPro; IPRO0134; Peptidase S1.
InterPro; IPRO0134; Peptidase S1A.
InterPro; IPRO0134; Peptidase S1A.
InterPro; IPRO0134; Peptidase S1A.
InterPro; IPRO0134; Peptidase S1A.
InterPro; IPRO0134; Peptidase S1A.
PRAM; SMO020; SEA; I.
PROSITE; PSS0246; ERA; I.
PROSITE; PSS0246; ERYPSIN_DOM; I.
 16-00T-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Airway trypsin-like protease precursor (EC 3.4.21.-).
 418 AA.
 PRT;
 Homo sapiens (Human)
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23 KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV 82
 241 TSG----ISTTFPKLRMRVRNILIHMNYKSAT--HENDIALVRLENS----VTFTKDIHS
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 83 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT
 ICLPSMYNDPOFGTSCEITGFGKENSTDYLYPBQLKMTVVKLISHRECQOPHYYGSEVTT
 203 KMLCAADPQWKTDSCOGDSGGPLVCSLOGRM-TLTGIVSWGRGCALKDKPGVYTRVSHFL
 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CATALYTIC
 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 SEA.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
INTERCHAIN (BY SIMILARITY).
 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCHAC. .) (POTENTIAL).

F4BC1DB020CFBBD0 CRC64;
 TRYPSIN-LIKE PROTEASE, NON-
 DB 1; Length 418;
 TISSUE=Prostate;
MEDLINE=95286644; PubMed=7768952;
Yu J.X., Chao L., Chao J.;
"Molecular cloning, tissue-specific expression, and cellular localization of human prostasin mRNA.";
J. Biol. Chem. 270:13483-13489(1995).
 CATALYTIC CHAIN.
AIRWAY TRYPSIN-LIKE PROTEASE,
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Transmembrane; Signal-anchor; 3Glycoprotein.
1 186 AIRWAY TRYPSIN-LIKE PROTEASE, CHAIN
 28.1%; Score 423.5; DB 1; Length 4 36.4%; Pred. No. 7.9e-31; tive 47; Mismatches 93; Indels
 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
 016651, 09UCA3;
01-NVV-1997 (Rel. 35, Created)
01-NVV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
PRSS8.
 343 AA.
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
 46263 MW;
 l Similarity 36.4³
90; Conservative
 1418
11648
12222
12328
13933
1444
 20
41
 262 PWIRSHT 268
 DWIRQQT 416
 42
184
187
222
222
222
338
333
334
418
48
48
43,
 SEQUENCE FROM N.A. TISSUE=Placenta;
 187
 2 7
 HUMAN
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ACT SITE
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DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
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TRANSMEM
 350
 410
 Query Match
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 DOMAIN
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 Matches
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ACTIVATION PEPTIDE

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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altasnar R.D., Collins F.S., Wagner L., Shamenc C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Zeeberg B., Bardow K.B., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Workernan K.G., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergen B.G., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergen B.G., Lu X., Gibbs R.A.,
Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerd, A., Schein J.E., Jones S.J.M., Marra M.A.,
Human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 TISSUE=Semen,
MEDLINE=94308140; PubMed=8034638;
Yu J.X., Chao L., Chao J.;
"Prostasin is a novel human serine proteinase from seminal fluid.
Purification, tissue distribution, and localization in prostate
 MIMI, 600823, -...

R GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0008236; C:plasma membrane; TAS.

R InterPro; IPR001203; Cyp Ser trypsin.

InterPro; IPR001204; Peptidase_S1.

InterPro; IPR001214; Peptidase_S1.

R Pfam; PR001314; Prpsin. 1.

R PRMITS; PR00032; CHTMOINVEIN.

R PROSITE; PSC0040; TRYPSIN. DOM; 1.

R PROSITE; PSC00134; TRYPSIN DOM; 1.

R PROSITE; PSC00134; TRYPSIN HIS; 1.

R PROSITE; PSC00135; TRYPSIN ERR; 1.

R HYDGOIDS: TRYPSIN ERR; 1.
 -!- SIMILARITY: Belongs.to peptidase family S1.
 POTENTIAL
 EMBL; L41351; AAC41759.1; -...
EMBL; U33446; AAB1971.1; -...
EMBL; BC001462; AAB10462.1; -...
PIR, A57014; A57014.
HSSP, P00763; 1DPO.
MEROPS; S01.159; -...
Genew; HGNC:9491; PRSS8.
 59
 SEQUENCE OF 45-64.
 Transmembrane
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

SEGUENCE FROM N.A., AND PARTIAL SEQUENCE.

X SELINE-91090844; PubMed=2264928;

X SELINE-91090844; PubMed=2264928;

X SELIAD N.G., Sawyer N., Hamelin J., Mion P., Beaubien G.,

X Brachpapa L., Rochemont J., Molkay M., Chretien M.,

Mouse plasma kallikrein: cDNA structure, enzyme characterization,

The protein and mRNA levels among species.";

The cell Biol. 9:737-748(1990).

Y FUNCTION: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It

Ard comparation in a recipional reaction, factor XII after its binding

C atlivates, in a recipional reaction, factor XII after its binding

C to a negatively charged surface. It also releases bradykinin from

HWM kininogen and may also play a role in the renin-angiotensin

System by converting procenin into renin.

C -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Xaa and Lys-|-Xaa

bonds, including Lys-|-Arg and Arg-|-Ser bonds in (human)

kininogen to release bradykinin.
 85 HCFPSEKHKEAYEVKLGAHQLDSYSEDAKVSTLKDIIPHPSYLQE--GSQGDIALLQL-- 140
 141 --SRPITFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISR 198
 69 HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 128
 84
 129 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK-ENSTDYLYPEQLKMTVVKLISH
 188 REC------QOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTG
 CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTY----VCGGSLISPCWVISAT
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FRB-2003 (Rel. 41; Last annotation update)
Plasma kallikrein precursor (BC 3.4.21.34) (Plasma prekallikrein)
(Kininogenin) (Fletcher factor).
 37;
 .) (POTENTIAL)
 Query Match 27.1%; Score 408.5; DB 1; Length 343; Best Local Similarity 36.6%; Pred. No. 1.4e-29; Matches 100; Conservative 36; Mismatches 100; Indels 37,
 POTENTIAL.
SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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CHARGE RELAY SYSTEM.
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N. LINKED (GLORAC. . .) (POTEN'
N. JINKED (GLORAC. . .) (POTEN'
 PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
 238 IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
 255 IVSWGDACGARNRPGVYTLASSYASWIQSKVTE
 638
STANDARD;
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CC27C93AB1086599 CRC64;

638 AA;

EMEL; M58588; AAA63393.1; -.

EMEL; M38589; AAA63393.1; -.

RENDPS; S01212; -.

MEROPS; S01212: -.

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InterPro; IPR001314; Peptidase\_S1A

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"TWERSS, a new type II transmembrane serine protease.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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254 YVLWIR 259
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 TISSUE=MEABLE.

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ridanner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Zeeberg B., Bonaldo M.F., Casninci P., Prange C.,

B. Antachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Vilalon D.K., Murny D.M., Schergen B.D., Dickson M.C.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

T. "Generation and initial analysis of more than 15,000 full-length

P. T. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., A Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Slaan D., Song L., Mang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhan G., Chissoe S., Murray J., Miller N., Minx P., A Cordes M. Du Z., Fulton E., Goela D., Graves T., Hawkins J., A Hinds K., Kemp K., Latrelle P., Layman D., Ozersky P., Rolson J., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., A Edlemann L., Kim U.J., Shrauya H., Simon M.I., Dumanski J.P., A Poyraxd M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., Khan A.S., Lane L., Tilahun Y., Wright H.; The DNA sequence of human chromosome 22.";
 SEQUENCE OF 9-811 FROM N.A. (ISOPORM 1), AND TISSUE SPECIFICITY.

TISSUE=Fetal liver;

MEDILINE=22241917; PubMed=12149247;

Velasco G., Cal S., Quesada V., Sanchez L.M., Lopez-Otin C.;

"Matriptase-2, a membrane-bound mosaic serine proteinase predominantly expressed in human liver and showing degrading activity against extracellular matrix proteins.";

J. Biol. Chem. 277:37637-37646(2002).
 Isold=081U80-2; Sequence=VSP 008379, VSP 008380;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Liver specific.
SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 3 LDL-receptor class A domains.
 Event=Alternative splicing; Named isoforms=2;
 IsoId=Q8IU80-1; Sequence=Displayed;
 SEQUENCE FROM N.A. (ISOFORM 2).
 TISSUE=Brain;
 REVIEW
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67 ATHCFIDYPKKED-----YIVYLGRSRLNSNTQCEMKFEVENLILHKDYSADTLAHHN 119
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 99
 LCGLRILOPYAERIPVVATAGITINFTSQISLTGPGVRVHY
GLYNOSDPCPGE -> YHFLSSLWLPFLPPPPSLPSSTVTP
 7 EELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
 SLEAGVPNLRGAARGASRGWGWCQACCP (in isoform
 Gaps
 CUB 1.

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM.

N-LINKED (GLCNAC...) (POTENTIAL).

 33;
 Query Match 26.8%; Score 404.5; DB 1; Length 811; Best Local Similarity 36.8%; Pred. No. 9.5e-29; Matches 99; Conservative 48; Mismatches 89; Indels 33.
 /Frid=VSP 008380.
A -> V (IN REF. 4).
7EEF193F655DE9D CRC64;
 FTIG=VSP 008379
 116 116 7
811 AA; 89999 MW;
 811
 462
 CONFLICT
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
 CARBOHYD
CARBOHYD
CARBOHYD
 CARBOHYD
VARSPLIC
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 VARSPLIC
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DECURENCE FROW N.A. (ISOPORM 1).

SEQUENCE FROW N.A. (ISOPORM 1).

X AMAIN-CSTAL/6J; TISSUE-Kidney;

X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Konno H., Kasukawa T., Saito R.,

A Alzawa K., Izawa M., Ashburner M., Batalov S., Casavant T.,

Radota K., Metuada H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,

Browstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Browstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

Nyasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nyasachisal.
 321 QKVDVQLIPQDLCSEVYRY--QVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLA 778
 615. AAHCF----QEDSMASTVLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEED--SHDY 667
 178 KMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVC-SLQGRMTLT
 DIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFG--KENSTDYLYPEQL
 668 DVALLQLDHPVVR----SAAVRPVCLPARSHFFEPGLHCWITGWGALREGGP---ISNAL
 -!- FUNCTION: Plays an essential role in cell growth and maintenance of cell morphology.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATUVE PRODUCTS:
--- B. Event = Alternative splicing; Named isoforms = 2;
Name = 1; Synonyms = 1a;
 Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLIFES9339944; PubMed=10411637;
Kawamura S., Kurachi S., Deyashiki Y., Kurachi K.;
Complete nuclectide sequence, origin of isoform and functional characterization of the mouse hepsin gene.";
Bur. J. Blochem. 262:755-764(1999).
 SEQUENCE FROM N.A. (ISOFORM 2).
TISSUB-LIVE-8805912,
Wu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard B.W.;
"Identification and cloning of the membrane-associated serine
procease, hepsin, from mouse preimplantation embryos.";
J. Biol. Chem. 272:31315-31320(1997).
 HERS MOUSE STANDARD; PRT; 436 AA. 035453; Q9CW97; 15-UL-1998 (Rel. 36, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Serine procease hepsin (EC 3.4.21.-).
 GIVSWGRGCALKDKPGVYTRVSHFLPWIR 265
 |:|||| || : ||||| GLVSWGLGCGRPNYFGVYTRITGVISWIQ 807
 NCBI_TaxID=10090;
 120
 237
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (FOTENTIAL). 43; 26.7%; Score 402.5; DB 1; Length 436; 35.7%; Pred. No. 6.7e-29; ive 54; Mismatches 85; Indels 43 E MBL; AP030065; AAB84211.1; -.

R MBLS; AC02664; BAB22289.2; ALT\_FRAME.

HSSP; PO07631 1DPO.

R MEXOPS; S01.224; Peptidase.

R MGD; MGI:1186620; Hpn.

R InterPro; IPR001034; Peptidase S1.

R InterPro; IPR001134; Peptidase S1.

R InterPro; IPR001134; Peptidase S1.

R Pfan; PP00089; LTYPSin; D.

R Pfan; PP00089; LTYPSin; D.

R SMART; SM00202; CHYMOTRYPSIN.

R SMART; SM00202; TYPSIN; D.

R SMART; SR00123; TRYPSIN DM; 1.

R PROSITE; PS50134; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R Hydrolase; Serine protease; Transmembrane; Signal-anchor; I Hydrolase; Serine S1.

R Alternative splicing. IsoId=035453-1; Sequence=Displayed;
Note=Minor isoform;
Note=Ai. Synonyms=2a;
IsoId=035453-2; Sequence=VSP\_007232;
Note=Major isoform;
SIMILARITY: Belongs to peptidase family S1.
CAUTION: Ref. 3 sequence differs from that shown due to frameshifts in positions 155, 191 and 233. /FTIGA'SEP 007232.

L -> F (IN REF. 3).

G -> R (IN REF. 3).

NR -> ET (IN REF. 3).

NR -> ET (IN REF. 3).

P -> L (IN REF. 3).

P -> L (IN REF. 3).

H -> N (IN REF. 3).

W, 4A0993148C620BD0 CRC64; EXTRACELLULAR (POTENTIAL). 46787 MW; Query Match Best Local Similarity 35.7% Matches 101, Conservative 85 204 214 223 264 281 436 36 63 204 204 214 228 264 281 436 AA; 182 21 64 2222 2222 2722 2722 2722 2723 3411 1311 25 DOMAIN TRANSMEM CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE DOMAIN DOMAIN ACT SITE ACT SITE ACT SITE DISULFID DISULFID DISULFID DISULFID CARBOHYD VARSPLIC 13 225 CHAIN à 원 ò g

CARBOHYDRATE-LINKAGE SITE ASN-453.

MEDLINE-22660472; PubMed=12754519;
A Zhang H., Li X.-J., Martin D.B., Abebraold R.;
Alang H., Li X.-J., Martin D.B., Abebraold R.;
Identification and quantification of N-linked glycoproteins using
T "identification and quantification of N-linked glycoproteins using
T "Identification and quantification of N-linked glycoproteins using
T "Identification and quantification of N-linked glycoproteins using
T Not Explored To Table isotope labeling and mass spectrometry.";
I Nat. Biotechnol. 21:660-666(2003).
I PUNCTION: The arctiprocal reaction, factor XII after its binding
t or a negatively charged surface. It also releases bradykinin from
HWW kiningen and may also play a role in the renin-angiotensin
System by converting prorent into renin.

C -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Xaa and Lys-|-Xaa
Donda, including Lys-|-Arg and Arg-|-Ser bonds in (human)
kiningen to release bradykinin.

-!- SUBUNIT: The zymogen is activated by factor XIIa, which cleaves LIKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQ---LKM 179 PARTIAL SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-91152016; Pubmed-1998666;
MCMullen B.A., Fujikawa K., Davie E.W.;
"Location of the disulfide bonds in human plasma prekallikrein: the presence of four novel apple domains in the amino-terminal portion of 180 TVVKLISHRECQOPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVC--SLQG--RMTL SEQUENCE FROM N.A., AND VARIANTS SER-143; THR-178; GLN-202; CYS-269; VAL-311; ALA-388; ALA-381; PRO-442 AND GLN-560.
Rieder M.J., Armel T.Z., Carrington D.P., Coura M., Kuldanek S.A., Rajkumar N., Toch B.J., Yi Q., Nickerson D.A.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. NEDLINE-20487549; PubMed=11031105; WEDLINE-20487549; PubMed=11031105; Yu H., Anderson P.J., Freedman B.I., Rich S.S., Bowden D.W.; "Genomic structure of the human plasma prekallikrein gene, identification of allelic variants, and analysis in end-stage renal KAL HUMAN STANDARD, PRT, 638 AA.
P03952,
23-007-1986 (Rel. 02, Created)
23-007-1986 (Rel. 02, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation update)
Plasma kallikrein precursor (BC 3.4.21.34) (Plasma prekallikrein)
KIKBI OR KLKS.
Homo sapiens (Human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; SEQUENCE FROM N.A. PDMed=3521732; Church D.W.; Evikawa K., McMullen B.A., Davie E.W.; Churg D.W.; Fujikawa K., McMullen B.A., Davie E.W.; "Human plasma prekallikrein, a zymogen to a serine protease that contains four tandem repeats."; Biochemistry 25:2410-2417(1986). the molecule."; Biochemistry 30:2050-2056(1991). Genomics 69:225-234(2000). disease."; RESULT 30 KAL\_HUMAN d ò ద ਨੇ 임

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and a besay Chain, which associates with HW kiningen. These contains are altitled by one or more distillated bonds.

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 STATE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
 MGD, MGI:1933407; Tupres5.

R MID: MGD, MGI:1933407; Tupres5.

R InterPro; IPR009003; Cye_Ser_trypsin.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001134; Peptidase_S1.

R InterPro; IPR001134; Peptidase_S1A.

R PROMOS9; Lrypain; I.

R PRIMIS; PR00012; CHYMOTRYEN.

R PRIMIS; PR00120; TYPY SPC: 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

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R PROSITE; PS00136; TRYPSIN SER; 1.

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R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

 EXTRACELLULAR (POTENTIAL). SRCR.
 Mitsui S., Yamaguchi N.;
"cDNA cloning of mouse spinesin.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
 IsoId=Q9ER04-2; Sequence=VSP_005397, VSP_005398;
 Name=3;
ISOZd=Q9ER04-4; Sequence=VSP_005396;
SIMILARITY: Belongs to peptidase family Sl.
SIMILARITY: Contains 1 SRCR domain.
 Name=2;
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EMBL; AB0416423; BAB20278 1;
EMBL; AB041037; BAB40328 1;
HSSP; P00763; LDPO.
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 rissum=Brain;
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 436
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 132 RCAQPSRTIQTICLPSMYNDPQFGTSCEITGFG--KENSTDYLYPEQLKMTVVKLISHRE 189
 909
 548 CÓK-RYODYKITORMYCAGYKEGGKDACKGDSGGPLYCKHNGMRLVGITSWGBGCARRE
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 17 TLRPRFKIIGGEFTTIENOPWFAAIY-----RRHRGGSVTYVCGGSLISPCWVISATHCF
 72 IDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEG
 Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 26.7%; Score 402; DB 1; Length 638;
llarity 33.1%; Pred. No. 1.2e-28;
Conservative 56; Mismatches 98; Indels 2
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10-02P264; QSER02; QSER03;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annocation update)
Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
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 R -> Q. _________/FTId=VAR_016286.
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 FTId=VAR_016280.
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 -> Q.
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|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|-------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------|------------------------------------------------|
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| 170<br>319<br>319<br>144<br>10<br>192<br>325<br>49632                                                                                                                                                                                                                                                                                             | 26.<br>34.<br>vative                                                                                          | - FOCGC<br> -  <br> SECGF                                    | CFIDYE                                                | AHHNDIA<br>   : <br>-HDYDVA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | OLKMTV1<br> : : <br>TLQDTM1                      | TGIVSV<br> - - <br>VGVVSV                      |
| 3170<br>375<br>1<br>1<br>1<br>1<br>183<br>325<br>455 AA;                                                                                                                                                                                                                                                                                          | h<br>Similarity 34.<br>96; Conservative                                                                       | PSSPPEELK<br>                                                | PCWVISATHCFIDYP<br>      ::     :<br>  HWVYTAAHCMYSF- | HKDYSADTL.<br>       <br>HPLYSAQN-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | NSTDYLYPE<br>: :<br>DPSHTHSSD                    | CSLQGRMTL<br> <br>CPSGDTWHL                    |
| CARBOHYD<br>CARBOHYD<br>CARBOHYD<br>VARSPLIC<br>VARSPLIC<br>VARSPLIC<br>CONFLICT<br>SEQUENCE                                                                                                                                                                                                                                                      | Query Match<br>Best Local Si<br>Matches 96;                                                                   | 197                                                          | 61 250                                                | 107                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 351                                              | 227                                            |
| 0.11.11.11.11.11.11.11.11.11.11.11.11.11                                                                                                                                                                                                                                                                                                          | MBe                                                                                                           | \$ 8<br>8                                                    | දු පු                                                 | \$ A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | දු දු                                            | \$ g                                           |

TISSUBERDATE FROM N.A.

TISSUBERDATERS, and Spleen;

TISSUBERDATERS, pubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine MEDLINE-88209431; PubMed-2835076; Leyrus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.; A novel trypain-like serine procease (hepsin) with a pucative transmembrane domain expressed by human liver and hepatoma cells."; Biochemistry 27:1067-1074(1988). Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 417 AA. STANDARD: SEQUENCE FROM N.A. NCBI\_TaxID=9606; HPN OR TMPRSSI. TISSUE=Liver; HUMAN HEPS HUN P05981; HEPS\_ 

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MEDLINE=91358502; PubMed=1885621;
Tsuji A., Terres-Rosado A., Arai T., le Beau M.M., Lemons R.S., Chou S.H., Kurachi K.;
"Hepsin, a cell membrane-associated protease. Characterization, tissue distribution, and gene localization.";
J. Biol. Chem. 266:16948-16953(1991). 

(POTENTIAL). CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) Transmembrane; Signal-anchor.
SERINE PROFERSE HEFSIN, NON-CATALYTIC
CHAIN (POTENTIAL)
SERINE PROTEASE HEPSIN, CATALYTIC CHAIN R EMBL; X07732; CAA30558.1; -R EMBL; X07732; CAA30558.1; -R EMBL; X07732; CAA30558.1; -R EMBL; X07702; CAA30558.1; -R EMBL; S00845; S00845
R HSSP; PO0763; LDPO.
R MRXOPS; S01.224; -R Genew; HGNC:5155; HPN.
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R InterPro; IPR001054; Peptidase S1.
R InterPro; IPR001054; Peptidase S1.
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R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN HIS; 1.
R PROSITE; PS0135; TRYPSIN HIS; 1.
R HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, HYDROLASE; HEPSIN, NON-CHAIN HYDROLASE; HEPSIN, HYDROLAS (POTENTIAL). EXTRACELLULAR (POTENTIAL) SERINE PROTEASE. 417 417 17 44 163 급 원 DOMAIN TRANSMEM CHAIN

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243 AA
 Similarity 38.7
4; Conservative
 STANDARD;
 WIQ 242
 WIR 265
 TRY1 BOVIN
 94;
 Query Match
Best Local S
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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 205
 123
 LKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQ---LKWT 180
 261 VHLSSP----LPLTEYIQPVCLPAAGQALVDGKICTVTGWG---NTQY-YGQQAGVLQEA 312
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 DYPKKEDYIVYLGRSRLNSNTQGB-----MKFEVENLILHKDY----SADTLAHHNDIAL
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 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
11-P29 precursor (EC 3.4.21.4).
Gallus gallus (Chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gaps
 Blocken. J. 307:471-479(1995).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- COPACTOR: Binds I calcium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.
-!- SIMILARITY: Belongs to peptidase family S1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
W, B2086FF661E551D7 CRC64;
 TISSUE=Pancreas;
MEDLINE=95251611; PubMed=7733885;
Wang K., Gan L., Lee I., Hood L.E.;
"Isolation and characterization of the chicken trypsinogen gene family.";
 41;
 DB 1; Length 417;
 26.3%; Score 396.5; DB 1; Length 4.2 35.8%; Pred. No. 2.2e.28; Mismatches 89; Indels
 GIVSWGRGCALKDKPGVYTRVSHFLPW----IRSHTKEENGL 274
 373 GIVSWGIGCALAQKPGVYTKVSDFREWIFQAIKTHS-EASGM 413
 45011 MW;
 EMBL; U15157; AAA79914.1; -. PIR; S55066; S55066.
 101; Conservative
 STANDARD;
203
257
257
353
188
322
342
342
112
112
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9031;
 TRY3 CHICK Q90629;
ACT_SITE
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143 ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 202
 73
 25 KIVGGYTCPEHSVPYQVSL-----KSRIQV
 RIGEYNIDVQEDSEVVRSSSVIIRHPKYSSITL--NNDIMLIKLAS----AVEYSADIQP
 128 IALPS--SCAKAGTECLISGWGNTLSNGYNYPELLQCLNAPILSDQECQEA--YPGDITS
 KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV
 203 KMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLP
 83 YLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT
 (Fragment).
Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;
Bovidae, Bovinae; Bos.
NCBI_TaxID=9913;
 25;
 26.2%; Score 395.5; DB 1; Length 248; 38.7%; Pred. No. 1.4e-28; Live 40; Mismatches 84; Indels 25.
 21-JUL-1986 (Rel. 01, Created)
1-JUNO-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypainogen, cationic precursor (EC 3.4.21.4) (Beta-trypsin)
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22-JAN-02.
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 22-JAN-02.
27-APR-02.
12-SEP-01.
 0-SEP-00.
 26-58P-01.
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 7-JAN-01
 7-JAN-01
 6-SEP-01
 5-SEP-01
 2-JAN-02
 8-NOV-01
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 MEDILINE=66079271; PubMed=5892911;

Kauffman D.L.;

"The disulphide bridges of trypsin.";

"The disulphide bridges of trypsin.";

-! CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.

-! CORACYON: Binds I calculm ion per subunit.

-! SUBCELLULAR LOCATION: Extracellular.

-! TISSUE SPECIFICITY: Synthesized in the acinar cells of the
 pencreas.

PTM: AUTOCATALYTIC CLEAVAGE AFTER LYS-20 LEADS TO BETA-TRYPSIN I RELEASING A TERMINAL HEXAPEPTIDE. SUBSEQUENT CLEAVAGE AFTER LYS-145 LEADS TO ALPHA-TRYPSIN, FURTHER CLEAVAGE AFTER LYS-190 YIZELDS ESEUDOTRYPSIN, A CLEAVAGE MAY ALSO OCCUR AFTER ARG-119. SIMILARITY: Belongs to peptidase family S1.

DATABASE: NAME-Worthington enzyme manual;

WWW="http://www.worthington-biochem.com/TRY/".
 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF CALCIUM-BINDING SITE. MEDLINE=76072097; PubMed=512; Bode W., Schwager P.; "The refined crystal structure of bovine beta-trypsin at 1.8-A resolution. II. Crystallographic refinement, calcium binding site, benzanidine binding site and active site at pH 7.0."; J. Mol. Biol. 98:693-717(1975).
 the
 [2]
SEQUENCE OF 15-243, AND DISULFIDE BONDS.
MINES O., HOLESOVSKY V., Tomasek V., Sorm F.;
Mikes O., Holegovsky V., Tomasek V., Sorm F.;
"Covalent structure of bovine trypsinogen. The position of remaining amides.";
Enothem. Biophys. Res. Commun. 24:346-352(1966).
 Hartley B.S.;
"Homologies in serine proteinases.";
Philos. Trans. R. Soc. Lond., B, Biol. Sci. 257:77-87(1970)
 MEDLINE=77112431; PubMed=556951;
Kosaiakoff A.A., Chambers J.L., Kay L.M., Stroud R.M.;
"Structure of bovine trypsinogen at 1.9-A resolution.";
Biochemistry 16:654-664(1977).
[1]
SEQUENCE FROM N.A.
TISSUE-Pancreas,
Okajima T., Maniwa M., Nagao S., Fujikawa H., Goto S.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
 REVISIONS.
MEDLINE=75146445; PubMed=1092332;
Titani K., Eriosson L.H., Neurath H., Walsh K.A.;
"Amino acid sequence of dogfish trypsin.";
Biochemistry 14:1358-1366(1975).
 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 [3]
REVISIONS.
MEDLINE-72035053; PubMed=4399051;
 EMBL; D38507; BAA07516.1;
PDB; 1AQ7; 25-FBB-98.
PDB; 1AU7; 14-OCT-98.
PDB; 1AZ8; 13-UAN-99.
PDB; 1BJU; 13-UAN-99.
 13-JAN-99,
13-JAN-99,
29-JAN-96,
15-OCT-95,
 DISULFIDE BONDS
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products.
-!- BNZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Bolongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Bolongs to least, 2 kringle domains.
-!- SIMILARITY: MELSS.
-!- SIMILARITY: MELSS.
 S PPEELKFQCGQKTLRPR---FKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISP
 Schaller J., Straub C., Kampfer U., Rickli E.E.;
"Complete amino acid sequence of ovine miniplasminogen.";
Protech. Seq. Data Anal. 5:21-55(1992).

"Complete amino acid sequence of ovine miniplasminogen.";
Protech. Seq. Data Anal. 5:21-55(1992).

-I. FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as embryonic development, tissue remodaling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Gradian follode. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as Cl and CS. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys- |-Xaa > Arg- |-Xaa; higher selectivity than trypsin. Converts fibrin into soluble
 Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
 59
 26.0%; Score 392.5; DB 1; Length 343; llarity 36.0%; Pred. No. 4e-28; Conservative 35; Mismatches 107; Indels 29
 37662 MW; 8DF6EBA92D596EE0 CRC64;
 HEAVY CHAIN A.
LIGHT CHAIN A.
KRINGLE 4.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
 15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Plasminogen (EC 3.4.21.7) (Fragment).
 InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR0010001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR003166; Peptidase_S1A.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
 SEQUENCE.
MEDLINE=93149995; PubMed=1492092;
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Best Local Similarity
Matches 96; Conserv
 343 AA;
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 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 142
 143 ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 202
 203 KMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLP 262
 179 NMFCAGYLEGGKDSCQGDSGGPVVCS--GK--LQGIVSWGSGCAQKNKPGVYTKVCNYVS 234
 82
 68
 KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV
 Gaps
 25;
 h. 26.2%; Score 394.5; DB 1; Length 243; Similarity 37.4%; Pred. No. 1.7e-28; 91; Conservative 41; Mismatches 86; Indels 25.
 A.
 343
 PLMN SHEEP

ID PLMN SHEEP STANDARD;

AC P81286;

DT 15-DEC-1998 (Rel. 37, Created)
PDB, 1PPB, 31-JAN-94, PDB, 1PPB, 31-JAN-94, PDB, 1QA0, 10-APR-00, PDB, 1QB0, 29-APR-00, PDB, 1QB0, 30-APR-00, PDB, 1QB0, 30-APR-00, PDB, 1QB0, 30-APR-00, PDB, 1QB0, 30-APR-00, PDB, 1QB0, 19-JAN-00, PDB, 1QB0, 19-JAN-00, PDB, 1ZEI, 09-JUL-94, PDB, 1ZEI, 09-JUL-94, PDB, 1TAM, 24-JUL-94, PDB, 1TAM, 24-JUL-94, PDB, 1TAM, 24-JUL-94, PDB, 1TAM, 24-JUN-97, PDB, 1TAM, 24-JUN-97, PDB, 1TAM, 20-NOV-94, PDB, 1TAM, 30-NOV-94, PDB, 1XUM, 11-NOV-98,
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 WIR 265
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 RESULT 35
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247 AA;
 SEQUENCE FROM N.A.
 262 PWIR 265
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 121
 199
 237
 CWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDI
 KMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTG
 EWVLTAAHCLDSILGPSFYTVILGAHYEMAREASVQEIPVSRLFLEPSRA-----DI
 ALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF----GTSCEITGFGKENSTDYLYPEQL
 trypsin family.";

Bur. J. Blochem. 193:767-773 (1990).

Bur. J. Blochem. 193:767-773 (1990).

-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-xaa, Lys-|-Xaa.

-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

-!- SUBCELDULAR LOCATION: Extracellular.

-!- SIMILARITY: Belongs to peptidase family $1.
 SEQUENCE FROM N.A.
STRAIN=Holstein-Friesian, TISSUE=Pancreas;
MEDLINE=91065383, PubMed=1701147,
MEDLINE=91065383, PubMed=1701147,
MICHEROU I., Wicker C., Guilloteau P., Toullec R., Puigserver A.;
"Isolation and nucleoride sequence of cDNA clone for bovine
pancreatic anionic trypsinogen. Structural identity within the
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
12-OCT-2003 (Rel. 50-OCT)
13-OCT-2003 (Rel. 50-OCT)
13-OCT-2003 (Rel. 50-OCT)
14-OCT-2003 (Rel. 50-OCT)
15-OCT-2003 (Rel. 50-OCT)
16-OCT-2003 (Rel. 50-
 MEROPS, SO1.258; ...
InterPro; IPR00903; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001144; Peptidase_S1.
InterPro; IPR001144; Peptidase_S1A.
Pfam; PF00089; trypsin, 1.
PRONTS; RR00722; CHYMOTRYPSIN.
SMART; SM00020; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIG; 1.
PROSITE; PS00135; TRYPSIN_HIG; 1.
PHOTOLASE; Serine protease; Digestion; Pancreas; Zymogen; Calcium-binding; Signal.
 POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN, ANIONIC.
 247 AA.
 : ||| ||| :|||| 336
310 VTSWGLGCARPNKPGVYVRVSTYVPWI 336
 238 IVSWGRGCALKDKPGVYTRVSHFLPWI 264
 PRT;
 EMBL; X54703; CAA38513.1; -.
 STANDARD;
 PIR; S13813; S13813.
HSSP; P00763; 1DPO.
 NCBI_TaxID=9913;
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Q29463;
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 is in no "... d for commercia
 71 VRLGEYNIDVLEGGEQPIDASKIIRHPKYSSWTL--DNDILLIKLSTP----AVINARVS 124
 142 IICLPSMYNDPQFGTSCELTGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVT 201
 202 TKMLCAADPQWKTDSCOGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFL 261
 VYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ 141
 23 KIVGG-YTCAENSVPYQVSLNAGY-----HPCGGSLINDQWVVSAAHCY-----QYHLQ 70
 23 KIIGGEFTTIENO-PWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYI
 Proc. Natl. Acad. Sci. U.S.A. 80:7486-7490(1983).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Lou-|-Xaa. Extracellular.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: Belongs to peptidase family S1.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
NCBL_TaxID=9615;
 MEDLINE-84170253; PubMed-6584866; Pinsky S.D. Laforge K.S., Luc V., Scheele G.; pinsky S.D., Laforge K.S., Luc W., Scheele G.; pinsky S.D., Laforge K.S., Luc W., Scheele G.; scheelend of CDNA closes encoding secretory isoenzyme form sequence determination of canine pancreatic prechymotrypsinogen
 27;
 ch 25.9%; Score 390.5; DB 1; Length 247; I Similarity 38.1%; Pred. No. 4e-28; 93; Conservative 41; Mismatches 93; Indels 27.
 CALCUTM (VIA CARBONYL CALCUTM (VIA CARBONYL CALCUTM (VIA CARBONYL CAYGEN)
(BY SIMILARITY).
(BY SIMILARITY).
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(CALCUTM (BY SIMILARITY).
(CHARGE RELAY SYSTEM.
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 REQUIRED FOR SPECIFICITY.
50A070495A7731DB CRC64;
RELAY SYSTEM.
I (BY SIMILARITY)
 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
28-EFBE-2003 (Rel. 41, Last annotation update)
Chymctrypainogen 2 precursor (BC 3.4.21.1).
Canis familiaris (Dog)
 263 AA
 CALCIUM
 26289 MW;
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MEDLINE=97053999; PubMed=8898378;
 (See http://www.isb-sib.ch/announce/
 126
 186
 182
 246
 ATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI 126
 72
 9
 127 RSKEGRCAQPSRIIQIICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLIS
 FOCGOKTLRPRF----KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
 127 ATP----ARFSKTVSAVCLPQATDDFPAGTLCVTTGWGLTKHTNANTPDKLQQAALPILS
 187 HRECOOPHYYGSEVTTKMLCAADPQWKTDSCOGDSGGPLVCSLOGRMTLTGIVSWGRGCA
 Gaps
 15-DEC-1998 (Rel. 37, Created)
10-DEC-2009 (Rel. 37, Last enotation update)
10-OCT-2003 (Rel. 42, Last enotation update)
Kallikrein 6 precursor (EC 3.4.21.-) (Protease M) (Neurosin) (Zyme)
 KIKG OR PRSS9.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
IPR00132; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC, 1.
PROSITE; PS00134; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
Bydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
SIGNAL
 22;
 25.9%; Score 390; DB 1; Length 263; larity 33.2%; Pred. No. 4.8e-28; Conservative 51; Mismatches 100; Indels 2
 CHYMOTRYPEIN 2, A CHAIN.
CHYMOTRYPEIN 2, A CHAIN.
CHYMOTRYPEIN 2, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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 2A2F449D813B3961 CRC64;
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or send an email to license@isb-sib.ch).
 247 LKDKPGVYTRVSHFLPWIR 265
 STSTPGVYARVTKLIPWVQ 257
 27787 MW;
 EMBL, K01173, AAA30841.1; -. PIR, A21195. A21195. PISP, P00766; IACB. MESCPS, S01.152; -.
 STANDARD;
 19 2 3 4 1 1 1 1 1 2 2 1 1 2 2 2 2 3 3 A 3 ,
 Similarity
 NCBI_TaxID=9606;
 86;
 KLK6 HUMAN
Q92876;
 DISULFID
DISULFID
DISULFID
SEQUENCE
 Query Match
Best Local S
 CHAIN
CHAIN
CHAIN
CHAIN
ACT SITE
ACT SITE
ACT SITE
DISULFID
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 17
 67
 RESULT 38
KLK6_HUMAN
 SP59)
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[1] SEQUENCE FROM N.A.

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TISSUB—COLOD,

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RETAUSPERS R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Joederg B., Buetow K.H., Schaefer C.F., Bhat: N.K.,

RA Altschul S.F., Joederg B., Buetow K.H., Schaefer C.F., Bhat: N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Wagner R.B., Toshiyuki S., Carninci P., Prange C.,

RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., World N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rohards S.W., Worth D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Murny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Murny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Hakesley R.W., Touchman J.W., Schoergren E.J., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Schwutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rum and mouse CDNA sequences."; N. Warra M.A.,

R. Proc. Natl. Acad. Sci. U.S.A., 99:169916903(2002).

- SUBCELLUAR LOCATION: Secreted.

- TISSUE SPECIFICITY: Preferentially expressed in brain. Also found in colon and kidney.

In colon and kidney.
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 TIŜSUE-COlon,
MEDLINE-97157069; PubMed-9003450;
MEDLINE-97157069; PubMed-9003450;
Yamashiro K., Tsuruoka N., Kodama S., Tsujimoto M., Yamamura Y.,
Tanaka T., Nakazato H., Yamaguchi N.;
"Molacular cloning of a novel trypsin-like serine protease (neurosin)
Preferentially expressed in brain.";
Ejochim. Biophys. Acta 1350:11-14(1997).
 MEDLINE=20079158; PubMed=10610719;
Yousef G.M., Luo L.Y., Scherer S.W., Sotiropoulou G., Diamandis E.. Molecular characterization of Zyme/protease M/neurosin(PRSS9), a hormonally regulated kallikrein-like serine protease.";
Genomics 62:251-259(1999).
 TISSUE=Brain,
MEDLINE=97460104; PubMed=9312124;
MEDLINE=97460104; PubMed=9312124;
MEDLINE=97460104; PubMed=9312124;
MEDLINE=97460104; PubMed=9312124;
Johnson B.P., Nariek T., Miller J.R., Mackellar W.,
Hepburn D., Corvalan J., McClure D., Liu X., Stephenson D.,
Clemens J., Johnstone B.M.;
"Zyme, a novel and potentially amyloidogenic enzyme cDNA isolated
from Alzheimer's disease brain.";
J. Biol. Chem. 272:25135-25142(1997).
 SEQUENCE FROM N.A. MEDLINE=2051030) FubMed=11054574; MEDLINE=20510030) FubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J. Moss P., Paeper B., Wang K.; Mang K.; Mang K.; Sequencing and expression analysis of the serine protease gene cluster located in Chromosome 19q13 region."; eque 257:119-130(2000).
 Anisowicz A., Sotiropoulou G., Stenman G., Mok S.C., Sager R. "A novel protease homolog differentially expressed in breast ovarian cancer.";
 Mol. Med. 2:624-636(1996)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
11-ACR-2004 (Rel. 43, Last annotation update)
Transmembrane protease, serine 3 (EC 3.4.21.-)
 SRCR.
 ACT_SITE
ACT_SITE
ACT_SITE
SITE
 DOMAIN
TRANSMEM
 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 83 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAOPSRTIOT 142
 143 ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMTVVKLISHRECQQPHYYGSEVTT 202
 125 --LPLERDCSANTTSCHILGWGKTADGD--FPDTIQCAYIHLVSREECE--HAYPGQITQ 178
 203 KMICAADPQWKTDSCOGDSGGPLVCSLOGRMTLTGIVSWGR-GCALKDKPGVYTRVSHFL 261
 179 NMLCAGDEKYGKDSCQGDSGGPLVCGDH----LRGLVSWGNIPCGSKEKPGVYTNVCRYT 234
 70
 KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV
 th Similarity 37.7%; Pred. No. 4.9e-28; Score 36; Mismatches 89; Indels 27; Gaps
 POTENTIAL.
ACTIVATION PEPTIDE (POTENTIAL).
KALLIKREIN 6.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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W, ARAO3F9145DB7AAB CRC64;
 (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
 EMBL: D78203; BAB07113.1; ---

R EMBL: D78203; BAB07113.1; ---

R EMBL: AF013988; AAB66483.1; ---

R EMBL: AF143527; AAG33359.1; ---

R EMBL: AF15518.1 ---

R EMBL: AF143527; AAG33359.1; ---

R EMBL: AF15518.1 ---

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R EMBL: AF15518.1 ---

R EMBL: AF15518.1 ---

R EMBL: AF15518.1 ---

R EMBL: AF1518.1 ---

R EMBL: AF1518.1 ---

R EMBL: AF1518.1 ---

R EMBL: AF16618.1 ---
 ż
 453
 26856 MW;
 STANDARD;
 16
244
244
1197
1197
2331
2033
218
1182
134
 17
522 2
62 1
106 1
197 1
131 2
138 2
133 2
24 4 AA,
 PWIR 265
 NWIQ 238
 TMS3 MOUSE
ID TMS3 MOUSE
AC Q8K1T0; Q8VDE0;
 DISULFID
CARBOHYD
SEQUENCE
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Matches 92
 23
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 DISULFID
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 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
 Hancock M.
 reticulum.
-- TISSUE SPECIFICITY: Expressed in the spiral ganglion, the cells supporting the organ of Corti and the stria vascularis.
-- PTM: Undergoes autoproteolytic activation.
-- SIMILARITY: Belongs to peptidase family S1.
-- SIMILARITY: Contains 1 LDL receptor class A domain.
-- SIMILARITY: Contains 1 SRCR domain.
 CLEAVAGE.

MEDLINE=2281255; PubMed=12393784;

MEDLINE=2281255; PubMed=12393784;

Guipponi M., Vuagniaux G., Mattenhofer M., Shibuya K., Vazquez M.,

Guipponi M., Vuagniaux G., Humele E., Okui M., Rossier C., Hancock M.

Buchet K., Reymond A., Hummler E., Marzella P.L., Kudoh J.,

Shimizu N., Scott H.S., Antonarakis S.B., Rossier B.C.;

"The transmembrane serine protease (TMPRS3) mutated in deafness

PFNB810 activates the epithelial sodium channel (ENAC) in vitro.";

Hum. Mol. Genet. 11:2829-2836 (2002).

-!-FUNCTION: Probable protease. Seems to be capable of activating
 PRINTS, PRO0022; CHYMOTRYPSIN.
SMART; SMO0122; CHYMOTRYPSIN.
SMART; SMO0122; DLLA.
SMART; SMO01202; SR; 1.
SMART; SMO0200; SR; 1.
PROSITE; PS51006; LDLRA_1; 1.
PROSITE; PS50067; SRCR_2, 1.
PROSITE; PS50067; SRCR_2, 1.
PROSITE; PS50040; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_DIS; 1.
PROSITE; PS00135; TRYPSIN_SIR; 1.
PROSITE; PS00135; TRYPSIN_SIR; 1.
PROSITE; PS00135; TRYPSIN_SIR; 1.
PROSITE; PS00135; TRYPSIN_SIR; 1.
PROSITE; PS00135; TRYPSIN_SIR; 1.
PROSITE; PS00135; TRYPSIN_SIR; 1.
PROSITE; PS00135; TRYPSIN_SIR; 1.
PROGIASE; SEIGH PACEGASE; 1.
PROGIASE; SEIGH PACEGASE; 1.
PROGIASE; SEIGH PACEGASE; 1.
PROGIASE; SEIGH PACEGASE; 1.
PROGIASE; SEIGH PACEGASE; 1.
PROGIASE; SEIGH PACEGASE; 1.
PROGIASE; SEIGH PACEGASE; 1.
PROGIASE; 1.
PROGIA
Mus musculus (Wouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
[1]
 SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CLEAVAGE (POTENTIAL).
 -1- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
 SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND FUNCTION IN ENAC
 EXTRACELLULAR (POTENTIAL).
LDL-RECEPTOR CLASS A.
 EMBL; AJ429216; CAD22137.1; EMBL; AJ429216; CAD22137.1; EMBL; AJ300738; CAC83350.1; ...
HSSP; PO0761; 1AN1.
MGD; MGI:2155445; Tmprse3.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR00112; LDL receptor A.
InterPro; IPR001134; Peptidase_SI.
InterPro; IPR001134; Peptidase_SI.
InterPro; IPR001134; Peptidase_SIA.
InterPro; IPR001190; Src_receptor.
Pfam; PF00087; 1dl recept a; 1.
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KIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKL 184
 (See http://www.isb-sib.ch/announce
 313 RLQT----ALNESDTVGAVCLPAKEQHFPKGSRCWVSGMGHTHPSHTYSSDMLQDTVVPL
 185 ISHRECQOPHYYGSEVTTKMLCAADPOWKTDSCOGDSGGPLVCSLOGRMTLTGIVSWGRG
 QCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCF
 72 IDY--PKKEDYIVYLGRSRLNSNT-----QGEMKPEVENLILHKDYSADTLAHHNDIALL
 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
 SRCR.
SERINE PROTEGES.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CLEAVAGE (POTENTIAL).
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
 MENOPS, S01.313; -.

MEROPS, IPRO01024; Peptidase S1.

METAPRO, IPRO01104; Peptidase S1.

METAPRO, IPRO01104; Peptidase S1.

READ, PRO01029; Trypsin; 1.

READ, SMART; SMOOTO20; Trypsin; 1.

READ, PROSITE; PS00134; TRYPSIN DOM; 1.

READSITE; PS00134; TRYPSIN DOM; 1.

READSITE; PS00135; TRYPSIN DOM; 1.

READSITE; PS00136; TRYPSIN DOM; 1.

READSITE; PS00136; TRYPSIN SRR; 1.

READSITE; PS00136; TRYPSIN SRR; 1.

READSITE; PS00136; TRYPSIN SRC; 1.

MACOLORS, PSCR 1; FALSE NEG.

MACOLORS, SRCR 1; FALSE NEG.
 25.7%; Score 388; DB 1; Length 457; 34.2%; Pred. No. 1.5e-27;
 47; Mismatches 102; Indels
 EXTRACELLULAR (POTENTIAL)
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 342
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or send an email to license@isb-sib.ch).
 CALKDKPGVYTRVSHFLPWIRSHTKE 270
 CAEPNHPGVYAKVAEFLDWIHDTAQD
 49574 MW;
 EMBL; AB028140; BAB20375.1; -.
 HSSP; P00763; 1DPO.
Genew; HGNC:14908; TMPRSS5.
 91; Conservative
 STANDARD;
 49
70
 1112
2112
2258
3008
3008
2017
2017
2019
2019
2019
319
457 AA,
 Similarity
 Glycoprotein.
DOMAIN
TRANSMEM
 RESULT 41
PSS8_RAT
ID PSS8_RAT
 DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
SITE
DISULFID
 DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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 187
 259
 RECOOPHYYGSEVITKWLCAADPQWKIDSCOGDSGGPLVCSLOGRMTLIGIVSWGRGCAL 247
 367 KICNHRDVYGGIISPSMLCAGYLKGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAE 426
 207 CGTRIGYSPR--IVGGNMSSLTQWPWQVSL--QFQG---YHLCGGSVITPLWIVTAAHCV
 ---SEPLTFDETIQPICLPNSEENFPDGKLCWTSGWGATEDGGDASP-VLNHAAVPLISN
 260 YDLYHPKSWTVQVGLVSLMDSPVPSHL---VEKIIYHSKYKPKRLG--NDIALMKL----
 131 GRCAQP---SRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLXMTVVKLISH
 CGOKT-LRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCF
 72 IDYPKKEDYIVYLGR-SRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE
BY SIMILARITY.
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L = N H (IN REF. 1) (POTENTIAL).
L -> I (IN REF. 1) CAC83350).
V -> I (IN REF. 1) CAC83350).
W7. 1ABCBF10AF6E1EF6 CRC64;
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Similarity 35.6%; Pred. No. 1.3e-27; Similarity 453; Mismatches 102; Indels 25)4; Conservative 43; Mismatches 102; Indels 25
 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
18-DEPEB-2003 (Rel. 41, Last annotation update)
Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
 457 AA
 248 KDKPGVYTRVSHFLPWIRSHTKEE 271
 49491 MW;
 STANDARD;
 453 AA;
 94;
 TMS5_HUMAN
 DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
CARBOHYD
CONFLICT
SEQUENCE
 188
 13
 Query Match
 о9н383;
 Local
 RESULT 40
TMS5 HUMAN
 Matches
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HIGEPPC; IPR003003; Cys Ser trypsin.
InterPrc; IPR001254; Peptidase\_S1.
InterPrc; IPR001314; Peptidase\_S1.
InterPrc; IPR001314; Peptidase\_S1.
InterPrc; IPR001254; Peptidase\_S1.
PRINTS; PR00722; CHYMCTRYPSIN.
SMART; SM00202; Tryp\_SRC; 1.
PROSITE; PS50240; TRYPSIN DCM; 1.
PROSITE; PS00134; TRYPSIN DCM; 1.
PROSITE; PS00135; TRYPSIN JCM; 1.
PROSITE; PS00135; TRYPSIN SR; 1.
PROSITE; PS00135; TRYPSIN SR; 1. eimilarity).
--- SUBUNIT: Heterodimer of two chains, light and heavy, held by a disulfide bond (By similarity).
--- SUBCELULIAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
--- SIMILARITY: Belongs to peptidase family SI. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus. (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(POTENTIAL). ACTIVATION PEPTIDE (BY SIMILARITY) PROSTATIN LIGHT CHAIN. PROSTATIN HEAVY CHAIN. "Molecular cloning and expression of rat prostasin.", Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: Possesses a trypsin-like cleavage specificity (By BY SIGNATION OF THE PROTEGES.

SERINE PROTEGES.

INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIYCHARGE  (GLCRAC.) IISSUE=Kidney; Adachi M., Kitamura K., Miyoshi T., Tomita K.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. SED1AF05D9213B98 CRC64; I -> V (IN REF. 1) A -> V (IN REF. 1) Q9ES87; Q9ER01; 16-CCT-2001 (Rel. 40, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 18-DEFEB-2003 (Rel. 41, Last annotation update) Prostasin precursor (EC 3.4.21.-). 36843 MW; (Rat) Rattus norvegicus SEQUENCE FROM N.A. [2] SEQUENCE FROM N.A. NCBI\_TaxID=10116; ransmembrane SIGNAL PROPEP CHAIN CHAIN PROPEP TRANSMEM DOMAIN DISULFID DISULFID ACT SITE ACT SITE ACT SITE CARBOHYD CONFLICT DISULFID CONFLICT PRSS8 Wang 

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 R InterPro; IPR009003; Cys Ser_trypsin.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1A.
R InterPro; IPR001319; Perceptor.
R Pfam; PF00089; trypsin; 1.
R PRINTS; PR00722; CHYMOTRYPSIN.
R SMART; SM00202; SR; 1.
R PROSITE; PS00240; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN HIS; 1.
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 maintenance
 TISSUBELIVER;
MEDLINE=93305733; PubMed=8318546;
Farley D., Reymond F., Nick H.;
"Cloning and sequence analysis of rat hepsin, a cell surface serine
 Biochim. Biophys. Acta 1173:350-352(1993).
-!- FUNCTION: Plays an essential role in cell growth and of cell morphology.
-!- SUNCELLUIAR LOCATION: Type II membrane protein.
-!- SIMILARITY: Belongs to peptidase family 51.
 IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine protease hepsin (EC 3.4.21.-).
 416
 EMBL; X70900; CAA50256.1; -.
 PIR; S33777; S33777.
HSSP; P00763; 1DPO.
MBROPS; S01.224; -.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 proteinase.
 238
 HEPS RAT
ID HEPS RAT
 a
 à
```

Gaps

25.6%; Score 386.5; DB 1; Length 342; 36.3%; Pred. No. 1.4e-27; ive 29; Mismatches 108; Indels 37;

Conservative

:66

Similarity

Query Match Best Local

Best Loca Matches

143 P----VTFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLQTPRPLQQLEVPLISR 198

REC------QOPHYYGSEVITRMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTG

188

129 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK-ENSTDYLYPEQLKWTVVKLISH 187

HCFPREHSKEEYEVKLGAHOLDSFSNDIVVHTVAQIISHSSYREE--GSQGDIALIRLSS

HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 128

69 69

8 8 8 8 8

37 CG-AVIQPR--ITGGGSAKPGQWPWQV-----SITYNGVHVCGSLVSNQWVVSAA

CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTY----VCGGSLISPCWVISAT

us-09-880-503-5.rsp

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 205 --PERNRVLSRWRVFAG--AVARTSPHAVQLGVQAVIYHGGYLPFRDPTID--ENSNDIA 258
 LLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQ---LKM 179
 180 TVVICLISHRECQOPHYYGSEVITIONLCAADPOWKIDSCOGDSGGPLVC----SLQGRMTL 235
 DYPKKEDYI----VYLGRSRINSNIQGEMKFEVENLILH-----KDYSADTLAHHNDIA 122
 7.5
 CYTOPLASNIC
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
SHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
 SEQUENCE FROM N.A.
MEDILNE-91129236; PubMed=1993180;
Beaubien G., Rosinski-Chupin I., Mattei M.-G., Mbikay M., Chretien M.,
Seidah N.G.;
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90091743; PubMed=259871;
Seidah N.G., Ladenheim R., Mbikay M., Hamelin J., Lutfalla G.,
Stougeon F., Lazure C., Chretien M.;
"The cDNA structure of rat plasma kallikrein.";
DNA 8:563-574(1989).
-!- FUNCTION: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It
activates, in a reciprocal reaction, factor XII after its binding
 CGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRRGGSVTYVCGGSLISPCWVISATHCFI
 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
 "Gene structure and chromosomal localization of plasma kallikrein.";
Biochemistry 30:1628-1635(1991).
CHAIN (POTENTIAL).
SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
(POTENTIAL).
 TAL RAT STANDARD; PRT; 638 AA.
P14272;
01-37N-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein)
KLKB1 OR PK.
 N-LINKED (GLCNAC. . .) (POTENTIAL)
ESA9F8FA9550E180 CRC64;
 25.6%; Score 386.5; DB 1; Length 416;
.larity 35.0%; Pred. No. 1.8e-27;
Conservative 51; Mismatches 90; Indels 43;
 44926 MW;
 16
43
 Best Local Similarity
Matches 99; Conserv
 DOMAIN
ACT SITE
ACT SITE
ACT SITE
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
 DOMAIN
TRANSMEM
 13
 152
 123
 73
 Query Match
 DOMAIN
 CHAIN
 RESULT 43
KAL RAT
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ubfamily.

Subfamily.

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Subfamily.

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 EMBL; M62357; AAA74563.1; JOINED.
BRBL; M62346; AAA74563.1; JOINED.
BRBL; M62346; AAA74563.1; JOINED.
BRBL; M62347; AAA74563.1; JOINED.
BRBL; M62349; AAA74563.1; JOINED.
BRBL; M62351; AAA74563.1; JOINED.
BRBL; M62351; AAA74653.1; JOINED.
BRBL; M62353; AAA74653.1; JOINED.
BRBL; M62353; AAA74653.1; JOINED.
BRBL; M62353; AAA74653.1; JOINED.
BRBL; M62353; AAA74653.1; JOINED.
BRBL; M62353; AAA74653.1; JOINED.
BRBL; M62353; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74653.1; JOINED.
BRBL; M62355; AAA74663.1; JOINED.
BRBL; M62355; APPLEDOWAIN.
BRITCHEPTO; IPRO01314; Peptidase_S1A.
BRRT; SM00223; APPLEDOWAIN.
BRINTS; PRO0134; PRYPSIN SPC: 1.
BRRT; SM00233; AAPELE; 4.
BRRS; MART; SM00230; TRYPSIN JOM; 1.
BROSITE; PRO0134; TRYPSIN JOM; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
BROSITE; PRO0135; TRYPSIN SER; 1.
to a negatively charged surface. It also releases bradykinin from system by converting prorenin into renin.

Bygstem by converting prorenin into renin.

CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Xaa and Lys-|-Xaa bonds, including Lys-|-Arg and Arg-|-Ser bonds in (human)

Kininogen to release bradykinin.

SUBUNIT: The Zymogen is activated by factor XIIa, which cleaves and a heavy chain, which chain, which contains the active site, and a heavy chain, which associates with HWM kininogen. These chains are linked by one or more disulfide bonds.

SMINIARITY: Belongs to peptidase family SI. Plasma kallikrein shifanily.
 PLASMA KALLIKREIN HEAVY CHAIN.
PLASMA KALLIKREIN LIGHT CHAIN.
APPLE 1.
APPLE 2.
APPLE 3.
APPLE 4.
SERINE POTEASE.
N-LINKED (GLCNAC. . .) (PROBABLE).
N-LINKED (GLCNAC. . .) (PROBABLE).
N-LINKED (GLCNAC. . .) (PROBABLE).
N-LINKED (GLCNAC. . .) (PROBABLE).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
 W 14224 W 1444
 CHAIN
CHAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
CARBOHYD
 CARBOHYD
ACT_SITE
ACT_SITE
ACT_SITE
 CARBOHYD
 TARBOHYD
```

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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Rah S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley D.M., Sodergen E.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M.J., Madan A.M., Gabbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ablaceley R.W., Touchman J.W., Schautz J., Myers R.M., Butterfield Y.S.N., Krzyniski M.I., Skalska U., Smilus D.E., Beneration and initial analysis of more than 15,000 full-length human and mouse offs Generation and initial analysis of more than 15,000 full-length human and mouse offs Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
- Insubalinia specificity Expressed in many tissues subfamily.
- Insubalinia specificity Expressed in many tissues cubfamily.
 23 KIIGGEFITIENOPWFAAIYRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV
 29 RIVGGHAAPAGTWPWQASL-RLHK----VHVCGGSLLSPEWVLTAAHCFSGSVNSSDYQV
 83 YLGRSRLMSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Score 384.5; DB 1; Length 311;
Pred. No. 1.9e-27;
35; Mismatches 110; Indels 19; Gaps
 a sin il time
Salah il time
Salah il time
 POTENTIAL.
TRYPTASE GAMMA LICHT CHAIN.
TRYPTASE GAMMA HEAVY CHAIN.
POTENTIAL.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (POTENTIAL).
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
M, 7PC9DGEF6A2A8808 CRC64;
 32656 MW;
 Query Match
Best Local Similarity 35.4%;
Matches 90; Conservative 35
 1117
1314
137
202
238
192
 Ą.
 30
277
70
117
214
518
151
188
192
192
 ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
 SIGNAL
CHAIN
CHAIN
TRANSMEM
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 137 SRTIQTICLPSMYNDPQFGTSCEITGFG---KENSTDYLYPBQLKMTVVKLISHRECQQP 193
 77 KEDYIVYLGRSELNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQP 136
 TLRPRFKIIGGEFTTIENQPWFAAIYRHRGGSVTYVCGGSLISPCWVISATHCFIDYPK 76
 194 HYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGV
 142 PDVWRIYGGILNLSEITUKTPFSSIKELIHQKYKMSEGSY--DIALIKLQTP----LNY
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
 MOUSE STANDARD; PRT; 311 AA. 17YG MOUSE STANDARD; PRT; 311 AA. 0990L7; 16-00T-2001 (Rel. 40, Last sequence update) 115-MAR-2004 (Rel. 43, Last annotation update) Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase) TPSG1 OR TMT.
 16;
 25.5%; Score 385; DB 1; Length 638; 32.3%; Pred. No. 4.1e-27; ive 56; Mismatches 106; Indels
 SEQUENCE FROM N.A.
STRANSFVB/N; TISSUR=Colon;
MEDLINE-2238825; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
 454BEB27E8CA8F88 CRC64;
 SIMILARITY.
SIMILARITY.
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 254 YTRVSHFLPWIRSHTKEENGLAL 276
 Biol. Chem. 274:30784-30793(1999)
 ||:|: :: || : || YTKVAEYIDWILEKIQSSKERAL
 71273 MW;
 Query Match
Best Local Similarity 32.37
Best Local Similarity
Best Local Similarity
Local BS; Conservative
 lydrophobic extension.
 Mus musculus (Mouse)
 638 AA;
 611
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 A MEDLINE=8818529; PubMed=3356193;

A MEDLINE=8818529; PubMed=3356193;

A Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,

Gerufg G.J., van Halbeek H., Vliegenthart J.F.;

"The N- and O-linked carbohydrate chains of human, bovine and porcine
plasminogen. Species specificity in relation to sialyiation and
fucosylation patterns.";

Eur. J. Blochem. 173:57-63(1988).

-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including
embryonic development, tissue remodeling, tumor invasion, and
inflammation; in ovultation it weakens the walls of the Graafian
collagenases and several complement zymogens, such as Cl and CS.

It claaves fibrin, fibronectin, thrombospondin, laminin and von
Willebrand factor.

Higher selectivity than trypsin. Converts fibrin into soluble
 199
 200 VITIKMLCAADPQWKIDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYIRVSH 259
196 IQPDMLCARGP---GDACQDDSGGPLVCQVAGTWQQAGVVSWGBGCGRPDRPGVYARVIA 252
 84 HLGELTVTLSPH----FSTVKRIIMYTGSPGPPGSSGDIALVQLSSPVALSSQ----VQP 135
 products.

--- ENZYME REGULATION: Converted into plasmin by plasminogen activators being bound to fibrin. Cannot be activated with streptckinase.

--- PTM: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINB, SIALIC ACID AND IS CORE FUCOSYLLAND. O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).

--- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

--- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.

--- SIMILARITY: Contains 5 kringle domains.
 [1] SEQUENCE OF 1-560.
SCAULINCE J. Marti T., Roesselet S.J., Kaempfer U., Rickli E.E.;
"Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the carbohydrate attachment sites with the human and bovine species.";
 143 ICLPSMYNDPQFGTSCEITGFGKENSTDYLYPE-QLKMTVVKLISHRECQQPHY--YGSE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
 SEQUENCE OF 450-790.
MEDLINE=85203907; PubMed=3846533;
Marti T., Schaller J., Rickli B.E.;
"Determination of the complete amino-acid sequence of porcine miniplasminogen."
Eur. J. Biochem. 149:279-285(1985).
 D06867. 190 AA. 190 AA. 1906867. 190 AA. 1906867. 190 AA. 1908687. 190 AA. 1908687. 190 AA. 1908687. 190 AA. 1908687. 190 AA. 1908887. 190 Rel. 17, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Plasminogen (EC 3.4.21.7). Sus scrofa (Pig).
 790 AA
 Fibrinolysis 1:91-102(1987).
 253 YVNWIHHHIPEAGG 266
 260 FLPWIRSHTKEENG 273
 STANDARD;
 PLMN_PIG
ID _PLMN_PIG
 RESULT 45
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762 68 THCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR 127 652 SKEGRCAOPSRTIQTICLPSMYNDPQF----GISCEIIGFGKENSTDYLYPEQLKMTVVK 183 601 KHCLEKSSSPSSYKVILGAHEEYHLGEGVQRIDVSKLF--KEPS-----EADIALLKLS 184 LISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGR 11 FQCGQKTLRPR---FKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISA ch 25.4%; Score 383.5; DB 1; Length 790; 11 Similarity 36.0%; Pred. No. 7.3e-27; 94; Conservative 39; Mismatches 99; Indels 29; Gaps Ş 263 GCALKDKPGVYTRVSHFLPWI 264 PRT; Query Match Best Local Similarity RESULT 46 CTRB RAT ID CTRB RAT 244 128 763 Matches

Page

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127 ATP----AQFSETVSAVCLPNVDDDFPPGTVCATTGWGKTKYNALKTPEKLQQAALFIVS 182
 342 AA.
 EMBL; AF188613; AAG17054.1; ALT_FRAME. HISSP; P00794; 1UVS.
 247 LKDKPGVYTRVSHFLPWIR 265
 | ||:||:
239 STSTPAVYSRVTALMPWVQ 257
 RESULT 47
PSS8 MOUSE
ID PSS8 MOUSE
 SIGNAL
PROPEP
CHAIN
CHAIN
PROPEP
TRANSMEM
 ö
 MEDLINE=85054881; PubMed=6209274;

MEDLINE=85054881; PubMed=6209274;

MEDLINE=85054881; PubMed=6209274;

MEDLINE=85054881; PubMed=6209274;

MEDLINE=85054881; PubMed=6209274;

Rutter W.J.

"Isolation and sequence of a rat chymotrypsin B gene.";

"Isolation and sequence of a rat chymotrypsin B gene.";

"Isolation and sequence of a rat chymotrypsin B gene.";

"Isolation and sequence of a rat chymotrypsin B gene.";

"Isolation and sequence of a rat chymotrypsin B gene.";

"Isolation = 1-xaa, Leu-|-xaa,

"Isolation = 1-xaa, Leu-|-xaa,

"Isolation = 1-xaa, Leu-|-xaa,

"Isolation = 1-xaa, Leu-|-xaa,

"Isolation = 1-xaa,

"Isolation = 1-xa
 67 ATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI 126
 127 RSKEGRCAQPSRTICTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKOTTVVKLIS 186
 17 FGCGVPTIQPVLTGLSRIVNGEDAIPGSWPWQVSLQDK----TGFHFCGGSLISEDWVVT 72
 11 FOCGOKTLRPRF----KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS 66
 Query Match
25.3%; Score 382; DB 1; Length 263;
Best Local Similarity 33.6%; Pred. No. 2.6e-27;
Matches 87; Conservative 47; Mismatches 103; Indels 22; Gaps
 R WIEL; K02298; AAA488732.1; -.
R RAIDS, K02298; KYRTB.
R HSSP, P00766; LCHG.
R InterPro; IPR009003; Cys Ser_trypsin.
R InterPro; IPR001294; Peptidase $1.
R InterPro; IPR001294; Peptidase $1.
R Pfan; P700069; trypsin, 1.
R PROMITS; PR00722; CHYMOTRYPSIN.
R PROSITE; PS0020; Tryp SPC; 1.
R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
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R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS00135; TRYPSIN DOM; 1.
R PROSITE; PS000135; TRYPSIN DOM; 1.
R PROSITE; PS000135; TRYPSIN DOM; 1.
R PROSITE; PS000135; TRYPSIN
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 CHYMOTRYPEINOGEN B.
CHYMOTRYPEIN B, A CHAIN.
CHYMOTRYPEIN B, C CHAIN.
CHYMOTRYPEIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Chymotrypainogen B precursor (EC 3.4.21.1).
 263
31 CH
31 CH
264 CH
263 CH
120 CH
213 CH
76 BY
219 BY
219 BY
2184 MW
 Rattus norvegicus (Rat)
 154 2
186 2
209 2
263 AA;
 NCBI TaxID=10116;
 DISULFID
DISULFID
SEQUENCE
 CHAIN
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 SEQUENCE FROM N.A.

MEDLINE=20235202; PubMed=10770960;
Wagniaux G., Vallet V., Jaeger N.F., Pfister C., Bens M., Farman N., Vuagniaux G., Vallet V., Jaeger N.F., Pfister C., Bens M., Farman N., Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E.;
Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E.;
Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E.;
The series protease mcAPI expressed in a mouse cortical by the series mcAPI expressed in a mouse cortical collecting duct cell line.;
The series mcAPI expressed in a mouse cortical collecting and cell line.;
The series a trypsin-like cleavage specificity (By inilarity). Activates aniloride-sensitive sodium channels.

SUBGNIT: Heterodime of two chains, light and heavy, held by a disulfide bond (By similarity).

SUBCELDULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).

SIMILARITY: Belongs to peptidase family 31.

LIAMBARIY: Ref. 1 sequence differs from that shown due to a frameshift in position 339.
187 HRECQQPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCA
 Farman N.,
 POTENTIAL.
ACTIVATION PEPTIDE (BY SIMILARITY).
PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
BY SIMILARITY.
POTENTIAL.
SERINE PROTEASE.
 Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCEL_TaxID=10090;
 Q9ESDI;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostasin precursor (BC 3.4.21.-) (Channel activating protease 1)
PRSSB OR CAP1.
 MEROPS, SO1.158; ---
MEROPS, SO1.158; ---
MEDP, MGI:1923810; Pres8.
MGD, MGI:1923810; Pres8.
InterPro; IPR001204; Peptidase_S1.
InterPro; IPR00124; Peptidase_S1.
InterPro; IPR00124; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
Rean; PP00089; trypsin; 1.
Rean; PP00089; trypsin; 1.
Rean; PP00175; PR00175; TRYPSIN, DOM; 1.
Recoilt; PS00134; TRYPSIN, DOM; 1.
Recoilt; PS00134; TRYPSIN, SER; 1.
Recoilt; PS00135; TRYPSIN, SER; 1.
Recoilt; PS00135; TRYPSIN, SER; 1.
Recoilt; PR00175; TRYPSIN, SER; 1.
Recoilt; PR00175; TRYPSIN, Signal; Glycoprotein; Recoilt; Recoilt; PR001786; PR001787
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FT FT FT FT SO

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InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR00189; LTypsin; I.
PRINTS; PR00020; Trypsin; I.
PROSITE; PS00134; TRYPSIN DOW; I.
PROSITE; PS00135; TRYPSIN DOW; I.
PROSITE; PS00135; TRYPSIN ER; I.
Hydrolase; Serine protease; Zymogen; Signal; 3D-structure.
I 1 16 PROPEP
 25.2%; Score 380; DB 1; Length 269; 34.1%; Pred. No. 4e-27; ive 50; Mismatches 106; Indels 1
 249 DKPGVYTRVSHFLPWIRS 266
 HKPSVFTRVSNYIDWINS 264
 EMBL; M16651; AAA11027.1; --
EMBL; D00237; BAA01166.1; --
PIR; A26823; A26823.
PDB; 1BRU; 25-AUG-99.
MEROPS; S01.155; --
 88; Conservative
 Query Match
Best Local Similarity
 CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
 CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 DISULFID
DISULFID
CONFLICT
 16
 Matches
 RESULT 49
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 142
 .29 KEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGK-ENSTDYLYPEQLKMTVVKLISH 187
 143 P----VTFSRYIRPICLPAANASFPNGLHCTVTGWGHVAPSVSLQTPRPLQQLEVPLISR 198
 237
 HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 128
 84
 188 REC------OOPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTG
 CG-AVIQPR--ITGGGSAKPGQWPWQV-----SITYDGNHVCGGSLVSNKWVVSAA
 HCFPREHSREAYEVKLGAHQLDSYSNDTVVHTVAQIITHSSYRBE--GSQGDIAFIRLSS
 MEDLINE-88198076; PubMed=2834346;

MEDLINE-88198076; PubMed=2834346;

Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N.,

Shimada Y., Janaka J., Ikanaga H.;

Tamai Y., Tanaka J., Ikanaga H.;

Molecular cloning and expression in Escherichia coli of a cDNA rending human pancreatic elastase 2.";

"Molecular cloning and expression in Escherichia coli of a cDNA rending human pancreatic elastase 2.";

"Diochem. 102:1555-165(1987).

"I Biochem. 102:1555-165(1987).

"I Subcatton Acts upon elastin.

"I SURCELULAR LOCATION: Secreted.

"I SUBCELLULAR LOCATION: Secreted.

"I SUBCELLULAR LOCATION: Secreted.

"I SIMILARITY: Belongs to peptidase family S1. Elastase subfamily.
 CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTY----VCGGSLISPCWVISAT
 Gaps
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
 subfamily.
 SEQUENCE FROM N.A.
MEDLINE=87217962; PubMed=3646943;
Kawashima I., Tani T., Shimoda K., Takiguchi Y.;
Characterization of pancreatic elastase II cDNAs: two elastase II
"RMNs are expressed in human pancreas.";
DNA 6:163-172 [1987].
 Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
 37;
 Score 380.5; DB 1; Length 342; Pred. No. 4.8e-27; 30; Mismatches 109; Indels 37
 SIMILARITY)
 0620DE88ED187D0F CRC64;
 238 IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Blattase 2 precursor (EC 3.4.21.71).
 INTERCHAIN (BY
 269
 MW;
 36729
 97; Conservative
 STANDARD;
 342 AA;
 Query Match
Best Local Similarity
 NCBI_TaxID=9823;
 37
70
168
234
234
134
1130
159
DISULFID
DISULFID
DISULFID
DISULFID
ACT SITE
ACT SITE
ACT SITE
ACT SITE
CARBOHYD
CARBOHYD
 69
 13
 85
 EL2 PIG
P08419;
 SEQUENCE
 Best Loca
Matches
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 187
 192 QPHYYGSBYTTKALCAADPQWKTDSCOGDSGGPLVC-SLQGRMTLTGIVSWGR--GCALK 248
 131
 75
 188 KPGWWGSTVKTNMICAGG-DGIISSCNGDSGGPLNCQGANGQWQVFGIVSFGSSLGCNYY
 13 CGQKTLRPRF-KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCF
 72 IDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEG
 RCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREÇQ
 14; Gaps
 (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
 TRY3_HUMAN

ID TRXY HUMAN STANDARD, PRT; 304 AA.

1D TRXY HUMAN STANDARD, Q9UQV3,

DT 01-APR-1990 (Rel. 14, Created)

DT 01-RPS-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sannotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT Trypsin III precursor (EC 3.4.21.4) (Brain trypsinogen)
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us-09-880-503-5.rsp

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 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) (ISOFORM A).
MEDLINE=21686310; PubMed=11827488;
Katona G., Berglund G.I., Hajdu J., Graf L., Szilagyi L.;
"Crystal structure reveals basis for the inhibitor resistance of human
 U. Mol. Biol. 315:1209-1218(2002).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- COPACTOR: Binds 1 calcium ion per subunit.
-!- SUBCELLULAR LOGATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
 TISSUE-Pancreas;
MEDLINE-9021895; PubMed-2326201;
Tani T., Kawashima I., Mita K., Takiguchi Y.;
"Nucleotide sequence of the human pancreatic trypsinogen III cDNA.";
Nucleic Acids Res. 18:1631-1631(1990).
(Mesotrypsinogen) (Trypsin IV).
PRSS3 OR TRY3 OR PRSS4 OR TRY4.
Home sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 SEQUENCE FROM N.A. (ISOFORMS A AND B).

TISSUE=Brain;
MEDLINE=94123994; PubMed=8294000;
MEDLINE=94123994; PubMed=8294000;
MEDLINE=94123994; PubMed=8294000;
Micgand U., Corbach S., Minn A., Kang J., Mueller-Hill B.;
"Cloning of the cDNA encoding human brain trypsinogen and characterization of its product.";
Gene 136:167-175(1993).
 Fukuoka S.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
 EWEL, X72781; CABS8178.1; --
EWEL, X71345; CAA504841.; --
EWEL, X71345; CAA504841.; --
EWEL, X71345; CAA504841.; --
EWEL, X71345; CAA3527.1; --
EWEL, Z33496; CAA3357.1; --
EWEL, Z33496; S33496.
EWEN, S33496; PESS --
EWEN, HONC: 9486; PESS --
EWEN, HONC: 9486; PESS --
EWEN, PROFOSOS --
EWEN, PROFOSOS --
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 Event=Alternative splicing; Named isoforms=3;
 Isold=P35030-3; Sequence=VSP_005410;
TISSUE SPECIFY: Pancreas and brain.
SIMILARITY: Belongs to peptidase family S1.
 IsoId=P35030-2; Sequence=VSP_005409;
 Name=A;
IsoId=P35030-1; Sequence=Displayed;
 SEQUENCE FROM N.A. (ISOFORM C).
 SEQUENCE FROM N.A. (ISOFORM C).
 orain trypsin.";
 Name=B;
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202 TKYLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFL 261 238 NSWFCVGFLEGGKDSCQRDSGGPVVCNGQ----LQGVVSWGHGCAWKNRPGVYTKVYNYV 293 142 IICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVT 201 80 KIVGG-YTCEENSLPYQVSL-----NSGSHFCGGSLISEQWVVSAAHCY-----KTRIQ 127 82 VYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ 141 /FILS=VSP\_005409. MCGPDDRCPARMPGRGRAVKGKGLAAARPGRVERGCAQRG MCGPDLGCRTWAARABAGGCEALGT -> MNPFLILA FVGAA (in isoform C). /FILS=VSP\_005410. MISSING (IN REF. 1; CAA50484). TQ -> RE (IN REF. 2). Y -> C (IN REF. 2). Y -> C (IN REF. 2). WA; 4C4316C31F1D0FFC CRC64; REQUIRED FOR SPECIFICITY (BY SIMILARITY). MCGPDDRCPARWPGPGRAVKCGKGLAAARPGRVERGGAQRG 23 KIIGGEFTTIENQ-PWFAALYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYI 25.2%; Score 379.5; DB 1; Length 304; ilarity 37.7%; Pred. No. 5.2e-27; Conservative 38; Mismatches 87; Indels 27; Gaps Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. PROSITE; PS00135; TRYPSIN SER; FALSE NEG.
Hydrolase; Serine protease; Digestion; Zymogen; Calcium-binding; Signal, Multigene family; Alternative splicing; 3D-structure.
Signal, proper chair and analy; Alternative splicing; 3D-structure.
PROPER ; 80 ACTIVATION PEPTIDE.
CHAIN 81 304 TRYPSIN III.
ACT SITE 120 132 CALCIUM.
METAL 132 134 CALCIUM (VIA CARBONYL OXYGEN).
METAL 137 CALCIUM (VIA CARBONYL OXYGEN).
METAL 142 142 CALCIUM. CALCIUM.
CALCIUM (VIA CARBONYL OXYGEN).
CALCIUM (VIA CARBONYL OXYGEN).
CALCIUM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM. ψ.Υ Σ.Ε 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CAPMOOTYPSin-like protease CTRL-1 precursor (EC 3.4.21.-).
CTRL OR CTRL!
Homo sapiens (Human). -> M (in isoform B) = VSP 005409. 264 AA PRT; [1] SEQUENCE FROM N.A. MEDLINE=94093544; PubMed=8268911; 32499 MW; STANDARD; 5 Query Match Best Local Similarity Matches 92; Conserva 89 224 232 253 253 304 AA; ||: 294 DWIK 297 262 PWIR 265 NCBI\_TaxID=9606; CTRL HUMAN P40313; ACT\_SITE ACT\_SITE DISULFID DISULFID DISULFID DISULFID DISULFID CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE SITE VARSPLIC VARSPLIC RESULT 50 CTRL HUMAN ò 쉱 a ઠે 유 ठे 유 ò ઠ

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Boinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
 129
 69 HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 128
 129 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR 188
 189 ECQQPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWG-RGCAL 247
 89
 74
 19 CGIPAIKPALSFSQRIVNGENAVLGSWPWQVSL----QDSSGFHFCGGSLISQSWVTAA
 13 CGOKTLRPRF----KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISAT
 ACTIVATION PEPTIDE (POTENTIAL).
CHYMOTRYBEIN-LIKE PROTEASE CTRL-1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCKAC. .) (POTENTIAL).
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 23;
 Query Match 25.1%; Score 378.5; DB 1; Length 264; Best Local Similarity 35.0%; Pred. No. 5.3e-27; Matches 90; Conservative 43; Mismatches 101; Indels 23.
Larsen F., Solheim J., Kristensen T., Kolsto A.B., Prydz H.; "A Light cluster of five unrelated human genes on chromosome HG422.1."; Mol. Genet. 2:1589-1595(1993).
-!- SIMILARITY: Belongs to peptidase family S1.
 3F629F02FA6DDFB4 CRC64;
 248 KDKPGVYTRVSHFLPWI 264
 R-APAVYTRVSKFSTWI 257
 28002 MW;
 264 AA;
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| GenCore version 5.1.6<br>Copyright (c) 1993 - 2004 Compugen Ltd. | OM protein - protein search, using sw model | May 25, 2004, 14:44:05 ; Search time 45.7178 Seconds (without alignments) 1904.795 Million cell updates/sec | US-09-880-503-5<br>score: 1508<br>e: 1 KPSSPPEELKFQCGQKTLRPVSHFLPWIRSHTKEENGLAL 276 | table: BLOSUM62<br>Gapop 10.0, Gapext 0.5 | d: 1017041 seqs, 315518202 residues | Total number of hits satisfying chosen parameters: 1017041 | Minimum DB seq length: 0<br>Maximum DB seq length: 2000000000 | Post-processing: Minimum Match 0%<br>Maximum Match 100% |
|------------------------------------------------------------------|---------------------------------------------|-------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|-------------------------------------------|-------------------------------------|------------------------------------------------------------|---------------------------------------------------------------|---------------------------------------------------------|
|                                                                  | OM protein - p                              | Run on:                                                                                                     | Title:<br>Perfect score:<br>Sequence:                                               | Scoring table:                            | Searched:                           | Total number o                                             | Minimum DB seq<br>Maximum DB seq                              | Post-processin                                          |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SPTREMBL\_25:\*
1: Sp\_archea:\*
2: Sp\_bacteria:\*
3: Sp\_tungi:\*
4: Sp\_human:\*
5: Sp\_invertebrate:\*
6: Sp\_mammal:\*
7: Sp\_mhc:\*!
7: Sp\_mhc:\*!
8p\_phage:\*
10: Sp\_phage:\*
11: Sp\_rodent:\*
11: Sp\_rodent:\*
12: Sp\_virus:\*
13: Sp\_virus:\*
14: Sp\_unclassified:\*
15: Sp\_virus:\*
16: Sp\_bacteriap:\*
17: Sp\_roteriap:\*
18: Sp\_virus:\*
19: Sp\_virus:\*
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14: Sp\_virus:\*
15: Sp\_virus:\*
16: Sp\_bacteriap:\*
17: Sp\_archeap:\*

|           |          |        | Description     | 10 oryctolagus | 7 oryctolagus | 10 oryctolagus | 37 oryctolagus | 99 homo sapien | k8 homo sapien | wl homo sapien | 23 sus scrofa | Q8mkb1 oryctolagus | cs4 mus musculu | 89 equus cabal | E3 homo sapien | 0y7 meleagris g | z5 homo sapien | 07 sus scrofa | and the property of the |
|-----------|----------|--------|-----------------|----------------|---------------|----------------|----------------|----------------|----------------|----------------|---------------|--------------------|-----------------|----------------|----------------|-----------------|----------------|---------------|-------------------------|
|           |          |        | Desci           | Q8mi10         | Q8mhy         | Q9xt           | 097587         | 66nq60         | Q86yk8         | 12q60          | Q88Q,         | O8mki              | 08v             | 095m           | Q96e1          | 080             | OBiz           | 0975          | ,,,,,                   |
| SUMMARIES |          |        | ΩI              | QBMILO         | QBMHY7        | Q9XT70         | 097587         | 66DE60         | Q86YK8         | Q9BZW1         | 088023        | Q8MKB1             | Q8VCS4          | Q95M89         | Q96EF3         | Q800Y7          | Q8IZZS         | 097507        | 0001172                 |
|           |          |        | DB              | 9              | 9             | 9              | v              | 41             | 4              | 41             | ø             | ø                  | 11              | w              | 4              | 13              | 4              | 9             | ц                       |
|           |          |        | Match Length DB | )<br>!<br>!    |               |                |                |                |                |                |               | 564                |                 |                |                |                 |                |               |                         |
|           | de<br>de | Query  | Match           | ;              |               |                |                |                |                |                |               | 36.2               | 33.0            | 32.8           | 32.8           | 32.6            | 32.6           | 31.0          | 0.0                     |
|           |          |        | Score           | 1321           | 1316          | 670            | 585            | 583            | 583            | 573            | 553           | 545.5              | 497.5           | 495            | 495            | 492             | 492            | 467           | 2 6 7 6                 |
|           |          | Result | No.             | 1              | (7)           | m              | 4              | Ŋ              | 9              | 7              | 80            | 6                  | 10              | 11             | 12             | 13              | 14             | 15            | 7.                      |

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| 035727 Q80YC5 Q80NT31 Q80NT31 Q96NT47 Q966V4 Q99GVG Q99GVG Q99GVG Q99GVG Q99GVG Q99GVG Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE Q96CFE | ALIGNMENTS  PRT; 433 AA.  Created) Last sequence update) Last annotation update) activator. |
| 29.9 29.9 29.9 29.9 29.9 29.9 29.9 29.9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PRELIMINARY;<br>(TEMBLEE]. 22,<br>(TEMBLEE]. 22,<br>(TEMBLEE]. 25,<br>YPE PLASMINGEN        |
| 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RESULT 1 Q8MIL0 ID Q8MIL0 AC Q8MIL0, DT 01-OCT-2002 DT 01-OCT-2003 DF Urokinase-ty GN PLAU. |

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 217
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 181 VVKLISHRECQQPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 9
 RECIENCE FROW N.A.

WEDLINE=22155945; PubMed=12149463;

RECIENCE FROW N.A.

Palkenbergy M., Tom C., DeYoung M.B., Wen S., Linnemann R.,

Dichek D.A.;

Dichek D.A.;

Dichek D.A.;

Increased expression of urokinase during atherosclerotic lesion development causes arterial constriction and lumen loss, and a ccelerates lesion growth.";

Procederates lesion.";

Procederates lesion.";

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 218 PCWVVSATHCFINHQKKEDYIVYLGRSRLNSMTPGEMKFEVEQLILHEGYSADTLAHHND
 338 VVKLVSYQECQQPHYYGSEVTTKALCAADPQWETDSCQGDSGGPLVCSVQGRATLTGIVS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
 ;
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 Length 433;
 87.6%; Score 1321; DB 6; Length 4:
87.3%; Pred. No. 4.1e-123;
tive 15; Mismatches 20; Indels
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKNKPGVYTRVSRFLPWIRSHIGEENGLAL 433
 Matches 241; Conservative
 Similarity
 NCBI_TaxID=9986,
 61
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181 VVKLISHRECQQPHYYGSEVTTKALCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 240
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHRND 120
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT 180
 RY SEQUENCE FROM N.A.

RY ALGO M., Watenabe M.;

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 278 IALLKILSNNGQCAQPSRSIQTICLPPWNADPNFGTSCBITGFGKENSTDYLYPBQLXOMT
 1 KPSSPPELIKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
 21; Indels
 Length
 K., Maruyama M.;
EMBL/GenBank/DDBJ databases
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Urokinase-type plasminogen activator.
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Query Match
87.3%; Score 1316; DB 6;
Best Local Similarity 87.0%; Pred. No. 1.3e-122;
Matches 240; Conservative 15; Mismatches 21;
 Anai
 SEQUENCE FROM N.A.
Sugiki M., Yoshida E., A.
Submitted (APR-2001) to
 SEQUENCE FROM N.A.
 NCBI_TaxID=9986;
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433 AA

PRELIMINARY;

Q8MHY7 Q8MHY7;

RESULT 2 Q8MHY7 ID Q8 AC Q8

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SECUENCE FROM N.A.
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ da
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 2 KRINGLE DOWAINS.
EMBL; BC002795; AAH02795.1; -.
 PRELIMINARY;
 157 SCEITGFG 164
 121 SCEITGFG 128
 Q9BU99;
 RESULT 5
Q9BU99
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 69 KPALPPGKLEFQCGQKALRPRFKIIGGEFTIIENQPWFAAIYRRHRGGSVTYVCGGSLIS 128
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 60
 0; Gaps
 09XT70 PRELIMINARY; PRT; 214 AA.
03XT70 0XYT70 DOXT01.
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
02-OCT-2003 (TrEMBLrel. 25, Last annotation update)
03-OCT-2003 (TrEMBLrel. 25, Last sequence)
03-OCT-2003 (TrEMBLrel. 25, Last sequence)
03-OCT-2003 (TrEMBLrel. 25, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
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03-OCT-2003 (TrEMBLrel. 12, Last sequence)
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03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
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03-OCT-2003 (TrEMBLrel. 12, Last sequence)
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03-OCT-2003 (TrEMBLrel. 12, Last sequence)
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03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
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03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequence)
03-OCT-2003 (TrEMBLrel. 12, Last sequenc
 Query Match
Best Local Similarity 84.2%; Pred. No. 1.5e-58;
Matches 123; Conservative 9; Mismatches 14; Indels
 Created)
Last sequence update)
Last annotation update)
398 WGRGCALKNKPGVYTRVSRFLPWIRSHIGEENGLAL 433
 121 IALLKIRSKEGRCAQPSRTIQTICLF 146
 189 IALLKILSNNGQCAQPSRSIQTICLP 214
 (TrEMBLrel. 10, C) (TrEMBLrel. 10, I) (TrEMBLrel. 25, I
 PRELIMINARY;
 NCBI_TaxID=9986;
 097587,
097587,
01-MAY-1999 ('01-MAY-1999 ('01-MAY-1999 ('01-MAY-1999) ('01-MAY-1
 RESULT 4
097587
1D 0975
AC 0975
DT 01-M
DT 01-M
 RESULT
Q9XT70
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97 MKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGT 156
 96
 1 WFAAIYRRHRGGSVTVVCGGSLISPCWVVSATHCFINHQKKEDYIVVLGRSRLNSMTPGE 60
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=99057575; PubMedia=9237780;

Reno C., Boykiw R., Martin=827780;

Reno C., Boykiw R., Martin=8277562;

Tam d'helint potential regulators in the healing medial collateral ingenent.";

Tigament.";

Indiament.";

L. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

EMBL, ARO69711; AAC95003.1; -..

SEMEL, ARO69711; AAC95003.1; -..

SEMEL, ARO69711; PELONGS TO PEPTIDASE FAMILY S1.

EMBL, ARO69711; PAC95003.1; -..

SEMEL, ARO69711; PELONGS TO PEPTIDASE FAMILY S1.

BEROPS; S01.231; -..

CO; GO:0016301; F:kinase activity; IEA.

CO;
 37 WFAALYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGE
 Similar to plasminogen activator, tissue.
Homo sapiens (Human)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
 ö
 Query Match 38.8%; Score 585; DB 6; Length 128; Best Local Similarity 84.4%; Pred. No. 2.3e-50; Matches 108; Conservative 6; Mismatches 14; Indels
 databases
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
 191 QQPHYYGSEVTTKMLCAAD----PQWKT-DSCQGDSGGPLVCSLQGRWTLTGIVSWGRG 244
 131 GRCAOPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREC
 477 ISOHLINRIVIDNMLCAGDIRSGGPQANLHDACQGDSGGPLVCLNDGRWTLVGIISWGLG
 13 CG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRH-RGGSVTYVCGGSLISPCWVISATHC
 97; Indels 10; Gaps
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sanotation update)
Neonatal thrombolytic agent alpha-form (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Length 562;
 R GO: GO: GO: GO: GENTRE SEA.

R GO: GO: GO: GO: GO: GENTRE SEA.

R GO: GO: GO: GO: GO: GENTRE SEA.

R GO: GO: GO: GO: GO: GES: F: chymacrypsin activity; IEA.

R GO: GO: GO: GO: GES: F: chymacrypsin activity; IEA.

R GO: GO: GO: GES: F: chymacrypsin activity; IEA.

R InterPro: IPRO00003; Cyg Ser trypsin. interPro: IPRO00003; Cyg Ser trypsin.

R InterPro: IPRO00003; Cyg Ser trypsin.

R InterPro: IPRO00003; EdF: Like.

R InterPro: IPRO00003; EdF: Like.

R InterPro: IPRO00003; Kringle.

R Ffam; PRO0009; EdF: 1.

R PRINTS; PRO0009; Kringle; 2.

R Pfam; PRO0009; Kringle; 2.

R PRINTS; PRO0009; Kringle; 2.

R PRINTS; PRO0009; Kringle; 2.

R SMART; SMO0000; KR; 2.

R SMART; SMO0000; KR; 2.

R PROSITE; PSO0022; EGF: 1: 1.

R PROSITE; PSO0022; EGF: 1: 1.

R PROSITE; PSO0021; KRINGLE: 2.

R PROSITE; PSO0031; KRINGLE: 2.

R
 SEQUENCE FROM N.A.
Dou D.:
"A brain-type plasminogen activator.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 Query Match
Best Local Similarity 44.9%; Pred. No. 2.4e-49;
Matches 119; Conservative 39; Mismatches 97;
 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
 PRELIMINARY;
 Q9BZW1
Q9BZW1;
 RESULT 7
Q9BZW1
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 71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREC 190
 191 QQPHYYGSEVTTKMLCAAD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRG 244
 CG-OKTLRPRFKIIGGEFTTIENOPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHC 70
 371 SRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRC
 97; Indels 10; Gaps
 OBGYKB PRELIMINARY, PRT; 562 AA.
OBGYKB;
OBGYKB;
OLJUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
11-Ssue plasminogen activator.
Homo sapiens (Human).
Eukaryota; Metazoa; Cordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
R GO; GO: 0004263; F: chymotrypsin activity; IEA.

R GO; GO: 0004223; F: chymotrypsin activity; IEA.

GO; GO: 0004229; F: tryptidase activity; IEA.

GO; GO: 0004229; F: tryptidase activity; IEA.

R GO; GO: 00056509; P: proteolysis and peptidolysis; IEA.

R GO; GO: 00056509; P: proteolysis and peptidolysis; IEA.

InterPro; IPR005009; EGF_like.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001144; Peptidase_S1.

R InterPro; IPR001144; Peptidase_S1.

R Pfam; Pr00009; EGF; I.

R Pfam; Pr00009; EGF; I.

R Pfam; Pr00018; KRINGIE.

R PRNTTS; PR00125; CHYMOTRYPSIN.

R PRNTTS; PR00129; KRINGIE.

R SMART; SM00120; Tryp_FC; I.

R RCSITE; PS00120; Tryp_FC; I.

R RCSITE; PS00130; Tryp_FC; I.

R RCSITE; PS00130; Tryp_FC; I.

R RCSITE; PS00134; TRYPSIN. DOM; I.

R RCSITE; PS00134; TRYPSIN. DOM; I.

R RCSITE; PS00134; TRYPSIN. DER; I.

R RCSITE; PS00134; TRYPSIN. SER; I.

R RCSITE; PS00135; TRYPSIN. SER; I.

R RCF-like domain; Glycoprofein; Hydrolase; Kringle; Protease;
 Query Match 38.7%; Score 583; DB 4; Length 516; Best Local Similarity 44.9%; Pred. No. 2.2e-49; Matches 119; Conservative 39; Mismatches 97; Indels
 SEQUENCE FROM N.A.
Liu Y., Xu L., Zeng Y., He X.;
"cDNA of tissue plasminogen activator ";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 516 AA; 57370 MW; BAB31901FDC96800 CRC64;
 GQQKDVPGVYTKVTNYLDWIRDNMR 515
 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
 Serine protease.
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us-09-880-503-5.rspt

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Ding Y., Xue J., Bartlett J.D.;

"T-plasminogen activator in tooch tissues.";

"T-plasminogen activator in tooch tissues.";

"Submitted (Mark-2001) to the EmBL/GenBank/DDBJ databases.

"I- SIMILARITY: CONTAINS 2 KRINGIE DOMAINS.

BMB1, AP546605, AAM00297.1;

"GO; GO:00008231; F:peptidate activity; IEA.

GO; GO:0008231; F:peptidate activity; IEA.

GO; GO:0008231; F:peptidate activity; IEA.

GO; GO:0008231; F:peptidate activity; IEA.

RO; GO:0008231; F:peptidate activity; IEA.

GO; GO:0008231; F:peptidate activity; IEA.

RO; GO:0008231; F:peptidate activity; IEA.

RO; GO:0008231; F:peptidate activity; IEA.

RO; GO:0008231; F:peptidate activity; IEA.

RITEPPO: IPRO00001; Kringle.

RITEPPO: IPRO00001; Kringle.

RITEPPO: IPRO00001; Kringle.

REMAIP: ROWOOTS: CHYMOTYPEIN.

REMAIP: ROWOOTS: CHYMOTYPEIN.

REMAIP: ROWOOTS: CHYMOTYPEIN.

REMAIP: SWOOTS: CHYMOTYPEIN.

REMAIP: SWOOTS: CHYMOTYPEIN.

REMAIP: SWOOTS: REMAIPE.

REMAIP: REMOILS: REMOMECTIN 1:

REMSITE: PSOOTS: REMSITE: REMOMECTIN 1:

REMSITE: PSOOTS
 Length 562;
 Query Match
36.7%; Score 553; DB 6; Length 56
Best Local Similarity 41.9%; Pred. No. 2.4e-46;
Matches 111; Conservative 43; Mismatches 101; Indels
 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
 CGOKDVPGVYTKVTNYLNWIRDNTR 561
 Query Match
 Q8MKB1
Q8MKB1;
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 130
 310 TSQHLLNRTVIDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLG 369
 131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLXMTVVXLISHREC 190
 250 SRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPPYSERLKEAHVRLYPSSRC 309
 70
 13 CG-QKTLRPREKIIGGEFTTIENQPWFAAIYRH-RGGSVTYVCGGSLISPCWVISATHC
 71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE
 192 FQERFPPHHLTVILGRTYRVVPGEEEQKFECEKYIVHKEFDDDT--YDNDIALLQLKSDS
 QQPHYYGSEVITXMLCAAD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRG
 Query Match 38.0%; Score 573; DB 4; Length 395;
Best Local Similarity 44.2%; Pred. No. 1.5e-48;
Matches 117; Conservative 39; Mismatches 99; Indels 10; Gaps
 Q8SQ23 PRELIMINARY, PRT, 562 AA.
Q8SQ23,
QBSQ23,
QBSQ23,
QB-CO2002 (TEMBLrel. 21, Created)
O1-UTN-2002 (TEMBLrel. 21, Last sequence update)
O1-OCT-2003 (TEMBLrel. 25, Last annotation update)
T-plasminogen activator.
Sus scrofa (Pig)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
C: -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

BMBL, PAPES0825, AAK11956.1; -

BMBL, PAPES0825, AAK11956.1; -

BMSD, POOTSO, IPRO.

R GO: GO:0004263; F: Proymotrypain activity; IEA.

GO: GO:0004293; F: Computation activity; IEA.

GO: GO:0004293; F: Computation activity; IEA.

GO: GO:0004295; F: Lrypsin activity; IEA.

R GO: GO:0004295; F: Lrypsin activity; IEA.

R GO: GO:0006508; P: Protectorysis and peptidolysis; IEA.

INTERPO: IPRO00003; F: DENCELLI.

R INTERPO: IPRO00114; Peptidase SI.

INTERPO: IPRO0114; Peptidase SI.

INTERPO: IPRO0114; Peptidase SI.

R PRON015; FROOTS2; FILMOTRYPSIN.

R PAMPY: PRO0039; Lrypsin, I.

R PRINTS; PRO0039; Kringle; I.

R PRINTS; PRO0129; Kringle; I.

R PROSTIE; PRO0129; KRINGLE I.

R PROSTIE; PSO0129; RINGLE I.

R PROSTIE; PSO0135; RYPSIN DON; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.

R PROSTIE; PSO0135; TRYPSIN SER; I.
 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
 SEQUENCE FROM N.A.
TISSUE=Enamel organ;
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 RESULT 8
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35
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 71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE
 131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREC
 191 QOPHYYGSEVTTKMLCAADPQW-----KTDSCOGDSGGPLVCSLOGRMTLTGIVSWGRG
 13 CGOKTLR-PRFKIIGGEFTTIENOPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHC
 Created)
Last sequence update)
Last annotation update)
 (TrEMBLrel. 22, C
(TrEMBLrel. 22, I
(TrEMBLrel. 25, I
 01-OCT-2002 (
01-OCT-2002 (
01-OCT-2003 (
 RESULT 9
Q8MKB1
ID Q8MK
AC Q8MK
DT 01-0
DT 01-0
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## Tue May 25 15:05:10 2004

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 67 ATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI 126
 127 RSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLIS 186
 187 HRECQQPHYYGSEVTTKMLCAADPQW-----KTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 475 SSRCTPQQLKNRTVTGNMLCAGDTRSGGAQVNLHDACQGDSGGPLVCMTDGHMTLIGIIS 534
 12 OCGOKTLR ---- PRFKIIGGEFTTIENOPWFAAIY-RRHRGGSVTYVCGGSLISPCWVIS 66
 Query Match

36.2%; Score 545.5; DB 6; Length 564;
Best Local Similarity 43.1%; Pred. No. 1.3e-45;
Matches 115; Conservative 36; Mismatches 103; Indels 13; Gaps
Tissue-type plasminogen activator.
Oryccolagus cumiculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REDURNCE FROM N.A.

SUGIKI M., Yoshida E., Anai K., Maruyama M.;

Lib. SIMILARITY, BEDLONGS TO PEPTIDASE FAMILY SI.

- SIMILARITY, BEDLONGS TO PEPTIDASE FAMILY SI.

- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.

RABL, AN029518; AAKAGGAU1, -

CO. GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

GO; GO: 000823; F: PEPTIDASE ACTIVITY; IEA.

RICEPPO: IPRO0620; CGF_like.

IN THERPO: IPRO0620; CGF_like.

IN THERPO: IPRO0620; FGF_like.

IN FRANTS; PRO0013; FGF_like.

IN FRANTS; PRO0013; FGF_like.

IN FRANTS; FROO022; FGF_like.

RAMART; SMO0121; FRINGLE.

REDURNING PRO0021; FRINGLE.

REDURNING PRO0022; FRINGLE.

REDURNING PRO0023; FRINGLE.

REDURNING PRO0023; FRINGLE.

REDURNING PRO0023; FRINGLE.

REDURNING PRO0023; FRINGLE.

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REDURNING PRO0023; FRINGLE.

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REDURNING PRO0023; FRINGLE.

REDURNING PRO0023; FRINGLE.

REDURNING PROO023; FRINGLE.

REDURNING PROOF PROOP PROOF P
 241 WGRGCALKDKPGVYTRVSHFLPWIRSH 267
 535 WGLGCGQKDVPGVYTKVVNYLGWIQQH 561
 NCBI_TaxID=9986;
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RESULT 10

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57 SLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLA 1
 2 PSSPPRELKFQCGQK----TLRPRFKIIGGBFTTIENQPWFALIYRRHRGGSVTYVCGG
 Query Match
33.0%; Score 497.5; DB 11; Length 653;
Best Local Similarity 38.5%; Pred. No. 9.9e-41;
Matches 105; Conservative 44; Mismatches 109; Indels 15; Gaps
 ## HSSP; POUTGI, 1ANI.

HSSP; POUTGI, 1ANI.

CO: 00004576; C:extracellular; IEA.

CO: 000045376; E:erypeain activity; IEA.

CO: 000045376; E:erypeain activity; IEA.

CO: 00004508; F:erypeain activity; IEA.

CO: 00004091; F:erypeain activity; IEA.

CO: 00004091; F:erypeain activity; IEA.

PRINTS; PRO001314; Peptidase_S1A.

PRINTS; PRO001314; Peptidase_S1A.

PRINTS; PRO0013; F:erypeain activity; IEA.

PRODOM; PRO00099; F:erypeain activity; IEA.

PRODOM; PRO00099; F:erypeain activity; IEA.

PROSTIE; PRO0022; F:erypeain activity; IEA.

PROSTIE; PRO0023; F:erypeain; EGF; 1.

PROSTIE; PRO0023; F:errypeain; EGF; 1
 01-WAR-2002 (TrEMBLE1. 20, Created)
01-WAR-2002 (TrEMBLE1. 20, Last sequence update)
01-OCT-2003 (TrEMBLE1. 25, Last annotation update)
01-OCT-2003 (TrEMBLE1. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Strauberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-: SIMILARITY: CONTAINS 1 KRINGLE DOWAIN.
EMBL; BC019376; AAH19376.1; -.
HSSP; P00761; 1ANI.
 653 AA.
 PRT;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 Q8VCS4
Q8VCS4;
Q8VCS4
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 37 WFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGE 96
 9
 :| |: |::: | || || |: || || || 493 NH-DLVLIRLKKKGERCAVRSQFVQPICLPBAGSSFPTGHKCQIAGWGHMDENVSSYSNS
 1 WFAAIYRRHRGGSVTYVCGGSLISPCWVLSATHCFINYPKKEDYIVYLGRSRLSSTSFGE
HHNDIALLKIRSKEGRCAOPSRTIOTICLPSMYNDPOFGTSCEITGFGKENSTDYLYPEO
 LXMTVVKLI SHRECQQPHYYGSEVTTXMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLT
 0; Gaps
 SEQUENCE FROM N.A. MEDINE 11421942; MEDINE 21314992; PubMed=11421942; Shubitne 21314992; PubMed=11421942; Shubitowski D.M., Venta P.J., Douglass C.L., Zhou R.-X., Ewart S.L.; "Polymorphism identification within 50 equine gene-specific sequence
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
 Query Match 32.8%; Score 495; DB 6; Length 103; Best Local Similarity 87.4%; Pred. No. 1.6e-41; Matches 90; Conservative 7; Mismatches 6; Indels
 MKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRT 139
 MKFEVEXLILHEDYSADTLAHHNDIALLKISSSTGQCAQPSRS 103
 103 AA; 11525 MW; 0B739514F6331180 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Plasminogen activator urokinase (Fragment).
 Created)
Last sequence update)
 237 GIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 269
 612 GIISWGDGCGRLNKPGVYTRVANYVDWINDRIR 644
 Hydrolase; Kinase; Protease; Serine protease.
NON TER 1 1 1
NON TER 103 103
 300 AA
 103 AA.
 PRT;
 (TrEMBLrel. 19, (TrEMBLrel. 19,
 PRELIMINARY;
 Equus caballus (Horse).
 Q96EF3;
Q96EF3;
01-DEC-2001 (
 SEQUENCE
 Q95M89
 RESULT 11
Q95M89
 RESULT 12
 096EF3
ID 099
AC 009
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83 AGSLIAPCWVLTAAHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAFS--P 14.
 17
 70
 174 PEQLKWIVVKLISHRECQOPHYYGSEVTIKMLCAADPOWKTDSCOGDSGGPLVCSLQG-- 23
 201 ASFLOEAQVPFLSLERCSAPDVHGSSILPGMLCAGFLEGGTDACQGDSGGFLVCEDQAAE 26
 54
 82
 55 GGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADT 11
 1 KPSSPPEELK---FOCGQ---KTLRPRFKIIGGEFTTIBNQPWFAAIYRRHRGGSVTYVC
 115 LAHHNDIALLKIR-SKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLY
 SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(TM) System Donor
 Query Match
32.8%; Score 495; DB 4; Length 300;
Best Local Similarity 38.5%; Pred. No. 6.5e-41;
Matches 107; Conservative 44; Mismatches 109; Indels 18;
 A GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:trypsin activity; IEA.

R GO; GO:0004508; F:trypsin activity; IEA.

R GO; GO:0004508; F:trypsin activity; IEA.

R InterPro; IPRO0124; Peptidase_S1.

R InterPro; IPRO0124; Peptidase_S1.

R InterPro; IPRO0124; Peptidase_S1.

R PRINT; PRO0125; CHYMOTRYPSIN.

R PRANT; SMO020; Tryp SPC; 1.

R PROSITE; PSO0134; TRYPSIN DOM; 1.

R PROSITE; PSO0134; TRYPSIN HIS; 1.

R PROSITE; PSO0135; TRYPSIN JES; 1.

R PROSITE; PSO0135; TRYPSIN JES; 1.

R PROSITE; PSO0135; TRYPSIN JES; 1.

R PROFICE | PSO0135; TRYPSIN JES; 1.

R PROSITE; PSO0135; TRYPSIN JES; 1.
 vector.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BC012390; AAH12390.1;
--- EMBL; BT007350; AAP36014.1;
HSSP; P00761; IAN1.
 080077;
01-JUN-2003 (TrEMBirel. 24, Created)
01-JUN-2003 (TrEMBirel. 24, Last sequence update)
01-JOCT-2003 (TrEMBirel. 25, Last annotation update)
Heparocyte growth factor activator (Fragment).
Meleagris gallopavo (Common turkey).
 232 -RMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT 268
 PRELIMINARY;
 Query Match
 Q800Y7
 RESULT 13
Q800Y7
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A. NCBI\_TaxID=9606;

Hypothetical protein (Coagulation factor XII) (Hageman factor). Homo appiens (Human).

Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris. NCBL\_TaxID=9103;

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398 AGSLIAPCWVLTAAHCLQDRPAPEDLTVVLGQBRRNHSCEPCQTLAVRSYRLHEAFS--P 4:
 1 KPSSPPBELK---FQCGQ---KTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVC 5
 55 GGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADT 1.
 A SEQUENCE FROM N.A.

A Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.,

Mada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.

I Submitted (NOV-2002) to the EMEJ/GenBank/DDBJ databases.

R EMEJ, AboSe45; BAC23095.1;

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005509; P:calcium ion binding; IEA.

GO; GO:0005509; P:calcium ion binding; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0006509; P:chymotrypsin activity; IEA.

R GO; GO:0006509; P:chymotrypsin activity; IEA.

R GO; GO:0006509; P:chymotrypsin activity; IEA.

R InterPro; IPR001081; EGF Ca.

R InterPro; IPR001081; Fibrachi.

R InterPro; IPR001014; Peptidase_Sl.

R InterPro; IPR001114; Peptidase_Sl.

R Pfam; PF00009; EGF; C:

R Pfam; PF00009; EGF; C:

R Pfam; PF00009; Fibrilli.

R Pfam; PF00009; Firingin 1.

R Pfam; PF00009; FIRINIERI.

R PRINTS; PR00013; FRINTERI.

R PRINTS; PR00013; FRINTERI.

R PRINTS; PR00013; FRINTERI.
 Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Query Match
32.6%; Score 492; DB 4; Length 615;
Best Local Similarity 38.5%; Pred. No. 3.2e-40;
Matches 107; Conservative 43; Mismatches 110; Indels 1
 R PEODON; PRO00195; RV. TYPE_II; 1.

R PEODON; PEORO0395; RV. TYPE_II; 1.

R SWART; SW00199; EGF_CA; 2.

R SWART; SW00199; EGF_CA; 2.

R SWART; SW00199; EN1; 1.

R SWART; SW00130; RR; 1.

R SWART; SW00130; RR; 1.

R PROSITE; PS01186; EGF_L; 2.

R PROSITE; PS01186; EGF_L; 2.

R PROSITE; PS00123; FIBRONECTIN_1; 1.

R PROSITE; PS00021; RRINGLE_1; 1.

R PROSITE; PS00021; RRINGLE_2; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_BN; 1.

R PROSITE; PS01135; TRYPSIN_HIS; 1.

R PROSITE; PS01135; TRYPSIN_HIS; 1.
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Coagulation factor XII-Mie.
Homo sapiens (Human).
 PRT;
 PRELIMINARY;
 NCBI_TaxID=9606;
RESULT 14
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 89
 394 KNGQRCAVKSQFVQPICLPESNTVFPD-QF--KCQISGWGHKHENITGYSDVLQETLIPI 450
 335 AHCFANSPOKSSIKVVLGQHFFNRTTDVTQTFEIEKYILYPQYSVFRPTEH-DIALIKLK 393
 185 ISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQQDSGGPLVCSLQGRMTLTGIVSWGRG 244
 283 CGRRHKKRSFYRPR--IIGGSSSLPGSHPWTAAIY---IGES---FCAGTLIQTCWVVSA 334
 68 THCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR 127
 128 SKEGRCAQPSRTIQTICLP---SMYNDPQFGTSCELTGFGKENSTDYLYPEQLKMTVVKL 184
 13 CGOK----TLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISA 67
 SEQUENCE FROM N.A.
MEDLINE=22122796; PubMed=12128063;
HOlsberger D.R., Becker A.E., Thurston R.J., Rice C.D.;
Holsberger D.R., Becker A.E., Thurston R.J., Rice C.D.;
"Expression of a hepacoyte growth-factor activator protein in turkey (Melaagris gallopavo) deferent duct epithelial cells.";
Comp. Biochem. Physiol. 132:769-777(2002).
 Query Match 32.6%; Score 492; DB 13; Length 540;
Best Local Similarity 40.8%; Pred. No. 2.7e-40;
Matches 106; Conservative 43; Mismatches 91; Indels 20; Gaps
 A SEQUENCE FROM N.A.

Holsberger D.R., Becker A.E., Thurston R.J., Rice C.D.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY216598, AAO46038.1, -.

GO; GO:0004263, F.Chymotrypsin activity; IEA.

InterPro; IPR000424; EGF_1ike.

InterPro; IPR006039; EGF_1ike.

InterPro; IPR006039; Firstype_II.

InterPro; IPR006039; Firstype_II.

R InterPro; IPR006124; Feptidase_S1A.

R InterPro; IPR001244; Peptidase_S1A.

R Pfam; PF00018; Kxingle, I.

R Pfam; PF00018; Kxingle, I.

R Pfam; PF000099; Lxingle, I.
 540 AA; 61159 MW; 0BB3B4A89C0B577F CRC64;
 PRINTS; PRO0722; CHYMOTYPEIN; TP PERINTS; PRO0722; CHYMOTYPEIN; PRO01018; KRINGIE.
PRINTS; PR001018; KRINGIE.
SMART; SM001081; EGF, 2.
SWART; SM001086; FNI; 1.
SWART; SM001087; RN; 1.
SWART; SM00100020; TRYP_SPC; 1.
PROSITE; PS001020; EGF_2; 1.
PROSITE; PS01166; EGF_2; 1.
PROSITE; PS00121; KRINGIE 1; 1.
PROSITE; PS00121; KRINGIE 1; 1.
PROSITE; PS00131; KRINGIE 1; 1.
PROSITE; PS00131; TRYPSIN_DOM; 1.
PROSITE; PS00131; TRYPSIN_DOM; 1.
 245 CALKDKPGVYTRVSHFLPWI 264 | :|||||||| :::||
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Gaps

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342 APPEQRGPLPSAGLVGCGQR-LRKRLSSLNRIVGGLVALPGAHPYIAALYWGQN----- 394
 113 DTLAHHNDIALLKIR-SKEGRCAQPSRIIQTICLP---SMYNDPQFGTSCEITGFGKENS 168
 169 IDYLYPEQLKWITVVKLISHRECQQPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVC- 227
 512 GAEBYSSFLÖBAQVPLISPERCSAADVHGAAFTPGMLCAGFLBGGTDACQGDSGGFLVCE 571
 REDIENCE FROM N.A.

RC STRAIN-white spot;

RX SEQUENCE FROM N.A.

STRAIN-white spot;

RX ONDAINE-99423646; PubMed=10491255;

RX ONDAINE-99423646; PubMed=10491255;

RX ONDAINE-99423646; PubMed=10491255;

RX ONDAINE-STRICKENSON OF STRAINE SI.

RX NELLARITY: BELONGS TO PEPTIDASE FAMILY SI.

C. --- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

RX ONDOGOS, 1DPO.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005045; F:chymotrypsin activity; IEA.

GO; GO:0005045; F:peptidase activity; IEA.

GO; GO:0005045; F:peptidase activity; IEA.

GO; GO:0005045; F:peptidase activity; IEA.

GO; GO:0005045; F:peptidase activity; IEA.

GO; GO:0005045; F:peptidase activity; IEA.

GO; GO:0005045; F:peptidase SI.

RICE-PRO; IRRO01214; Pan.app.

DR InterPro; IRRO01214; Peptidase SI.

RICE-PRO; IRRO01214; Peptidase SI.

RICE-PRO; IRRO01204; PAN; I.

DR Ffam; PP00024; PAN; I.

DR Ffam; PP00024; PAN; I.

DR Ffam; PP00089; trypsin; I.

DR RINTS; PR00122, CHRMOTRYPSIN.

DR RINTS; PR00122, CHRMOTRYPSIN.
 455 KTYQH--DLALVRLKETADGCCAHPSPFVQPVCLPRSVASSAEPE-GALCEVAGWGHQPE
 4 SPPEEL-----KFQCGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTY
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
Serine protease.
SEQUENCE 616 AA; 68012 MW; 4C5FR3D71FRRR1129 PPCA.
 Q9Y1V3;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tunicate retinoic acid-inducible modular protease precursor.
TRAMP.
 Query Match
31.0%; Score 467; DB 6; Length 616;
Best Local Similarity 37.8%; Pred. No. 1e-37;
Matches 107; Conservative 46; Mismatches 102; Indels 2
 --SLOGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT 268
 Bukaryota, Merazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Styelidae, Polyandrocarpa.
NCBI_TaxID=7723;
 PRT;
 Polyandrocarpa misakiensis.
 PRELIMINARY;
 Query Match
Best Local 9
 Q9Y1V3
 RESULT 16
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 516 ASPLQEAQVPPLSLERCSAPDVHGSSILPGMLCAGFLEGGTDACQGDSGGPLVCEDQAAE 575
 115 LAHHNDIALLKIR-SKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLY 173
 456 VSYQHDLALLRLQEDADGSCALLSPYVQPYCLPSGAARPSETTLCQVAGCGHQFEGASEY
 174 PEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQG--
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 TISSUE=Liver;
Takahashi T., Kihara T.,;
"Portine liver factor XII.";
Submitted (Javer factor XII.";
Submitted (Javer factor XII.";
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; AB02245; BAA37148.1; -.
HSSP; P00763; 1DPO.
 232 -RMILIGIVSWGRGCALKDKFGVYTRVSHFLPWIRSHT 268
 Last sequence update)
Last annotation update)
 616 AA
 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last seq. 01-OCT-2003 (TrEMBLrel. 25, Last ann. FXII.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 Sus scrofa (Pig).
 NCBI_TaxID=9823;
 RESULT 15
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RESULT 18
280YCS
10 080YC
AC 080YC
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 117 HHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDY-LYPE 175
 QLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQG--RM 233
 58 LISPCWVISATHCFI-DYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLA 116
 PSSPPEELKFQCGQKTL----RPRFKIIGGEFTTIENQPWFAAIYRHRGGSVTYVCGGS
 Gaps
 FT2...
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
 21;
 30.7%; Score 463.5; DB 5; Length 868; 38.9%; Pred. No. 3.5e-37; ive 44; Mismatches 103; Indels 21.
 TISSUB-Liver;
Schlosser M., Schwager S., Engel W.;
Schlosser M., Schwager S., Engel W.;
Submitted (UUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: ELLONGS TO PERTIDAGE FAMILY SI.
-!- SIMILARITY: CONTAINS I KRINGLE DOWAIN.
R. HSSP; POO760; LAQ7.
R. MSROPS; SO1.211; -.
R. MGD; MG1:1891012; FI2.
R. GO; GO:0004563; F:ctracellular; IEA.
R. GO; GO:0004263; F:ctracellular; IEA.
R. GO; GO:0004263; F:trypein activity; IEA.
R. GO; GO:0004263; F:trypein activity; IEA.
R. GO; GO:0006209; F:trypein activity; IEA.
R. GO; GO:0006209; F:trypein activity; IEA.
R. GO; GO:0006209; F:trypein activity; IEA.
R. GO; GO:0006209; F:trypein activity; IEA.
R. InterPro; IPR006009; Figr like.
R. InterPro; IPR006009; Fibrnctul.
R. InterPro; IPR006083; Fibrnctul.
R. InterPro; IPR006083; Fibrnctul.
R. InterPro; IPR006083; Fibrnctul.
R. InterPro; IPR006083; Fibrnctul.
 F71462865F36A6CA CRC64;
 035727;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pactor XII.
 234 TLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHT 268
 PRINTS; PRO0258; SPERACTRCPTR.
SMART; SM00473; PAN_AP; 1.
SWART; SM00473; PAN_AP; 1.
SWART; SM00202; SR_AP; 1.
SWART; SM00202; Tryp_SPc; 1.
PROSITE; PS01209; LDLEA_1; 3.
PROSITE; PS50240; LDLEA_2; 2.
PROSITE; PS50240; TRYPSIN_DO; 1.
PROSITE; PS00134; TRYPSIN_LS; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS0134; TRYPSIN_SER; 1.
PROSITE; PS01345; TRYPSIN_SER; 1.
PROSITE; PS0135; TRYPSIN_SER; 1.
PROCITE; PS0135; TRYPSIN_SER; 1.
PROCITE; PS0135; TRYPSIN_SER; 1.
PROCITE; PS0135; TRYPSIN_SER; 1.
PROCITE; PS0135; TRYPSIN_SER; 1.
PROFENANTAL
 POTENTIAL.
 SEQUENCE 868 AA; 97660 MW;
 Cuery Match
Best Local Similarity 38.99
Matches 107; Conservative
 PRELIMINARY;
 176
 N
 035727
 SIGNAL
 RESULT 17
01-3727
AC 035727
AC 035727
DT 01-478
DT 01-502
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ECOOPHYYGSEVITIKMLCAADPQWKTDSCOGDSGGPLVC---SLOGRWTLIGIVSWGRGC 245
 129 KEGRÇAQPSRIIÇTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWTVVKLISHR 188
 70 CFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-S 128
 13 CGQ---KTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATH
 Query Match
29.9%; Score 451.5; DB 11; Length 597;
Best Local Similarity 37.0%; Pred. No. 3.4e-36;
Matches 97; Conservative 47; Mismatches 103; Indels 15; Gaps
 080YCS;

080YCS;

01-JUN-2003 (TYEMBLrel. 24, Last sequence update)

01-JUN-2003 (TYEMBLrel. 25, Last annotation update)

01-OCT-2003 (TYEMBLrel. 25, Last annotation update)

Similar to coagulation factor XII (Hageman factor) (Fragment).

Bulks musculus (Mouse).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
F3AC07C37D0C0FBA CRC64;
 609 AA.
 246 ALKDKPGVYTRVSHFLPWIRSH 267
 573 GDRNKPGVYTDVANYLAWIQKH 594
 PRT;
 597 AA; 65638 MW;
 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
Strausberg R.;
 PRELIMINARY;
 Serine protease.
SEQUENCE 597 A
 189
 080YC5
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133 CAQPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYP-----EQLKMTVVKLI 185
 75 CGQPRMSSR--IVGGRDGRDGEWPWQASI--QHRG---AHVCGGSLIAPQWVLTAAHCFP 127
 186 SHREÇQQPHYYGSEVITK-----MLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGI 238
 73 DYPKKEDYIVYLGRSRLNSNTOGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGR
 13 CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
 Gaps
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Serine protease BOS.
Homo sapiens (Human).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 01-OCT-2002 (TrEMBLrel. 22, Created)
1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protease, serine, 8 (Prostasin) (Fragment).
Howo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 33;
 Query Match 29.3%; Score 442.5; DB 4; Length 327; Best Local Similarity 38.8%; Pred. No. 1.2e-35; Matches 104; Conservative 35; Mismatches 96; Indels 33.
 Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (MCG-2002) to the EMBL/GenBank/DDBJ databases
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; BO036846; AH36846 L; ...
GO; GO:0004233; Fichypain activity; IEA.
GO; GO:0004233; Fichphidase activity; IEA.
GO; GO:0004235; Fithypain activity; IEA.
GO; GO:0004235; Fithypain activity; IEA.
GO; GO:0004235; Fithypain activity; IEA.
GO; GO:0004235; Fithypain activity; IEA.
GO; GO:0004235; Fithypain activity; IEA.
InterPro; IPRO0303; Cys Ser Lrypsin.
InterPro; IPRO03124; Peptidase_SI.
InterPro; IPRO03124; Peptidase_SIA.
Fram; PFO:0089; trypsin, 1.
Fram; PFO:0089; trypsin, 1.
FRANT; SMO022; Tryp SPC; II.
FRANT; SMO022; Tryp SPC; II.
FRANT; SMO022; Tryp SPC; II.
FRANT; FROMO32; Tryp SPC; II.
FRANT; PROMO32; Tryp SPC; II.
FRANT; FRANT; SRM; TRYPSIN, SER; II.
FRANT; FRANT; TRYPSIN, SER; II.
FRANT; FRANT; TRYPSIN, SER; II.
 NON TER 1 1 SEQUENCE 327 AA, 35106 MW; 60458ED817AC1CF3 CRC64;
 SEQUENCE FROM N.A. Darrade-Gordon P., Chen C.; Darrow A.L., Qi J., Andrade-Gordon P., Chen C.; "DNA encoding the human serine protease EOS.";
 239 VSWGRGCALKDKPGVYTRVSHFLPWIRS 266
 ||||:|||| ::||||| |::||||::
VSWGKGCALPNRPGVYTSVATYSPWIQA 323
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Q8NF86
Q8NF86;
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 08NF86
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 464
 KEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR 188
 ECOOPHYYGSEVITIMALCAADPOWKIDSCOGDSGGPLVC---SLOGRMTLIGIVSWGRGC 245
 465 KTNSCAILSPHVOPVCLPSGAAPPSETVLCEVAGWGHQFEGAEBYSTFLQEAQVPFIALD 524
 69
 70 CFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR-S
 407 CLONRPAPEELT VVIGGDRHNQSCEWCQTLAVRSYRLHEGFSSITYQH--DLALLRLQES
 13 CGQ----KTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATH
 353 CGQRFRKGLSSFMRVVGGLVALPGSHPYIAALYWGNN-----FCAGSLIAPCWVJTAAH
 15;
 DB 11; Length 609;
Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL, BCO095576; C:extracellular; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005209; F:calcium ion binding; IEA.
GO; GO:0005209; F:calcium ion binding; IEA.
GO; GO:0005209; F:chymotrypsin activity; IEA.
GO; GO:0006209; F:chymotrypsin activity; IEA.
GO; GO:0006209; F:chymotrypsin activity; IEA.
GO; GO:0006209; F:chymotrypsin activity; IEA.
R InterPro; IPRO01801; GGF_Ca.
R InterPro; IPRO01801; GGF_Ca.
R InterPro; IPRO01801; Firtypsin.
R InterPro; IPRO01801; Firtypsin.
R InterPro; IPRO01244; Peptidase_S1.
R InterPro; IPRO01244; Peptidase_S1.
R InterPro; IPRO01244; Peptidase_S1.
R InterPro; IPRO01244; Peptidase_S1.
R Edm; PFO0009; EGF; 2.
F Fam; PFO0009; EMPORTEI.
R PRINTS; PRO0181; EMPORTEI.
R PRINTS; PRO0181; EMPORTEI.
R PRINTS; PRO0181; EMPORTEI.
R PRINTS; PRO0181; EMPORTEI.
R PRINTS; PRO0181; EMPORTEI.
R PRODON; PD000995; Kringle; 1.
R PRODON; PD000995; Kringle; 1.
R SWART; SW00185; FRZ; 1.
R SWART; SW00185; FRZ; 1.
R SWART; SW00185; FRZ; 1.
R SWART; SW00185; FRZ; 1.
R PROSITE; PS00121; KRINGLE 1.
R PROSITE; PS00121; KRINGLE 2; 1.
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R PROSITE; PS00121; KRINGLE 2; 1.
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R PROSITE; PS00121; KRINGLE 2; 1.
R PROSITE; PS00121; KRINGLE 2; 1.
R PROSITE; PS00121; TRYPSIN_BER; 1.
 29.9%; Score 451.5; DB 11; Length 37.0%; Pred. No. 3.5e-36; ive 47; Mismatches 103; Indels
 609 AA; 66783 MW; DF97D4DB2369B6D2 CRC64;
 327 AA.
 246 ALKDKPGVYTRVSHFLPWIRSH 267
 GDRNKPGVYTDVANYLAWIQKH 606
 97; Conservative
 PRELIMINARY;
 Query Match
Best Local Similarity
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Q8N171;
 RESULT 19
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ID Q8N17
AC Q8N17
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MEDINB=21326076; PubMed=11313341;

MEDINB=21326076; PubMed=11313341;

A Kodama E., Baba T., Yokosawa H., Sawada H.;

Kodama E., Baba T., Yokosawa H., Sawada H.;

A Kodama E., Baba T., Yokosawa H., Sawada H.;

A Baba T., Yokosawa H., Sawada H.;

A Baba T., Yokosawa H., Sawada H.;

A Kodama E., Baba T., Yokosawa H., Sawada H.;

A Kodama E., Baba T., Yokosawa H., Sawada H.;

A Baba T. Similakiriy Belongs Pamira S.

I Similakiriy: Belongs Pamira S.

B Baba T. Samilakiriy: Baba T. Samana S.

B Baba T. A Baba T. Samana S.

B Baba T. A Baba T. Samana S.

B Baba T. A Baba T. Samana S.

B Baba T. A Baba T. Samana S.

B CO, GO:0004295; F:crypsin activity; IEA.

B Ffam; PF00421; CUB; 2.

B Ffam; PF00421; CUB; 2.

B REAL; SMORZ1; SMO042; CUB; 2.

B REAL; SMART; SMO0020; Tryp. SPC; 1.
 72 IDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEG 131
 18 CGVQVINPVLNKIVGGDEAVPGSWPWQVMFRKRYWAGDYQF-CGGTLISDEWAVSAAHCF 76
 191 QOPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVC-SLQGRMTLTGIVSWGRGCALKD
 186 NRATWYGGEINDNMICAGFKEGGKDSCQGDSGGFFVCQSASGEVELVGVVSWGYGCADAR
 13 CGQKTLRPRF-KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCF
 15;
 Query Match
28.3%; Score 426.5; DB 5; Length 267;
Best Local Similarity 36.2%; Pred. No. 3.8e-34;
Matches 93; Conservative 42; Mismatches 107; Indels 15;
 Proacrosin.
ACR.
Halocynthia roretzi (Sea squirt).
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Prims, Pr00089; trypsin; 1.
PRIMS: PR00722; CHYMOIRYSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS0135; TRYPSIN SER; 1.
PROSITE; PS0135; TRYPSIN SER; 1.
PROSITE; PS0135; TRYPSIN SER; 1.
PROSITE; PS0135; TRYPSIN SER; 1.
PROSITE; PS0135; TRYPSIN SER; 1.
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Last sequence update)
Last annotation update)
 246 KPGVYAKVLNYVSWINN 262
 250 KPGVYTRVSHFLPWIRS 266
 01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
 PRELIMINARY;
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Q966V4;
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10966V4
10 0966V4
10 0966V4
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 132
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 135 PVPLSARVQPVCLPVPGARPPPGTPCRVTGWGS-----LRPGVPLPEWRPLQGVRVPLL 188
 186 SHRECQOPHYYGSEVITK-----MLCAADPOWKIDSCQGDSGGPLVCSLQGRMILIGI 238
 133 CAQPSRTIQTICLPSMYNDPOFGTSCEITGFGKENSTDYLYP------EQLKMTVVKLI 185
 72
 80
 28 CGQPRMSSR--IVGGRDGRDGEWPWQASI--QHPG---AHVCGGSLIAPQWVLTAAHCFP
 13 CGOXTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
 73 DYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGR
 Gaps
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N SEQUENCE FROM N.A.

N SEQUENCE FROM N.A.

MEDLINE=21100442; PubMed=11179669;

MICHAINZALION CLL., VICKETY M.S., MCClintock J.B., Amsler C.D.;

N Vickery M.C.L., Vickery W.S., MCClintock J.B., Amsler C.D.;

N Utilization of a novel deuteroetcme model for the study of regeneration genetics: Molecular cloning of genes that are differentially expressed during early stages of larval sea star regeneration."; Cene 26:73-80 (2001).

Cene 26:73-80 (2001).

SEMEL, AF312826; AAK15274.1; -..

REMEL, AF312826; AAK15274.1; -..

REMEL, AF312826; AAK15274.1; -..

RO; GO:0008233; F:cppridase activity; IEA.

GO; GO:0008233; F:tppridase activity; IEA.

RO; GO:0008235; F:trppsin activity; IEA.

RO; GO:0008235; F:trppsin activity; IEA.

RO; GO:0008236; P:trypsin activity; IEA.

RO; GO:00080303; P:trypsin activity; IEA.

RO; GO:0006508; P:trypsin activity; IEA.

RO; GO:0006508; P:trypsin.
 33;
 Query Match 28.9%; Score 435.5; DB 4; Length 284; Best Local Similarity 38.4%; Pred. No. 5.2e-35; Matches 103; Conservative 35; Mismatches 97; Indels 33;
 01-UN-2001 (TrEMBLrel. 17, Created)
01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Sea SLAR regeneration-associated protease SRAP.
Luidia follolata.
Eukaryota; Metacoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Valvatacea; Paxillosida; Luidiidae; Luidia.
NUSI_TAXID=105861;
 Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

2. GENEL, AFS36382; AAN04055.17;

3. GO; GO:0004233; F:chymocrypsin activity; IEA.

3. GO; GO:0004233; F:peptidase activity; IEA.

3. GO; GO:0004295; F:trypsin activity; IEA.

3. GO; GO:0006208; P:proteolysis and peptidolysis; IEA.

3. InterPro; IPR009003; Cya_Ser_trypsin.

3. InterPro; IPR009003; Cya_Ser_trypsin.

3. InterPro; IPR001314; Peptidase_S1.

3. RPRIMYS; PR001234; Peptidase_S1A.

3. RPRIMYS; PR001234; PEPTINGORYPSIN.

3. RPROSITE; PS00134; TRYPSIN DOM; 1.

4. RPROSITE; PS00134; TRYPSIN DOM; 1.

4. RPGOSITE; PS00134; TRYPSIN DOM; 1.

4. RPGOSITE; PS00134; TRYPSIN ER; 1.

4. RPGOSITE; PS00134; TRYPSIN ER; 1.

5. RPGOSITE; PS00134; TRYPSIN ER; 1.

6. RPGOSITE; PS00135; TRYPSIN ER; 1.
 VSWGKGCALPNRPGVYTSVATYSPWIQA 276
 PRELIMINARY;
 Q9BK47
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RESULT 21 Q9BK47

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099408
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 176 QLKMTVVKLISHREÇQQPHYYGSEVTTKMLCAADPQWKTDSÇQGDSGGPLVC----SLQ 230
 NDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYL---YPE 175
 13 CGOKTLRPRF-----KIIGGEPTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVI 65
 SATHCF-----IDYPKKEDYIVYLG-RSRLNSNTQGEMKFEVENLILHKDYSADTLAHH
 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Buks musculus (Mouse).

Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 Query Match 28.2%; Score 425.5; DB 5; Length 505; Best Local Similarity 35.5%; Pred. No. 1.1e-33; Matches 99; Conservative 47; Mismatches 92; Indels 41
 FERUDANCE FROM N.A.

A STRAUSBERGHOWN. A.

TISSUE-Kidney;

Strausberg R.;

Submitted (UIN-2002) to the EMBL/GenBank/DDBJ databases.

L. SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

-!- SIMILARITY: CONTAINS I KRINGIE DOWAIN.

R MEL; BCO1775; AAH31775.1; -.

R GO; GO:0006263; F:calcium ion binding; IEA.

R GO; GO:0006283; F:chymotrypsin activity; IEA.

R GO; GO:0006283; F:chymotrypsin activity; IEA.

R GO; GO:0006283; F:chymotrypsin activity; IEA.

R GO; GO:0006283; F:chymotrypsin activity; IEA.

R GO; GO:0006283; F:chymotrypsin activity; IEA.

R GO; GO:0006283; F:chymotrypsin activity; IEA.

R GO; GO:0006283; F:chymotrypsin activity; IEA.

R InterPro; IPR00003; Cys Ser_trypsin.

R InterPro; IPR001881; BGF_Ca.

R InterPro; IPR001881; BGF_Ca.

R InterPro; IPR001881; BGF_Ca.

R InterPro; IPR001881; BGF_Ca.

InterPro; IPR001881; BGF_Ca.

InterPro; IPR001881; BGF; 2.

R InterPro; IPR001881; Peptidase_SIA.

R Pfam; PF000089; Kringle; 1.

R Pfam; PR000089; Kringle; 1.

R PRINTS; PR00189; KRINGIE.

PROD; PR00189; KRINGIE.

R SMART; SM00181; RR; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135, TRYPSIN_ER; 1.
Hydrolase; Protease, Serine protease.
SEQUENCE SOS AA; 55002 MW; 79AlA917CElD9334 CRC64;
 231 GRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 269
 242 PTFFLQGIVSWGRGCALDGFPGVYTEVRXYSSWIANYTQ 280
 PRELIMINARY;
 SEQUENCE FROM N.A.
 99
 119
 Query Match
 Q8K0D2
Q8K0D2;
 RESULT 23
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76 KKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKBGRCAQ 135
 325 TKHLKVV-LGDQDLKKTESHEQTFRVEKILKYSQYNERDEIPHNDIALLKLKPVGGHCAL 383
 136 PSRTIQTICLPSMYNDP-QFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPH 194
 384 ESRYVKTVCLPS.--DPFPSGTECHISGWGVTETGE--GSRQLLDAKVKLIANPLCNSRQ 438
 439 LYDHTIDDSMICAGNLQKPGSDTCQGDSGGPLTCBKDGTYYVYGIVSWGQECG--KKPGV 496
 195 YYGSEVTTKMLCAADPQWK-TDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGV
 23 KIIGGEFTTIENQPWFAAIY-----RRHRGGSVTYVCGGSLISPCWVISATHCFIDYP
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 PEDUENCE FROM N.A.

Hintsch G., Sonderegger P.;

Hintsch G., Sonderegger P.;

Hintsch G., Sonderegger P.;

Hintsch G., Sonderegger P.;

Colonological and sequencing of the cDNA encoding rat neurotrypsin.";

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ31671; CAC35028.2; ---

EMBL; AJ31671; CAC35028.2; ---

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EMBL; EMBL; EMBL; EMBL; ---

EMBL;
PROSITE; PS00022; EGF 1; 3.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00040; KRYBGIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Hypothetical protein; EGF-1ike domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SEQUENCE 517 AA; 57326 MW; 3855A42035A5EA59 CRC64;
 Query Match
28.2%; Score 425; DB 11; Length 517;
Best Local Similarity 36.7%; Pred. No. 1.3e-33;
Matches 101; Conservative 36; Mismatches 102; Indels 22
 Created)
Last sequence update)
Last annotation update)
 497 YTQVTKFLNWIKTTWHREAGL 517
 254 YTRVSHFLPWIRSHTKEENGL 274
 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Meurotrypsin.
 PRELIMINARY;
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PROSITE; PS00135; TRYPSIN_SER; 1.
 Protease.
NON TER
SEQUENCE
 382
 248
 442
 Q80WM7
Q80WM7;
 RESULT 26
Q80WM7
DD Q80WM AC
Q80WM AC
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 184 LISHRECQOPHYYGSEVTTKMLCAADPQW--KTDSCQGDSGGPLVCSLQGR-MTLTGIVS 240
 125 KIRSKEGRÇAQPSRTIQTICLPSMYNDPQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVK 183
 66 SATHCFIDY-PKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALL 124
 65
 7 BELKFOCGOKTL-RPRFKIIGGEFTTIBNOPWFAAIYRRHRGGSVTYVCGGSLISPCWVI
 OBCFEO PRELIMINARY, PRT; 471 AA.

OBCFEO;

O1-MAR-2003 (TrEMBLrel. 23, Created)

O1-MAR-2003 (TrEMBLrel. 25, Last sequence update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Similar to mosaic serine protease (Fragment).

Bus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(1) TaxID=10090;
 DB 11; Length 761;
 A Straubberg R.,
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

B Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

B GO; GO:0016020; C:membrane; IEA.

GO; GO:0006233; F:peptidase activity; IEA.

GO; GO:000633; F:peptidase activity; IEA.

GO; GO:000633; F:peptidase activity; IEA.

GO; GO:0006508; F:trypsin activity; IEA.

GO; GO:006508; P:proteclysis and peptidolysis; IEA.

IN EAPLY: IRRO2122; LDL receptor A.

IN INTERPRO; IRRO2122; LDL receptor A.

IN INTERPRO; IRRO3134; Peptidase_SIA.

INTERPRO; IRRO3134; Peptidase_SIA.

INTERPRO; IRRO01934; Peptidase_SIA.

INTERPRO; IRRO01934; Peptidase_SIA.

INTERPRO; IRRO01934; Peptidase_SIA.

INTERPRO; IRRO0199; STCT_receptor.

P Fam; PRO0722; CHYMOTRYPSIN.

SMART; SMO022; GHYMOTRYPSIN.

SMART; SMO022; GHYMOTRYPSIN.

DR SMART; SMO022; CHYMOTRYPSIN.

DR PROSITE; PSSO2397; SRGZ 2.

DR PROSITE; PSSO2307; TRYPSIN JIS; 1.
 28.0%; Score 421.5; DB 11; Length
36.6%; Pred. No. 4.6e-33;
.ive 44; Mismatches 113; Indels
SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS00400; KRINGLE 2; 1.

PROSITE; PS00400; SRCR 1; 3.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

SEQUENCE 761 AA; 84165 WW; 91DC966ED3BACFE1 CRC64;
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHT 268
 732 WGYGCGIKDTPGVYTRVPAFVPWIKSVT 759
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Breast tumor;
 Query Match
Best Local Similarity 36.0.
The 98; Conservative
 RESULT 25
08GCPE
00GCPE
01-MA
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73 DYPKK---EDYIVYLGRSRLMSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSK 129
 72
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 221 CGLRAMTGR--IVGGALTSESKWPWQVSL---HFG--TTHICGGTLIDAQWVLTAAHCFF 273
 73 DYPKK--BDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
 274 VTREKLLEGWKVYAGTSNLHQLPEAA---SISQIIINGNYTDE--QDDYDIALI----- 322
 131 GRCAQP---SRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLXMTVVKLISH 187
 323 -RLSKPLTLSAHIHPACLPWHGQTFGLNETCWITGFGKTKETDEKTSPFLREVQVNLIDF 381
 188 RECOOPHYYGSEVITKMLCAADPQWKTDSCOGDSGGPLVCSLOGRMTLTGIVSWGRGCAL 247
 13 CGQKTLRPRFKIIGGBFTTIENQPWFAAIYRRRGGSVTYVCGGSLISPCWVISATHCFI 72
 13 CGOKTLRPREKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWISATHCFI
 25 CGQPRMSSR--IVGGRDAQDGEWPWQTSI--QHRG---AHVCGGSLIAPQWVLTAGHCF-
 Gaps
 Tryptase-6.

Tryptase-6.

Bukar musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBI_TaxID=10090;
 24;
 27.8%; Score 418.5; DB 11; Length 277; 36.9%; Pred. No. 2.5e-33; ive 41; Mismatches 91; Indels 39;
 Length 471;
 Query Match 27.9%; Score 420; DB 11; Length 47. Best Local Similarity 37.1%; Pred. No. 3.5e-33; Matches 98; Conservative 38; Mismatches 104; Indels
1
471 AA; 52535 MW; ED58CFE6B7C3BCC4 CRC64;
 Created)
Last sequence update)
Last annotation update)
 277 AA
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 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
 Query Match 27.8%
Best Local Similarity 36.9%
Matches 100; Conservative
 PRELIMINARY;
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73 DYPKK--EDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
 131 GRCAQP---SRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISH 187
 414 --RLSKPLTLSAHİHPACLPMHGQTFSLNETCMİTGFGKTRETDDKTSPFLREVQVNLİDF 472
 188 RECQOPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCAL 247
 389 -RLSKPLILSAHIHPACLPMHGQTFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDF 447
 RECOOPHYYGSEVITIMICAADPOWKIDSCOGDSGGPLVCSLOGRMTLIGIVSWGRGCAL 247
 3.5 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 | 3.4 |
 13 CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 24;
 Park T.J., Park W.J.;

A Park T.J., Park W.J.;

Park T.J., Park W.J.;

"Homo sapiens transmembrane protease, serine 6 (TMPRSS6) mRNP
"Homo sapiens transmembrane; new Go, Go. 00046020; C. membrane; new Go, Go. 0004262; F. chymotrypein activity; new.

GO, GO. 0004263; F. peptidase activity; new.

GO, GO. 000423; F. peptidase activity; new.

GO, GO. 0004295; F. chypsin activity; new.

GO, GO. 0004295; F. chypsin activity; new.

GO, GO. 0004295; F. chypsin activity; new.

R GO, GO. 0004295; F. chypsin activity; new.

InterPro; PR000129; F. crypsin.

InterPro; PR001314; Peptidase S1A.

InterPro; PR001314; Peptidase S1A.

InterPro; PR00129; Sr. receptor.

R PR00120; GY, I.Y.

R PR00120; SR; 1.

R PR011F PS00203; RY, 1.

R PR051TE; PS00201; Tryp SPC; 1.

R PR051TE; PS00201; Tryp SPC; 1.

R PR051TE; PS00201; TRYPSIN D0M; 1.

R PR051TE; PS00135; TRYPSIN JNS; PR0501TE; PS00135; TRYPSIN SRS; 1.
 Query Match

27.7%; Score 418; DB 4; Length 558;

Best Local Similarity 36.5%; Pred. No. 6.9e-33;

Matches 97; Conservative 39; Mismatches 106; Indels 2
 Protease.
SEQUENCE 558 AA; 60432 MW; 4AC817FCD70D7017 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Transmembrane protease serine 6.
 248 KDKPGVYTRVSHFLPWIRSHTKEENG 273
 248 KDKPGVYTRVSHFLPWIRSHTKEE 271
 RINKPGVYTKVTEVLPWIYSKMESE 531
 PRELIMINARY;
 NCBI_TaxID=9606;
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 DYPKK--EDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
 131 GRCAQP---SRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLLYPEQLKMTVVKLISH 187
 ---VSLSTRIQPVCLPAPGSHPPPGSPCWVIGWGS-----LSPGVPLPKGRPLQGVRV 182
 KLISHRECQQPHYYGSE-----VTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTL 235
 --PRRVWPSEYSVILGALSIDVRSSHELLVPVLRVLLPPDYSEDEA--RGDLALLQIRHP 132
 EGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYP ------EQLKMTVV 182
 CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 27.7%; Score 418; DB 4; Length 537; 36.7%; Pred. No. 6.6e-33;
 MEROPS; 801.003; 1.DFO.

READES; 801.003; 1.DFO.

READES; 801.001; C:integral to membrane; NAS.

RO; GO:0006508; P:proteolygis and peptidolysis; NAS.

InterPro; IPR002172; LDL receptor A.

InterPro; IPR00134; Peptidase S1.

InterPro; IPR00134; Peptidase S1.

InterPro; IPR00134; Peptidase S1.

InterPro; IPR00134; Peptidase S1.

REANTS; PR00057; Ldl receptor.

REANTS; PR00057; LTYDESIN; 1.

REANTS; PR00122; CHYMOTRYPSIN.

RAMRT; SM00122; CHYMOTRYPSIN.

RAMRT; SM00120; RF, 1.

ROSITE; PS00134; TRYPSIN DO;

RECOITE; PS00134; TRYPSIN LHIS; 1.

RECOITE; PS00134; TRYPSIN LHIS; 1.

RECOITE; PS00134; TRYPSIN LHIS; 1.

RECOITE; PS00134; TRYPSIN LHIS; 1.

RECOITE; PS00134; TRYPSIN LHIS; 1.

RECOITE; PS00134; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

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RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.

RECOITE; PS00135; TRYPSIN LHIS; 1.
 36.7%; Pred. No. 6.06-55.,
Live 38; Mismatches 105; Indels
 Created)
Last sequence update)
Last annotation update)
 243 VGVVSWGKGCALPNRPGVYINVAKYSPWIQA 273
 TGIVSWGRGCALKDKPGVYTRVSHFLPWIRS 266
 537 AA
 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25, Mosaic serine protease.
 Local Similarity 36.7
 PRELIMINARY;
 NCBI_TaxID=9606;
 £
 73
 Query Match
 183
 133
 Q9BYE1;
Q9BYE1;
 Best Loca
Matches
 RESULT 2

1099 X 21

1009 X 21

1009 X 21

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us-09-880-503-5.rspt

533 RNKPGVYTKVTEVLPWIYSKMESSAG 558

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Tomita M.; "Purification and characterization of a novel hyaluronan-binding protein (PHBP) from human plasma: it has three EGF, a kringle and a serine protease domain, similar to hepatocyte growth factor
 014520 PRELIMINARY; PRT; 560 AA.
014520; 000663;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-NOV-1996 (TEMBLrel. 25, Last amocation update)
01-OCT-2003 (TEMBLrel. 25, Last amocation update)
HGF activator like protein (Hyaluronan binding protein 2).
HGF activator | Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.
 SEĞUENCE FROM N.A.
MEDLINE-96425001; PubMed-8827452;
Chol-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
 Query Match 27.7%; Score 417; DB 4; Length 560; Best Local Similarity 36.2%; Pred. No. 8.7e-33; Matches 104; Conservative 40; Mismatches 113; Indels
 Kitamura N.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;
 J. Biochem. 119:1157-1165(1996).
 SEQUENCE FROM N.A.
 Serine protease
SEQUENCE 560
 activator.";
RESULT 29
 Q14520
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Gaps

30;

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288 PTEPSTKLPGFDSCGKTBIAERKIKRIYGGFKSTAGKHPWQASLQ----SSLPLTISMP 342
 52 --YVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKD 109
 110 YSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF--GTSCEITGFGKEN 167
 || : : | |:|| : || || CGLRANTGR--IVGGALASDSKWPWQVSL---HFG--TTHICGGTLIDAQWVLTAAHCFF 364
21
 13 CGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI
 168 STDYLYPROLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWK-TDSCQGDSGGPLV
2 PSSPPEELK--FOCGOKTLRPR--FKIIGGEFTTIENOPWFAAIYRRHRGGSVT----
 TISSUBELUNG;
MEDLINE=21167393; PubMed=11267681;
Kim D.R., Sharmin S., Inoue M., Kido H.;
Kim D.R., Sharmin S., Inoue M., Kido H.;
"Cloning and expression of novel mosalc serine proteases with and without a transmembrane domain from human lung.";
Embl., ABOA8796; BAB39741.1; --
HSSP; P00763; 1DPO.
 MSPL.

Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 27.5%; Score 414; DB 4; Length 581; 37.1%; Pred. No. 1.8e-32; Live 37; Mismatches 102; Indels 24
 515 CEKDGTYYVYGIVSWGLECG--KRPGVYTQVTKFLNWIKATIKSESG 559
 227 CSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENG 273
 RESPY; POUGES; LIDO.

RESPY; POUGES; LIDO.

RESPY; POUGES; Proposectory and apprincely sis; NAS.

RO; GO:0006508; Proposectory and apprincely sis; NAS.

GO; GO:0006508; Proposectory and apprincely sis; NAS.

RITHERPO: IPRO02172; LDL_receptor_A.

RITHERPO: IPRO01144; Peptidase_S1.

RITHERPO: IPRO01144; Peptidase_S1.

RITHERPO: IPRO01194; Serr_receptor.

R PARAT; PRO0057; LTYPSin; 1.

R PROVITS; PRO0122; CHYMOTRYPSIN.

R SMART; SM00122; LTYPSin; 1.

R SMART; SM00122; LTYPSin; 1.

R SMART; SM00124; RS; 1.

R PROSITE; PS50287; SR; 1.

R PROSITE; PS50287; SR; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PAGINES; RS0135; TRYPSIN HIS; 1.

R PAGINES; PS00135; TRYPSIN HIS; 1.

R PAGINES; PS00135; TRYPSIN HIS; 1.

R PAGINES; PS00135; TRYPSIN HIS; 1.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Membrane-type mosaic serine protease.
 PRT;
 Query Match
Best Local Similarity 37.1%;
Matches 96; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 312
 Q9BYE2
 RESULT :
Q9BYE2
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| Qy 198 SEVITRALCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGR-GCALKDKPGVYTR 256  | Oy 257 VSHFLPWIRSHTKRE 271  Db 252 VSKYLRWIREIIRNIPEQ 269                   | RESULT 32 QBROPS ID QBROPS AC QBROPS, DT 01-JUN-2002 (TrEMBLrel. 21, Created) DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) DT 01-OTT-2003 (TrEMBLrel. 25, Last annotation update) | ordata; Craniata; Vertebrat dentia; Sciurognathi; Murid bentia; Sciurognathi; Murid co the EMBL/GenBank/DDBJ dat 55.1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|--------------------------------------------------------------------------|-----------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| QY 73 DYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130<br> | Qy 131 GRCAQPSRIQTICLESMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISH 187<br>  :: | OY 188 RECOOPHYYGSEVITKMLCAADPOWKIDSCOCDSGCPLVCSLOGRWILIGIVSWGRGCAL 247  ::                                                                                                               | PRESULT 31  PRESULT 31  PRESULT 31  PRESULT 31  PRESULT 31  PRECASOR FRELIMINARY, PRT, 276 AA.  PRECASOR SOCRESSOR (TEXBELES, 25, Last sequence update)  DI 0.4AR.2033 (TEXBELES, 25, Last sequence update)  DI 0.4AR.2033 (TEXBELES, 25, Last sequence update)  DI 0.4AR.2033 (TEXBELES, 25, Last sequence update)  DI 0.4AR.2033 (TEXBELES, 25, Last sequence update)  SE GIADRILIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLIA)  MILLIA (MILLI |

PRT;

PRELIMINARY;

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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 Degree of the control of a rat adrenal mitochondrial protease.";

STRAIN-NEDH;

Omer S., Bicknell A.B., Lowry P.J.;

Identification of a rat adrenal mitochondrial protease.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

B MBL; AFS37098; AANO6771.1;

R GO: 001004263; F:chymotrypsin activity; IEA.

GO: 001004263; F:chymotrypsin activity; IEA.

GO: 001004263; F:chymotrypsin activity; IEA.

GO: 001004263; F:chymotrypsin activity; IEA.

R GO: 001004263; F:chymotrypsin activity; IEA.

R GO: 001004263; F:chymotrypsin activity; IEA.

R GO: 001004263; F:chymin activity; IEA.

R GO: 001004263; F:chymin activity; IEA.

R GO: 001004263; F:chymin activity; IEA.

R GO: 001004263; F:chymin activity; IEA.

R InterPro; IPR001264; Peptidase SI.

InterPro; IPR001264; Peptidase SI.

InterPro; IPR001190; Srcr.receptor.

R PROSITE; PRO0128; CHYMOTRYPSIN.

R PROSITE; PRO0128; CHYMOTRYPSIN.

R PROSITE; PRO0136; TRYPSIN HIS; 1.

R PROSITE; PRO0136; TRYPSIN HIS; 1.

R PROSITE; PRO0136; TRYPSIN HIS; 1.

R PROSITE; PRO0136; TRYPSIN HIS; 1.

R PROSITE; PRO0136; TRYPSIN HIS; 1.
 08C017;
01-WAR-2003 (TEMBLEEL. 23, Created)
01-WAR-2003 (TEMBLEEL. 23, Last sequence update)
01-OCT-2003 (TEMBLEEL. 25, Last annotation update)
Adrenal mitochondrial protease long variant.
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 RESULT 35
Q8CDR0
ID Q8CDR
AC Q8CDR
DT 01-MAD
DT 01-MAD
DD TTANS
GN TMPRS
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 166 PYWVVTAAHCMYSFRLSSWRVHAG---LVSHSAVRQHQGTM---VEKIIPHPLYSAQ 219
 61 PCMVISATHCFIDY--PKKEDYIVYLGRSRLNSNT-----OGEMKFEVENLILHKDYSAD 113
 220 N--HDYDVALLQLRTP----INFSDTVSAVCLPAKEQHFPQGSQCWVSGWGHTDPSHTHS 273
 274 SDTLQDTWVPLLSTDLCNSSCMYSGALTHRMLCAGYLDGRADACQGDSGGPLVCPSGDTW 333
 114 TLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLY 173
 174 PEQLIXMITVIKLISHRECQOPHYYGSEVITIYMLCAADPQWKTDSCQGDSGGPLVCSLQGRM 233
 2 PSSPPEELK-FOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRHRGGSVTYVCGGSLIS 60
 Rattus norvegicus (Rat)
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 SEQUENCE FROM N.A.

STRINIANDER:

A Omer S., Bicknell A.B., Lowry P.J.;

Omer S., Bicknell A.B., Lowry P.J.;

Comer S., Bicknell A.B., Lowry P.J.;

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF537099; AAN06758.1; -.

GO; GO:0016620; C:membrane; IEA.

GO; GO:0016023; F:chyprogram activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor.

RO; GO:0005044; F:scavenger receptor.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0005044; F:scavenger receptor activity; IEA.

RO; GO:0006508; F:scavenger receptor activity; IEA.

RO; GO:0006508; F:scavenger receptor activity; IEA.

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RO; GO:0006508; F:scavenger receptor activity; IEA.

RO; GO:0006508; F:scavenger receptor activity; IEA.

RO; GO:0
 26.7%; Score 402.5; DB 11; Length 371; 35.8%; Pred. No. 1.4e-31; cive 45; Mismatches 102; Indels 27;
 Protease.
SEQUENCE 371 AA; 40694 MW; 89A64081D9A1FE26 CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adrenal mitochondrial protease short variant.
 611 YTKVSEYMDWILEKTQSSDVRAL 633
 PRT;
 YTRVSHFLPWIRSHTKEENGLAL
 Local Similarity 35.8% les 97; Conservative
 PRELIMINARY;
 [1] —
SEQUENCE FROM N.A.
 254
 Query Match
 RESULT 33
Q8CJ16
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114 TLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLY 173
 348 SDILQDIMVPLLSTDLCNSSCMYSGALTHRMLCAGYLDGRADACQGDSGGPLVCFSGDTW 407
 240 PYWVVTAAHCMYSFRLSSWRVHAG---LVSHSAVRQHQGTM---VEKIIPHPLXSAQ 293
 174 PEQLKWIVVKLISHRECQQPHYYGSEVITKWLCAADPQWKTDSCQGDSGGPLVCSLQGRM 233
 294 N--HDYDVALLQLRTP----INPSDTVSAVCLPAKEQHFPQGSQCWVSGWGHTDPSHTHS
 2 PSSPPEELK-FOCGOXTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 61 PCWVISATHCFIDY--PKKEDYIVYLGRSRLNSNT-----QGEMKFEVENLILHKDYSAD
Query Match
26.7%; Score 402.5; DB 11; Length 445;
Best Local Similarity 35.8%; Pred. No. 1.8e-31;
Matches 97; Conservative 45; Mismatches 102; Indels 27; G
 408 HLVGVVSWGRGCAEPNRPGVYAKVAEFLDWI 438
 $
 234 TLIGIVSWGRGCALKDKPGVYTRVSHFLPWI
 PRELIMINARY;
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Transmembrane protease. TMPRSS5. Mus musculus (Mouse).

RESULT 34 Q8CJ17

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60 SPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHN 119
 178 KMIVVKLISHRECQQPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVC-SLQGRMTLT 236
 AND SEQUENCE FROM N.A.

AND SIDE SEQUENCE FROM N.A.

AND SEQUENCE FROM N.A.

AND SEQUENCE FROM W.K., Kim K.Y., Chung K.H., Park D.-H.;

AND "Cloning of a CDNA for a novel plasminogen activator from a Korean centipede Scolopendra";

RIST Considered (NOV-1996) to the EMBL/GenBank/DDBJ databases.

CC -: SIMILARITY BELONGS TO PEPTIDASE FAMILY S1.

REMBL, U79521; AAD00320.1; -.

BREADS, S01.125; -.

BREADS, S01.125; -.

BREADS, S01.125; -.

BREADS, S01.125; -.

BREADS, S01.125; -.

BREADS, S01.125; -.

BREADS, S01.125; -.

BREADS, S01.125; -.

BREADS, FILTPAPABIN activity; IEA.

GO; GO:0008233; Filtpapelidase activity; IEA.

BREADS, ROU0255; Filtpapelidase activity; IEA.

BREADS, S01.125; -.

BREADS, PROMO1264; Peptidase S1.

BREADS, RROWO1264; Peptidase S1.

BREADS, RROWO1264; Peptidase S1.

BREADS, RROWO1264; Peptidase S1.

BREADS, RROWO1264; PEPTIDAS, NO.

BREADS, RROWO1264; PEPTIDAS, NO.

BREADS, RROWO1264; PEPTIDAS, NO.

BREADS, RROWO1264; PEPTIDAS, NO.

BREADS, RROWO1264; PEPTIDAS, NO.

BREADS, RROWO1264; PEPTIDAS, NO.

BREADS, RROWO1264; PEPTIDAS, NO.

BREADS, RROWO1264; PEPTIDAS, NO.

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BREADS, RROWO1265; PEPTIDAS, NO.

BREADS, RROWO1265; PEPTIDAS, NO.

BREADS, RROWO1265; PEPTIDAS, NO.

BREADS, RROWO1265; PEPT
 120 DIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFG--KENSTDYLYPEQL
 2 PSSPPBBLKFQCGQKTLRPR--FKIIGGEFTTIBNQPWFAAIYRRHRGGSVTYVCGGSLI
MEDLINE=22784742; PubMed=12886014;

Cal S., Lopez-Octin C.;

"An alternative splicing of human polyserase lacking the last serine protease domain.";

Proc. Natl. Acad. Sci. U.S.A. 100:9185-9190(2003).

BMB1. AJG89846; CAD35758.1; -.

Alternative splicing.

SEQUENCE 1059 AA; 114020 MW; 17D27A2D99F2A264 CRC64;
 Plasminogen activator sPA.
Scolopendra subspinipes.
Bukaryota, Metazoa, Arthropoda; Myriapoda; Chilopoda;
Pleurostigmophos; Scolopendromorpha; Scolopendridae; Scolopendra.
 22;
 5; Length 277;
 Query Match

26.3%; Score 396; DB 4; Length 1059;
Best Local Similarity 35.0%; Pred. No. 2.5e-30;
Matches 96; Conservative 45; Mismatches 111; Indels 22
 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 1026 GVTSWGYGCGRPHFPGVYTRVAAVRGWIGQHIQE 1059
 237 GIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
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 Score 394.5;
 26.2%;
 PRELIMINARY;
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 107 HKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKE 166
 PCWVISATHOFIDYPKKEDYIVYLGRSRLNS------NTQGEMKFEVENLIL 106
 2 PSSPPEELK-FOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS 60
 167 NSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLV
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCPI_TaxID=10090;
 Query Match 26.3%; Score 396.5; DB 11; Length 455; Best Local Similarity 34.5%; Pred. No. 7.4e-31; Matches 96; Conservative 42; Mismatches 99; Indels 41;
 Created)
Last sequence update)
Last annotation update)
 Q72411 PRELIMINARY;
Q72411,
0.7411,
01-OCT-2003 (TEMBLE1. 25, L5
01-OCT-2003 (TEMBLE1. 25, L6
01-OCT-2003 (TEMBLE1. 25, L6
Polyserase lA protein.
 SEQUENCE FROM N.A.
TISSUE=Liver;
 227
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 RESULT 36
Q7Z411
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12;
 184 PLMTDEECSE--YY--NIVDTWLCAGYAEGGKDACQGDSGGPLVCPNGDGTYSLAGIVSW 239
 69 HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 128
 129 KEGRCAQP----SRTIQTICLPSMYNDPQFGTSCBITGFG--KENSTDYLYPEQLKMTVV 182
 133 ----- AEPLDLTPTAVGSICLPSQ-NNQEFSGHCIVTGWGSVREGGNS---PNILQKVSV 183
 183 KLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVC-SLQGRMTLTGIVSW
 QCGQKT---LRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISAT
 Gaps
 29;
 Indels
 Pred. No. 6.2e-31;
; Mismatches 99;
 242 GRGCALKDKPGVYTRVSHFLPWIRS 266
 240 GIGCAOPRNPGVYTOVSKFLDWIRN 264
Best Local Similarity 38.1%; Pr
Matches 101; Conservative 36;
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Created) Last sequence update) Last annotation update)

01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 11-OCT-2003 (TrEMBLrel. 25, 11-OCT-2003 (TrEMBLrel. 25, 11-OCT-2003)

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Guo J.H., Yu L.; "Molecular cloning and characterization of PRSS4B."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY052783; AAL14243.1; -. 261 AA; 28199 MW; 6B182C3BB9E7A5B3 CRC64; Q725F4 PRELIMINARY; PRT; 261 AA.
Q725F4;
01-0CT-2003 (TrEWBLrel. 25, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Protease serine 4 isoform B.
Homo sapiens (Human). SEQUENCE FROM N.A. NCBI\_TaxID=9606; Protease. SEQUENCE RESULT : Q7Z5F4 

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195 NSMFCVGFLEGGKDSCQGDSGGPVVCNGQ----LQGVVSWGHGCAWKNRPGVYTKVYNYV 250
 82 VYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ 141
 102 TKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFL 261
 8
 84
 ||:||:|| || ||: |: || ||: ||: ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
 KIIGGEFTTIENQ-PWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYI
 142 TICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVT
 27;
 261;
 th 26.0%; Score 391.5; DB 4; Length Similarity 38.1%; Pred. No. 1.1e-30; 93; Conservative 39; Mismatches 85; Indels
 262 PWIR 265
 DWIK 254
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PRELIMINARY;

RESULT 39 Q7Z410 ID Q7Z410

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ALLKIRSKEGRCAQP---SRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPBQLK 178
 121
 237
 179 MTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVC-SLQGRMTLTG
 3 SSPPEELKFOCG-OKTLRPRFKIIGGEFTTIENOPWFAAIYRRHGGSVTYVCGGSLISP
 CWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDI
 MEDLINE-2784742; Pubmed=12886014;
Cal S., Lopez-Octin C.;
Cal S., Lopez-Octin C.;
Tan alternative splicing of human polyserase lacking the last serine protease domain.";
Proc. Natl. Acad. Sci. U.S.A. 100:9185-9190(2003).
EMBL; AJ488947; CAD35759.1; -.
Alternative splicing.
SEQUENCE 855 AA; 91352 MM; 8AF2759D9740CF3F CRC64;
 Gaps
 Q812A6 PRELIMINARY; PRT; 453 AA.
Q812A6;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transmembrane proteinase tmprss3.
Transmembrane proteinase tmprss3.
Bus musculus (Mouse).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 A RAO N.V., Rao G.N., Hoidal J.R.; Ransmembrane Proteinasses."; Genomic Organization of Murine Transmembrane Proteinasses."; "Genomic Organization of Murine Transmembrane Proteinasses."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. REMBL; AR479687; AA033581.1; -... GO GO:0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:0016203; F:crypsin activity; IEA. GO; GO:0016204; F:scavenger receptor activity; IEA. GO; GO:0016209; F:trypsin activity; IEA. GO; GO:0016209; F:trypsin activity; IEA. GO; GO:0016209; P:trypsin activity; IEA. GO; GO:00162003; Cys Ser trypsin.
R InterPro; IPR0012172; LDL_Ecceptor_A.
R InterPro; IPR001214; Peptidasse_S1.
R InterPro; IPR001214; Peptidase_S1.
 22;
 Query Match
25.9%; Score 390; DB 4; Length 855;
Best Local Similarity 34.4%; Pred. No. 7.4e-30;
Matches 96; Conservative 48; Mismatches 113; Indels 2
 Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Butel
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
 405 IVSWGIGCAEARRPGVYARVTRLRDWILEATTKASMPLA 443
 238 IVSWGRGCALKDKPGVYTRVSHFLPWI-RSHTKEENGLA 275
 Polyserase 1B protein.
PolyseRASE.
 Homo sapiens (Human)
 NCBI_TaxID=9606;
 62
 RESULT 40
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260 YDLYHPKSWTVQVGLVSLMDSPVPSHL---VEKIIYHSKYKPKRLG--NDIALMKL---- 310
 311 ---SEPLTFDETIQPICLPNSEENFPDGKLCWTSGWGATEDGGDASP-VLNMAAVPLISN 366
 XICNHRDVYGGIISPSMLCAGYLKGGVDSCQGDSGGPLVCQBRRLWKLVGATSFGIGCAE 426
 72 IDYPKKEDYIVYLGR-SRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
 131 GRCAQP --- SRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISH 187
 188 RECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCAL 247
 71
 13 CGOKT-LRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCF
 Gaps
 SEQUENCE FROM N.A. Swiss; TISSUE=Lung; STRAIN=129/SvJ, and Swiss; TISSUE=Lung; Verghese G.M., Caughey G.H.; Werghese G.M. and characterization of mouse prostasin, a type I membrane-associated serine protease of the gamma-tryptase/prostasin
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 25;
 25.8%; Score 389.5; DB 11; Length 453; 35.6%; Pred. No. 3.7e-30; ive 43; Mismatches 102; Indels 25;
 PEAN, PRO005) LIL RECEPTARY IN TRYPE IN TARGET PRO0099; LINE IN THE PROOF PROO
 SECUENCE FROM N.A.
Kitamura K., Takefumi N., Kimio T.;
Kitamura K., Takefumi N., Kimio T.;
Kitamura K., Takefumi N., the Journal of Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BECOA3851, AAHO3851.1; -.
EMBL; AF378086; AAHO6320.1; -.
 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protease, serine, 8 (Prostasin).
 339
 248 KDKPGVYTRVSHFLPWIRSHTKEE 271
 PRT;
interPro; IPR001190; Srcr_receptor
 94; Conservative
 PRELIMINARY;
 Best Local Similarity
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SEQUENCE FROM N.A.
 gene family.
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 367
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129 KEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGK-ENSTDYLYPEQLKMTVVKLISH 187
 143 P----VTFSRYIRPİCLEAANASFPNGLHCTVİĞMĞHVAPSVSLQTERPLQQLEVPLISR 198
 69 HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 128
 188 REC------QOPHYYGSEVTTKMLCAADPQWKTDSCOGDSGGPLVCSLQGRMTLTG 237
 The FANTON N.A.

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SECURIOR FROM N.A.

STRAIN=C57BL/61.

STRAIN=C57BL/61.

SA HE RIKE=22354683; PubMed=12466851;

The FANTON Consortium,

The FANTON Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of 60.770 full-length cDNAs.";

Analysis of the mouse transcriptome based on functional annotation of 60.770 full-length cDNAs.";

Analysis of the mouse transcriptome based on functional annotation of 60.770 full-length cDNAs.";

Analysis of From Strain Strai
 븅
 13 CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTY----VCGGSLISPCWVISAT
 Gaps
 Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 Query Match
25.5%; Score 384.5; DB 11; Length 339;
Best Local Similarity 35.9%; Pred. No. 8e-30;
Matches 98; Conservative 30; Mismatches 108; Indels 37;
R EMBL; AB378085; AAL06319.1; -.
R FREL; AB038244; BAB82496.1; -.
HSSP; PO0734; 1UV2
R MGD; MGI:192340; Prs88.
RGD; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004203; F:pptidase activity; IEA.
GO; GO:0005508; P:proteclysis and peptidolysis; IEA.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1.
R PRONO125; CHYMOTRYPSIN.
R SMART; SN00020; LTYPSIN DO;
R PROSITE; PS00134; TRYPSIN DO;
R PROSITE; PS0134; TRYPSIN DO;
R PROSITE; PS0134; TRYPSIN DO;
R PROSITE; PS0134; TRYPSIN DO;
R PROSITE; PS0134; TRYPSIN DO;
R PROSITE; PS0134; TRYPSIN DO;
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 238 IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
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01-WAR-2003 (TrEMBLrel. 23,
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01-OCT-2003 (TrEMBLrel. 25,
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MEDLINE=21085660; PubMed=11217851;

Xawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fhkunishi Y., Konno M., Kandoh J., Yamanaka I.,

A Arakawa T., Hara A., Fhkunishi Y., Konno M., Kasukawa T., Yamanaka I.,

A Arakawa T., Hara A., Fhkunishi Y., Konno M., Kasukawa T., Saito R.,

A Arakawa T., Hara A., Ashburner M., Batalov S., Casavant T.,

Saito T., Okacaki Y., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 127 RSKEGRCAQPSKTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLIS 186
 127 ATP----AQFSETVSAVCLPTVDDPFPAGTLCATTGWGKTKYNALKTPDKLQQAALPIVS 182
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 11 FQCGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
 17 FGCGVPAIQPVLTGLSRIVNGEDAIPGSWPWQVSLQDR----TGFHFCGGSLISENWVVT
 67 ATHCFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI
 22; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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 Length 263;
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33.2%; Pred. No. 8.1e-30;
tive 48; Mismatches 103; Indels
RESP: POOTOGO; BAB22539.1; -...
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 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
2200008B09Rik protein (Chymotrypsinogen B precursor)
2200008B09RIK.
 247 LKDKPGVYTRVSHFLPWIR 265
 STSTPAVYARVTALMPWVQ 257
 Query Match
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 129 KEGRCAQPSKTIQTICLPSMYNDPQFGTSCEITGFGK-ENSTDYLYPEQLKMTVVKLISH 187
 188 REC------QPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTG 237
 200 ETCSCLYNINAVPEEPH----TIQQDMLCAGYVKGGKDACQGDSGGPLSCPMEGIWYLAG 255
 13 CGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTY----VCGGSLISPCWVISAT 68
 37 CG-AVIQPRI-TGGGQWQSPGQWPWQV-----SITYDGNHVCGGSLVSNKWVVSAA
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InterPro; IPR001314; Peptidase_S1A.
Pfam; PR00089; Lrypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSTTE; PS50240; TRYPSIN_DOM; 1.
PROSTTE; PS00134; TRYPSIN_HIS; 1.
PROSTTE; PS00135; TRYPSIN_HIS; 1.
SEQUENCE 340 AA; 36503 WW; 3C254059B3A8IC8A CRC64;
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Last sequence update)
Last annotation update)
 Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
 238 IVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKE 270
 256 IVSWGDACGAPNRPGVYTLTSTYASWIHHHVAE 288
 263 AA.
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 PRELIMINARY;
 01-JUN-2001 (TremBlrel.
01-JUN-2001 (TremBlrel.
01-OCT-2003 (TremBlrel.
2200008D09Rik protein.
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 NCBI TaxID=10090;
 2200008D09RIK
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REDLINE=22354683; PubMed=12466851;

The FANTAN Consortium,

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A the FAIRTM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

REP SECOLOGIA TODAS.";

RADIAGISTS of the mouse transcriptome based on functional annotation of conformal follows.";

RADIAGISTS BELONGS TO PEPTIDASE FAMILY SI.

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BY RELIA PRO00429; FISHINGS ACTIVITY; IEA.

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 67 ATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI 126
 187 HRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCA 246
 99
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ljons P., Marchibonni L., Mashima J., Mazzarelli J., Monbaetrs P., Nordone P., Ring B., Ringald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
 11 FOCGOKTLRPRF----KIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
 127 RSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLIS
 22; Gaps
 "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
 ch 25.3%; Score 382; DB 11; Length 263; 1 Similarity 33.2%; Pred. No. 1e-29; 86; Conservative 48; Mismatches 103; Indels 2:
 247 LKDKPGVYTRVSHFLPWIR 265
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STSTPAVYARVTALMPWVQ 257
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--YPGNITDTWLCASVRKEGKDSCQGDSGGPLVCN----GSLQGIISWQQDPCAVTRKPG 230
134 AQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQP 193
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STRANT-GSTBL/GJT IISSUE-Tongue;
STRANTOW CONSORTIUM.
THE FANTOW CONSORTIUM.
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573(2002).
 Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.;
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Frruno M.,
Hangaaki T., Hara A., Hayatsu N., Hiramoto K., Hiraka T., Hori P.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Saaski D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshido M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 125 VOP-LILSPHCVAA-----GTSCLISGWGTTSPPOLRLPHSLRCANVSIIEHKECEKA
 194 HYYGSEVITYMLCAADPOWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRG-CALKDKPG
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
Hippostasin prostate type (Adult male tongue cDNA, RIKEN full-length enriched library, olone:3310015108 product; protease, serine, 20, full insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched library, olone:2310040F07 product; protease, serine, 20, full insert
 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 TISSUE=Prostate;
MEDLINE=20525460; PubMed=11072088;
Mitsui S., Okul A., Kominami K., Uemura H., Yamagushi N.;
Mitsui S., Okul A., Issue-specific splicing variants of mouse
hippostasin/TLSP (PRSS20).";
Biochim. Biophys. Acta 1494:206-210(2000).
 STRAIN-C57BL/6J; TISSUE-Tongue;
RIKEN FANTOM COMSOrtium;
"Functional annotation of a full-length mouse cDNA collection."
Nature 409:685-690(2001).
 SEQUENCE FROM N.A.
TISSUDE-Prostate,
Yamaquchi N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUE=Tongue;
 231 VYTKVCKYFNWI 242
 PRELIMINARY;
 VYTRVSHFLPWI
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 253
 RESULT 47
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 78 EDYIVYLGRSRLNSNTQGEMKFEVENLILHKDY--SADTLAHHNDIALLKIRSKE--GRC 133
 65 PHYVILLGEHNLEKTDGCEQRRMATESFPHPDFNNSLPNKDHRNDIMLVKMSSPVFFTRA. 124
 487
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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NCBI_TaxID=10090;
 SEQUENCE FROM N.A.
TISSUEBRAIN W.;
Mitsui S., Yamagushi N.;
"CDNA cloning of a novel brain serine protease, Hippostasin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016226; BAA88825.1; -.
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to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
 MEDCES, SOL. 227, C. MEDCES, SOL. 227, C. MEDCES, SOL. 227, Presco.

GO. GO: OODS 56, C: extracellular; IDA.
INTERPRO; IDRO09003, CYS CST LTYPSin.
INTERPRO; IDRO01254, Peptidase S1.
INTERPRO; IDRO01254, Peptidase S1.
INTERPRO; IDRO0134, Peptidase S1.
PRIME; PRO0172, CHYMOTYPSIN.
SWART; SWOO20; TYPP SPC; I. PROSITE; PSCO20; TRYPSIN DOM; 1.
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 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
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 Yamaguchi N., Mitsui
Submitted (JUL-1998)
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TISSUE=Brain;
 Hippostasin.
 382
 72
 131
 488
 538
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 Q9QYN4
 RESULT 46
Q9QYN4
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A SIDATA R. TENDENCE TONGUE;

MEDLINE=20530913; PubMed=11076861;

A SIDATA R. TLOH M. AJEAWA K., Nagaoka S., Sasaki N., Carninci P.,

A Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,

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Pubik Matole S.T. Bahases S.I.;

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PROSITE; PSO0134; Peptidase S.I.

PROSITE; PSO0134; TRYPSIN HIS; I.

PROSITE; PSO0134; TRYPSIN HIS; I.

PROSITE; PSO0134; TRYPSIN HIS; I.

PROSITE; PSO0134; TRYPSIN HIS; I.

PROSITE; PSO0134; TRYPSIN HIS; I.

PROSITE; PSO0134; TRYPSIN SENIM; 90BDC0348ABBI78D6 CRC64; STRAIN=CS7EL/6J; TISSUE=Tongue;
MEDLINE=20499174; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1830(2000). SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Tongue;
MEDLINE=99279553; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length, CDNA cloning.";
Meth. Enzymol. 303:19-44(1999). SEQUENCE FROM N.A. SEQUENCE FROM N.A. 

Query Match
25.3%; Score 381; DB 11; Length 276;
Best Local Similarity 35.7%; Pred. No. 1.4e-29;
Matches 90; Conservative 41; Mismatches 85; Indels 36;

78 EDYIVYLGRSRLNSNTQGEMKFEVENLILHKDY--SADTLAHHNDIALLKIRSKE--GRC 133 204 --YPGNITDTWLCASVRKEGKDSCQGDSGGPLVCN----GSLQGIISWGQDPCAVTRKFG 257 152 VQP-LTLSPHCVAA-----GTSCLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKA 203 91 42 VGGETRIIKGYECRPHSQPWQVALFQXTR----LLCGATLIAPKWLLTAAHC----RK 134 AQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQP HYYGSEVITYMICAADPQWKTDSCQGDSGCPLVCSLQGRWTLTGIVSWGRG-CALKDKPG |||:| : || VYTKVCKYFNWI 269 253 VYTRVSHFLPWI 264 92 194 g g ઠ ò g  $\delta$  $\dot{\delta}$ ò

185 680 740 127 627 69 HC-FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR 128 SKEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGK--ENSTDYLYPEQLKMTVVKLI 186 SHRECQOPHYYGSEVITIMALCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGC CGQXTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYV----CGGSLISPCWVISAT SEQUENCE FROM N.A. PubMed=10903452;
MEDLINE=20363741; PubMed=10903452;
Yamada K., 7284744; PubMed=10903452;
"Isolation and characterization of three novel serine protease genes" Isolation and characterization of three novel Xenopus laevis (African clawed frog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus. 26; Query Match 25.3%; Score 381, DB 13; Length 767; Best Local Similarity 34.8%; Pred. No. 5.1e-29; Matches 92; Conservative 38; Mismatches 108; Indels 26 TEGENETION and Characterization of three moves serving the from Xenopus leavis.";

Gene 252:209-216(2000).

C -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

EMBL; ABIO38497; BAB08217.1; -.

EMBL; ABIO38497; BAB08217.1; -.

R GO; GO:0004295; F:thymotrypsin activity; IEA.

GO; GO:0004295; F:thymotrypsin activity; IEA.

GO; GO:0004295; F:thymotrypsin activity; IEA.

GO; GO:0004295; F:thymotrypsin activity; IEA.

R GO; GO:0004295; F:thymotrypsin activity; IEA.

R GO; GO:0004295; F:thymotrypsin activity; IEA.

R GO; GO:0004295; F:thymotrypsin activity; IEA.

R GO; GO:0004295; F:thymotrypsin activity; IEA.

R GO; GO:0004295; F:thymotrypsin.

R InterPro; IPR001254; Peptidase\_SIA.

R InterPro; IPR001314; Peptidase\_SIA.

R PRIMTS; PR00267; LDLas.

R PRIMTS; PR00267; LDLas.

R PRIMTS; RN00122; CHYMOTRYPSIN.

R PROSITE; PS00139; LDLas.

R PROSITE; PS00139; TRYPSIN DOM; I.

R PROSITE; PS00139; TRYPSIN DOM; I.

R PROSITE; PS00139; TRYPSIN MIS; I.

R PROSITE; PS00139; TRYPSIN SER; I.

R PROSITE; PS00139; TRYPSIN SER; I.

R PROSITE; PS00139; TRYPSIN SER; I.

R PROSITE; PS00139; TRYPSIN SER; I.

R PROSITE; PS00139; TRYPSIN SER; I. 01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Embryonic serine protease-2. 246 ALKDKPGVYTRVSHFLPWIRSHTK 269 13 Q9DGR2 RESULT 48 Q9DGR2 g g ઠ a ઠે ਨੇ g 

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4007 OT:CO.CT C7

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25 IGGEFTTIE-----NOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKK

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Search completed: May 25, 2004, 14:57:14 Job time: 48.7178 secs
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 248 KDKPGVYTRVSHFLPWI 264
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 185 NSMFCVGFLEGGKDSCQRDSGGPVVCNGQ----LQGVVSWGHGCAWRNRPGVXTKVXNXV 240
 202 TKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFL 261
 82 VYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ 141
 75 VRLGEHNIKVLEGNEQFINAAKIIRHPKYNRDTL--DNDIMLIKLSSP---AVINARVS 128
 201
 129 TISLPTA--PPAAGTECLISGWGNTLSFGADYPDELKCLDAPVIJQAECKAS--YPGKIT 184
 27 KIVGG-YTCEENSLPYQVSL-----NSGSHFCGGSLISEQWVVSAAHCY-----KTRIQ
 23 KIIGGEFTTIENQ-PWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYI
 142 TICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVT
 PRELIMINARY; PRT; 269 AA.

01-UW0.
01-WAR-2003 (TrEMBLrel. 23, Created)
01-OCT-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to chymotrypsin-like (Fragment).
Home sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.

[1]
 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hymochetical protein (Fragment).
Biomachetical (Fragment).
Bukarjota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Lasuberg R.;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
FEMBL, BC0300238; AAH30238.1; --
GO, GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R HILTERPO; IPR001254; Peptidase_SI.
R InterPro; IPR001254; Peptidase_SI.
R InterPro; IPR00134; Peptidase_SIA.
R RINTS; PR00030; Crypsin, 1.
R RRINTS; PR00122; CHYMOTRYPEIN.
SMART; SM00020; Tryp SPC; I.
R RRINTS; PS00240; TRYPSIN, DOM; 1.
R ROSITE; PS00134; TRYPSIN HIS; 1.
R RYSTTE; PS00134; TRYPSIN HIS; 1.
R HYDOLHELICAI protein; Hydrolase; Protease; Serine protease.
NOW TER.
1 1 1
SEQUENCE 251 AA; 27091 MW; 53D3993ES85AB328 CRC64;
 ch 25.2%; Score 379.5; DB 4; Length 251; l Similarity 37.7%; Pred. No. 1.7e-29; 92; Conservative 38; Mismatches 87; Indels 27
 251 AA
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 SEQUENCE FROM N.A.
 262 PWIR 265
 241 DWIK 244
 TISSUE=Prostate;
 NCBI_TaxID=9606;
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QBN2U3;
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AC 081UW
AC 081UW
DT 01-MAD
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69 HCFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 128
 129 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR 188
 189 ECOOPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWG-RGCAL 247
 24 CGIPAIKPALSFSQRIVNGENAVLGSWPWQVSL----QDSSGFHFCGGSLISQSWVTAA 79
 13 CGOKTLRPRF----KIIGGEFTTIENOPWFAAIYRHRGGSVTYVCGGSLISPCWISAT
 Gaps
 Query Match
25.1%; Score 378.5; DB 4; Length 269;
Best Local Similarity 35.0%; Pred. No. 2.4e-29;
Matches 90; Conservative 43; Mismatches 101; Indels 23;
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## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 25, 2004, 14:43:00 ; Search time 67.4882 Seconds (without alignments) 1155.508 Million cell updates/sec Run on:

US-09-880-503-5 1508 1 KPSSPPBELKFQCGQXTLRP.....VSHFLPWIRSHTKBENGLAL 276 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2002s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|            | ion         | Human LMW | Human uPA | Delta 1-4 | Bifunctio | ifunc    | Bifunctio | Bifunctio | Bifunctio | Bifunctio | Bifunctio | Bifunctio | Bifunctio | Bifunctio | Bifunctio | Bifunctio | Bifunctio |          | -        | ifunct   | Bifunctio |          | =        | neri     | ime      | M36: fibr |
|------------|-------------|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|----------|----------|-----------|----------|----------|----------|----------|-----------|
|            | Description | Aae16546  | 4         | Aar68854  | Aar66266  | Aar66245 | Aar66247  | Aar66260  | 9         | 'n        | Aar66259  |           | 525       | Aar66263  | 525       | Aar66256  | Aar66257  | Aar66251 | Aar66253 | Aar66249 | Aar66252  | 524      | Aar66250 | Aar99597 | 5        | Aar99885  |
| ٠          | 1           |           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |           |          |          |          |           |          |          |          |          |           |
|            | QI          | AAE16546  | ŝ         | AAR68854  | AAR66266  | 524      | AAR66247  | AAR66260  | AAR66264  | AAR66255  | AAR66259  | ø         | AAR66258  | AAR66263  | AAR66254  | AAR66256  | AAR66257  | AAR66251 | AAR66253 | 24       | AAR66252  | AAR66244 | AAR66250 | AAR99597 | AAR99596 | AAR99885  |
|            | BB :        | Ŋ         | ß         | N         | 7         | 7        | N         | (7        | C)        | €         | C3        | 7         | N         | ~         | ~         | ~         | ~         | ~        | ~        | ~        | 7         | ~        | ~        | ~        | N        | 7         |
|            | Length      | 7         | 2         | 9         | æ         | σ        | σ         | ω         | σı        | σı        | O)        | σ         | σ         | σ         | σı        | σ         | σ         | σ        | σ        | σ        | σ         | σ        | σ        | 393      | 6        | 393       |
| %<br>Query |             |           | 00        | 00        | 100.0     | 100.0    | 00        | 00        | 00        | 00        |           | 100.0     |           | 100.0     | 100.0     | 100.0     | 100.0     | 100.0    | 100.0    |          |           |          | 100.0    | 100.0    | 100.0    | 100.0     |
|            | Score       | 1508      | 50        | 50        | 50        | 1508     | 50        | 50        | 50        | 50        | 50        | 1508      | 50        | 1508      | 50        | 50        | 50        | 1508     | 50       | 50       | 50        | 50       | 50       | 1508     | 1508     | 20        |
| Result     | No.         | П         | α         | m         | 4         | S        | 9         | 7         | 00        | σ         | 10        | 11        | 12        | 13        | 14        | 15        | 16        | 17       | 18       | 19       | 20        | 21       | 22       | 23       | 24       | 25        |

| 626<br>626<br>626<br>626<br>626<br>626<br>63<br>63<br>63<br>63<br>63<br>63<br>63<br>63<br>63<br>63<br>63<br>63<br>63                                          | 1904 Human pri<br>1902 Human pri<br>1902 Human pri<br>1903 Human pri<br>1903 Human pri<br>2991 Pro-urok<br>9343 Human pri<br>2836 Urokinasi<br>1999 Human pri<br>1997 Prourokii<br>4797 Prourokii | 0114 Seque<br>0014 Seque<br>0074 Modifico<br>0250 Seque<br>0430 Debuo<br>1204 Pro<br>1219 Natu<br>17112 Human<br>1425 Human<br>1425 Human<br>1425 Human<br>1427 Human | 14605 Amino<br>7128 Huma<br>9228 Huma<br>9224 Huma<br>9226 Huma<br>9226 Huma<br>9226 Huma<br>6547 Lung<br>66708 Lung<br>6677 Huma<br>85854 Huma<br>85854 Huma<br>85854 Huma<br>85875 Huma |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 626<br>626<br>624<br>624<br>624<br>624<br>635<br>637<br>635<br>637<br>635<br>637<br>635<br>637<br>637<br>637<br>637<br>637<br>637<br>637<br>637<br>637<br>637 | 4 O O O B O 4 B B B O 4 F F                                                                                                                                                                       | 147922421121686                                                                                                                                                       | AA19291<br>AAB84605<br>AAU9222<br>AAU99228<br>AAU99236<br>AAU99236<br>AAU99236<br>AAU56547<br>ABU56547<br>ABU56708<br>ABU1076<br>ABU50337<br>AAB92137                                     |
| 10.10.10.10.10.10.10.10.10.10.10.10.10.1                                                                                                                      |                                                                                                                                                                                                   | 44444444                                                                                                                                                              | .4.v.v.v.v.v.v.v.v.v.v.v.v.v.v.v.v.v.v.                                                                                                                                                   |
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ALIGNMENTS

AAE16546 standard; protein; 276 AA. AAE16546;

09-APR-2002 (first entry)

Human LMW-urokinase-type plasminogen activator (uPA) protein.

Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; anglogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome; LMM-uPA. 

sapiens Ношо

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The invention relates to a composition comprising one or more domains of muckinase-type plasminogen activator (uPA). The composition is used to endothelial cell or tissue. The composition is used to endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypotension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pilmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human LMM-urokinase-type plasminogen activator (uPA) protein
 Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.
 Claim 5; Fig 1E; 117pp; English
 13-JUN-2001; 2001WO-US018976
 20-JUN-2000; 2000US-0212874P
 UYPE-) UNIV PENNSYLVANIA.
 Higazi AA;
 WPI; 2002-122240/16.
N-PSDB; AAD27079.
 WO200197752-A2
 27-DEC-2001
 Cines DB,
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Sequence 276 AA;

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120
 180
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 VVKLISHRECQOPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 9
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 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 Gaps
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100.0%; Score 1508; DB 5; Length 100.0%; Pred. No. 1.8e-125; ive 0; Mismatches 0; Indels
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 276; Conservative
 Similarity
 61
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241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
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 AAE16548 standard; protein; 323
 09-APR-2002
 AAE16548;
 RESULT 2
 AAE16548
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Human uPA deltakringle-scuPA and deltakringle-tcuPa mutant

Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke, hypotension; attoke, hypotension; attoke, hypotension; astionsis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthme; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; olletting disorder; uterine contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome; tcuPA; scuPA; two chain urokinase; single chain urokinase; mutant; mutein.

sapiens Synthetic. Homo 

WO200197752-A2.

27-DEC-2001.

13-JUN-2001; 2001WO-US018976.

20-JUN-2000; 2000US-0212874P.

(UYPE-) UNIV PENNSYLVANIA.

Cines DB, Higazi AA;

WPI; 2002-122240/16. N-PSDB; AAD27081.

composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator.

Claim 23; Fig 1G; 117pp; English

The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (upA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, andothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, suspically induced thrombotic disorders, angiogenic disorders, upulmonary fibrosis, asthma, tumour cell angiogenesis, tumour cell metastasis, glaucoma, clabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sequence is human urokinase-type plasminogen activator (upA) deltakringle chain urokinase (scuPA) and deltakringle-two chain urokinase deletion mutant

Sequence 323 AA;

```
KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHGGSVTYVCGGSLIS
 0
100.0%; Score 1508; DB 5; Length 323; 100.0%; Pred. No. 2.1e-125; ive 0; Mismatches 0; Indels 0;
 Conservative
 Best Local Similarity
Matches 276; Conserva
 Query Match
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| Db  | 48<br>7 | 48 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 107   | .07 |
|-----|---------|-----------------------------------------------------------------------|-----|
| ογ  | 61 E    | 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120   | 20  |
| Db  | 108     | 108 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNIQGEMKFEVENLILHKDYSADTLAHHND 167  | .67 |
| Š   | 121     | 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180  | 081 |
| QQ  | 168 1   | 168 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT 227  | 227 |
| λŏ  | 181     | 181 VVKILISHRECQOPHYYGSEVITYMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 240 | 240 |
| ٠ ۾ | 228     | 228 VVKG.ISHRECOOPHYYGSEVITKALCAADPOWKTDSCOGDSGGPLVCSLOGRATLIGIUS 287 | 287 |

241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276

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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivs. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to know plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 240
 210 VVKLISHRECQQPHYYGSEVITKWLCAADPQWKTDSCQGDSGGFLVCSLQGRWTLTGIVS 329
210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 269
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS

 .365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"

 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 ď
 Wnendt S, Schneider J, Heinzel-Wieland
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKBENGLAL
 Example 1; Page 11 and Fig 1; 34pp; German.
 365. .366
/label= X1
/note="peptide bond"
366. .386
/label= Y1
 Location/Qualifiers
 AAR66266 standard; protein; 386 AA
 Bifunctional urokinase variant M33
 93DE-04323754.
 93DE-04323754.
 (revised)
(first entry)
 (CHEP) GRUENENTHAL GMBH
 WPI; 1995-015191/03.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
 Disulfide-bond
Disulfide-bond
 Steffens GJ,
Saunders DJ;
 15-JUL-1993;
 15-JUL-1993;
 DE4323754-C1
 01-DEC-1994.
 25-MAR-2003
17-AUG-1995
 Synthetic.
 AAR66266;
 181
 Key
Region
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 Region
 RESULT 4
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 Amino acid residues 1-46 contain the EGF region of human urokinase. Delection of this region results in a plasminogen activator with reduced affinity for liver cell membranes; the mutant protein is not cleared from the circulation as rapidly as is wild-type tPA. The specification only gives the sequence around the deletion and not the full-length sequence of "delta 1-46 urokinase"; the sequence in AAR68854 has been obtained by amending a previously disclosed wild-type human urokinase sequence (from WO9501427) according to the description given in Example 3. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise
 KPSSPPEELKRQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 149
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 209
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT 180
 Human, des-epidermal growth factor homologous plasminogen activator; uPA;
liver membrane; reduced affinity; EGF homologous; thrombosis;
thrombolytic; increased half-life; urokinase.
 New modified plasminogen activator cpds. - having regions removed to reduce affinity for liver membranes and increase circulation half-life.
 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 /note= "amino acids 1-46 of wild-type urokinase have deleted"
 ÷
 Length 365;
 0; Indels
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.5e-125;
iive 0; Mismatches 0;
 288 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 323
 Location/Qualifiers
 (AMHP) AMERICAN HOME PROD CORP.
 standard; protein; 365
 Claim 1; Page ?; 26pp; English.
 Kalyan NK;
 88US-00150267.
 87US-00008795.
 (revised)
(first entry)
 (engineered)
 Conservative
 (revised)
 Delta 1-46 urokinase.
 WPI; 1995-043464/06.
 Query Match
Best Local Similarity
Matches 276; Conserv
 Lee SL,
 Sequence 365 AA;
 Key
Misc-difference
 Homo sapiens;
 29-JAN-1988;
 30-JAN-1987;
 US5376547-A
 27-DEC-1994
 25-MAR-2003
22-NOV-1995
 16-OCT-2003
 field)
 61
 Hung PP,
 150
 121
 AAR68854;
 AAR68854
 RESULT 3
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(revised)
(first entry)
 Wnendt S,
 WPI; 1995-015191/03
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 390 AA;
 Steffens GJ,
Saunders DJ;
 25-MAR-2003
17-AUG-1995
 Synthetic
 AAR66247;
 181
 121
 Key
Region
 RESULT 6
AAR66247
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 269
 209
 180
 270 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 329
 90 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWPAAIYRRHRGGSVTYVCGGSLIS 149
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 9
and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHGGSVTYVCGGSLIS
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 Gaps
 Location/Qualifiers
1. .365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
25. .67
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urckinase; variant; mutein.
 ,
 Length 386;
 0; Indels
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.6e-125;
ive 0; Mismatches 0;
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 urokinase variant M12.
 Ą
 RESULT 5
AAR66245
ID AAR66245 standard; protein; 390
 93DE-04323754
 151. .222
247. .316
279. .295
306. .334
366. .371
/label= X1
372. .390
/label= X1
 (revised)
(first entry)
 Query Match
Best Local Similarity 100.
Matches 276; Conservative
 (CHEF) GRUENENTHAL GMBH
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 386 AA;
 15-JUL-1993;
 DE4323754-C1
 Bifunctional
 01-DEC-1994
 25-MAR-2003
17-AUG-1995
 Synthetic
 AAR66245;
 181
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149
 120
 209
 180
 269
 240
 270 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 329
 and
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR65244-R66266 are specific examples of such deriva, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac scerebral infarct, pulmonary embolism, etc.
 90 KPSSPPEELKPQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMT
 VVKLISHRECQOPHYYGSEVTTKMLCAADPOWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPRELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 1. .365
1. .365
1/label= M4
1/note= "unglycosylated prourokinase(Ser47-Leu411)"
14. .85
25. .67
56. .80
1192. .233
 fibrinolygis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 0
 Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 276; Conservative 0; Mismatches 0; Indels 0
я
;
Heinzel-Wieland
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 276
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Example 1; Page 10 and Fig 1; 34pp; German.
 Schneider J,
 Location/Qualifiers
 Bifunctional urokinase variant M14.
 Ş
 AAR66247 standard; protein; 390
```

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1. 365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 Schneider J, Heinzel-Wieland
 Location/Qualifiers
 urokinase variant M27
 93DE-04323754
 102. .233
143. .159
151. .222
277. .295
306. .334
366. .371
/label= x1
/label= x1
 (CHEF) GRUENENTHAL GMBH
 4. .85
25. .67
56. .80
 Wnendt S,
 WPI; 1995-015191/03
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 3,5
2,5
 15-JUL-1993;
 Bifunctional
 DE4323754-C1
 15-JUL-1993;
 17-AUG-1995
 01-DEC-1994
 Synthetic.
 Steffens (
Saunders 1
 Key
Region
 Region
 Region
 149
 120
 269
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derive, which have both improved flubrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, and cerebral infarction and pulmonary deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.)
 9
 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac scerebral infarct, pulmonary embolism, etc.
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 1ALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT
 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 1 ALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHGGSVTYVCGGSLIS
 Gaps
 ;
0
 100.0%; Score 1508; DB 2; Length 390; 100.0%; Pred. No. 2.7e-125; ive 0; Mismatches 0; Indels 0
 Heinzel-Wieland
 Example 1; Page 10 and Fig 1; 34pp; German.
 Schneider J,
 93DE-04323754
 93DE-04323754
 151. .222
247. .316
279. .295
366. .334
366. .371
/label= X1
/label= X1
 Best Local Similarity 100.
Matches 276; Conservative
 (CHEF) GRUENENTHAL GMBH
 Wnendt S,
 WPI; 1995-015191/03
 Sequence 390 AA;
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Steffens GJ,
Saunders DJ;
 15-JUL-1993;
 15-JUL-1993;
 DE4323754-C1
 01-DEC-1994
 210
 181
 Query Match
 61
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IALLKIRSKBGRCAOPSKTIGTICLPSMYNDPOPGTSCEITGFGKRNSTDYLYPEGLKMT 180
 120
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such deriva: which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, eag for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAX-2003 to correct PN field.)
 improved
cardiac a
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHDD
 0
New bifunctional urokinase derivs and related plasmids - with fibrinolytic and thrombin inhibiting activities, for treating cerebral infarct, pulmonary embolism, etc.
 Length 392;
 Indels
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
tive 0; Mismatches 0;
 Example 1; Page 11 and Fig 1; 34pp; German.
 Conservative
 Similarity
 Sequence 392 AA;
 Best Local Simi
Matches 276;
 121
 Query Match
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VYKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS

270 241

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WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365

25-MAR-2003

AAR66260 AAR66260;

RESULT 7
AAR66260
ID AAR6
XX
AC AAR6
XX
DT 25-M

149 120 209 180 269 240

Gaps

o

Length 392; Indels

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270 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 329
 90 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 150 PCWVISATHCFIDYPKKBDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 181 VVKLISHRECQQPHYYGSEVTTKALCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 1 KPSSPPBBLKFQCGQKTLRPRFKIIGGBFTTIBNQPWFAAIYRRHRGGSVTYVCGGSLIS
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic, urokinase; variant; mutein.
 Query Match
100.0%; Score 1508; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 276; Conservative 0; Mismatches 0;
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Bifunctional urokinase variant M22.
 AAR66255 standard; protein; 392 AA.
 93DE-04323754
 366. .371
/label= X1
372. .392
/label= Y1
 (revised)
(first entry)
 CHEF) GRUENENTHAL GMBH
to correct PN field.)
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 392 AA;
 Disulfide-bond
 Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
 DE4323754-C1
 LS-JUL-1993;
 LS-JUL-1993;
 01-DEC-1994.
 25-MAR-2003
17-AUG-1995
 Synthetic
 AAR66255;
 Key
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 RESULT 9
 AAR66255
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 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR6244-R66266 are specific examples of such derivs. which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003)
 210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 269
 270 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS

 .365
 label= M4
 note= "unglycosylated prourokinase (Ser47-Leu411)"

 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 Schneider J, Heinzel-Wieland R;
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Example 1; Page 11 and Fig 1; 34pp; German.
 Location/Qualifiers
 Bifunctional urokinase variant M31.
 AAR66264 standard; protein; 392 AA
 93DE-04323754
 93DE-04323754
 366. 371
/label= X1
372. 392
/label= Y1
 (revised)
(first entry)
 (CHEF) GRUENENTHAL GMBH
 Wnendt S,
 WPI; 1995-015191/03.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 DE4323754-C1
 .5-JUL-1993;
 15-JUL-1993;
 Steffens GJ,
Saunders DJ;
 25-MAR-2003
17-AUG-1995
 01-DEC-1994,
 Synthetic
 AAR66264;
 241
 181
 Region
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 RESULT B
AAR66264
ID AAR6
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Disulfide-bond
Disulfide-bond
Disulfide-bond
 15-JUL-1993;
 15-JUL-1993;
 Steffens GJ,
Saunders DJ;
 DE4323754-C1
 270
 AAR66261;
 121
 181
 241
 Query Match
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 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 120
 PCWVISATHCFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHND 209
 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 270 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 329
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 210 IALLKIRSKEGRCAOPSRTIQTICLPSMYNDPOFGTSCEITGFGKENSTDYLYPEQLKMT
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 /note= "unglycosylated prourokinase(Ser47-Leu411)"
 thrombin inhibition; thrombolytic; anti-thrombotic;
 ..
 Length 392;
 Heinzel-Wieland R;
 Indels
 Query Match

100.0%; Score 1508; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 276; Conservative 0; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Example 1; Page 10 and Fig 1; 34pp; German.
Schneider J,
 Location/Qualifiers
 Bifunctional urokinase variant M26.
 AAR66259 standard, protein, 392
 1. .365
/label= M4
 urokinase; variant; mutein
 (revised)
(first entry)
 25. .67
56. .80
102. .23
143. .153
 Wnendt S,
 WPI; 1995-015191/03
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 392 AA;
 fibrinolysis;
Steffens GJ,
Saunders DJ;
 25-MAR-2003
17-AUG-1995
 Synthetic
 AAR66259;
 90
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AAR66259
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244.R66266 are specific examples of such derives. which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, eag for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.)
 VVKLISHRECQQPHYYGSEVTTYMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS
 150 PCWVISATHCFIDYPKKEDYIVYLGRSRINSNYQGEMKFEVENLILHKDYSADTLAHHND
 90 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMT
 1 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 ö
 Length 392;
 ď
 Indels
 Heinzel-Wieland
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
ive 0; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 Example 1; Page 11 and Fig 1; 34pp; German.
 cerebral infarct, pulmonary embolism, etc.
 Wnendt S, Schneider J,
 AAR66261 standard; protein; 392
 93DE-04323754.
 93DE-04323754
279. .295
306. .334
366. .371
/label= X1
372. .392
/label= Y1
 (first entry)
 Conservative
 (CHEF) GRUENENTHAL GMBH
 (revised)
 WPI; 1995-015191/03
 Best Local Similarity
Matches 276; Conserv
 Sequence 392 AA;
 25-MAR-2003
17-AUG-1995
 RESULT 11
AAR66261
ID AAR66
XX
AX
DT 25-MA
DT 17-AU
```

```
New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 Bifunctional urckinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivar, which have both improved fibrinolytic and thrombin-imhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, and cerebral infarction and pulmonary, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.)
 270 VVKLISHRECQQPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 329
VVICLISHRECOOPHYYGSEVITIMICAADPOWKIDSCOGDSGGPLVCSLOGRMILIGIVS 240
 1. .365
Alabel= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
4. .5
25. .67
56. .80
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 Wnendt S, Schneider J, Heinzel-Wieland R;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Example 1; Page 11 and Fig 1; 34pp; German.
 Location/Qualifiers
 Bifunctional urokinase variant M25.
 AAR66258 standard; protein; 392
 93DE-04323754.
 93DE-04323754
 143. .159
151. .222
279. .316
279. .395
306. .334
366. .371
/label= X1
/label= X1
 (revised)
(first entry)
 (CHEF) GRUENENTHAL GMBH
 WPI; 1995-015191/03.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
 15-JUL-1993;
 Steffens GJ,
Saunders DJ;
 15-JUL-1993;
 DE4323754-C1
 01-DEC-1994.
 25-MAR-2003
17-AUG-1995
 Disulfide-h
Disulfide-h
 Synthetic.
 AAR66258;
 181
 330
 Key
Region
 Region
 Region
 RESULT 12
 AAR66258
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 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 149
 120
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 269
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derive. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 9
 90 KPSSPPEBLKFQCGQKTLRPRFKIIGGEFTTIBNQPWFAAIYRRHRGGSVTYVCGGSLIS
 150 PCWVISATHCFIDYPKKEDYIVYLGRSRINSNIQGEMKFEVENLILHKDYSADTLAHHND
 210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKWT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND

 .365
 /label= M4
 /note= "unglycosylated prourokinase (Ser47-Leu411)"

 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 ..
0
 Length 392;
 Schneider J, Heinzel-Wieland R;
 Indels
 Query Match
100.0%; Score 1508; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 276; Conservative 0; Mismatches 0;
 Example 1; Page 11 and Fig 1; 34pp; German.
 Location/Qualifiers
Bifunctional urokinase variant M28
 93DE-04323754
 93DE-04323754
 143. .159
151. .222
247. .316
279. .336
306. .371
/label= X1
/label= X1
 (CHEF) GRUENENTHAL GMBH
 Wnendt S,
 WPI; 1995-015191/03
 Sequence 392 AA;
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 15-JUL-1993;
 .5-JUL-1993;
 Steffens GJ,
Saunders DJ;
 DE4323754-C1
 01-DEC-1994
 121
 Synthetic
 61
 Key
Region
 Region
 Region
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derives. Which have both improved fibrinollytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.)
 210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 90 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 VVKLISHRECOQPHYYGSEVTTKMLCAADPQWKTDSCOGDSGGPLVCSLQGRMTLTGIVS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 1 KPSSPPEELKFQCGQKTLRPRFXIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 Location/Qualifiers
1. 365
1. Jabel= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
4. 85
 fibrinolysis, thrombin inhibition, thrombolytic, anti-thrombotic,
 .
 Length 392;
 Indels
 Query Match 100.0%; Score 1508; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-125; Matches 276; Conservative 0; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Example 1; Page 11 and Fig 1; 34pp; German.
 Bifunctional urokinase variant M21.
 AAR66254 standard; protein; 392
 urokinase; variant; mutein.
 25. .67
56. .80
102. .233
143. .159
151. .222
247. .316
 (revised)
(first entry)
 WPI; 1995-015191/03.
 Sequence 392 AA;
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Saunders DJ;
 25-MAR-2003
17-AUG-1995
 Synthetic
 61
 150
 121
 270
 241
 330
 181
 Key.
Region
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 180
 210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT 269
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 329
 149
 209
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 9
 KPSSPPEELKFQCGQXTLRPRFXIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 thrombin inhibition; thrombolytic; anti-thrombotic;
 .
 Length 392;
 Heinzel-Wieland R;
 Indels
 Score 1508; DB 2;
Pred. No. 2.7e-125;
; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 Schneider J,
 urokinase variant M30.
 AAR66263 standard; protein; 392
 Query Match
Best Local Similarity 100.0%; P
Matches 276; Conservative 0;
 93DE-04323754
 102. .233
143. .159
151. .222
247. .295
306. .334
/label= X1
/label= X1
 urokinase; variant; mutein.
 (revised)
(first entry)
 (CHEF) GRUENENTHAL GMBH.
 Wnendt S,
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 392 AA;
 fibrinolysis;
 Bifunctional
 15-JUL-1993;
 15-JUL-1993;
 Steffens GJ,
 DE4323754-C1
 25-MAR-2003
17-AUG-1995
 01-DEC-1994
 Synthetic
 270
 Н
 61
 150
 121
 241
 AAR66263
 90
 181
 Key
Region
 Region
 Region
 RESULT 13
 AAR66263
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149

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90 KPSSPPEELKFÖGGGXTLRPRFKIIGGEFTTIENGPWFAAIYRRHRGGSVTYVCGGSLIS 149
 PCWVISATHCFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 are claimed (see features table). Sequences AAR66244.R66266 are specific examples of such derive. which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac a cerebral infarct, pulmonary embolism, etc.
 210 IALLKIRSKEGRCAQPSRTIQTICLPSWYNDPQFGTSCEITGFGKENSTDYLYPBQLKWT
 1 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 0; Gaps
 1. .365
/label= M4
/note="unglycosylated prourokinase(Ser47-Leu411)"
4. 85
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 100.0%; Score 1508; DB 2; Length 392; 100.0%; Pred. No. 2.7e-125; ive 0; Mismatches 0; Indels 0;
 Schneider J, Heinzel-Wieland R;
 Example 1; Page 10 and Fig 1; 34pp; German.
Bifunctional urokinase variant M23.
 93DE-04323754
 93DE-04323754
 25. .67
56. .80
102. .233
143. .222
151. .222
247. .316
279. .295
306. .371
/label= X1
 372. .392
/label= Y1
 (CHEF) GRUENENTHAL GMBH.
 Query Match 100.
Best Local Similarity 100.
Matches 276; Conservative
 Wnendt S,
 Sequence 392 AA;
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
 Disulfide-bond
Disulfide-bond
 DE4323754-C1
 15-JUL-1993;
 15-JUL-1993;
 Steffens GJ,
Saunders DJ;
 01-DEC-1994.
 61
 121
 Synthetic
 Key
Region
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 Region
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 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 209
 180
 181 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVGSLQGRMTLTGIVS 240
 270 VVKLISHRECQOPHYYGSEVITIKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 329
 Bifunctional uroxinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derive, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activities or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombolytic agents, and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 9
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHEND
 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 .
 Length 392;
 Query Match 100.0%; Score 1508; DB 2; Length Best Local Similarity 100.0%; Pred. No. 2.7e-125; Matches 276; Conservative 0; Mismatches 0; Indels
 Heinzel-Wieland
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 Example 1; Page 10 and Fig 1; 34pp; German.
 Schneider J,
 Ź
 AAR66256 standard; protein; 392
 93DE-04323754
 93DE-04323754
279. .295
306. .334
366. .371
/label= X1
372. .392
/label= Y1
 (revised)
(first entry)
 (CHEF) GRUENENTHAL GMBH
 Wnendt S,
 WPI; 1995-015191/03.
 Sequence 392 AA;
Disulfide-bond
Disulfide-bond
Region
 Steffens GJ,
Saunders DJ;
 25-MAR-2003
17-AUG-1995
 15-JUL-1993;
 DE4323754-C1
 15-JUL-1993;
 01-DEC-1994.
 AAR66256;
 61
 121
 Query Match
Best Local S
 9
 Region
 AAR66256
ID AAR66256
XX
AC AAR66
XX
DT 25-MA
DT 17-AU
 EFFFFXVXUXFXXXXIIXXXXXFFFXXXXXOOOOOO
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PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 IALLKIRSKEGRCAOPSRTIQTICLPSMYNDPOFGTSCEITGFGKENSTDYLYPFQLKMT 180
 90 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 149
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 240
 150 PCWVISATHČFIDYPKKEDYIVYLGRSRLNSNTOGEMKFEVENLILHKDYSADTLAHHND
 1 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 /note= "unglycosylated prourokinase(Ser47-Leu411)"
45 . 85
25 . 67
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urckinase; variant; mutein.
 ò.
 Length 392;
 Wnendt S, Schneider J, Heinzel-Wieland R;
 Indels
 WGRGCALKDKRGVYTRVSHFLPWIRSHTKENGLAL 365
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
tive 0; Mismatches 0;
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Location/Qualifiers
 Bifunctional urokinase variant M18.
 Ą
 AAR66251 standard; protein; 393
 93DE-04323754
 366. .372
/label= X1
373. .393
/label= Y1
 l. .365
/label= M4
 (revised)
(first entry)
 (CHEF) GRUENENTHAL GMBH.
 Query Match
Best Local Similarity 100.
Matches 276; Conservative
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Sequence 392 AA;
 15-JUL-1993;
 Steffens GJ,
Saunders DJ;
 15-JUL-1993;
 DE4323754-C1
 25-MAR-2003
17-AUG-1995
 01-DEC-1994.
 Synthetic.
 AAR66251;
 210
 330
 61
 121
 181
 Key
Region
 Region
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 RESULT 17
 AAR6625
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 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, and creatment of arterial occlusions, deep vein thrombolysic agents, and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.)
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 329
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 굓.
 Wnendt S, Schneider J, Heinzel-Wieland
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Example 1; Page 11 and Fig 1; 34pp; German.
 urokinase variant M24.
 AAR66257 standard; protein; 392 AA
 93DE-04323754
 151. .222
247. .316
279. .295
306. .334
71abel= X1
372. .392
/label= X1
 (revised)
(first entry)
 CHEF) GRUENENTHAL GMBH.
 WPI; 1995-015191/03.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Steffens GJ,
Saunders DJ;
 DE4323754-C1.
 15-JUL-1993;
 Bifunctional
 15-JUL-1993;
 01-DEC-1994.
 25-MAR-2003
17-AUG-1995
 Synthetic
 AAR66257;
 330
 270
 241
 181
 Key
Region
 Region
 Region
 RESULT 16
 AAR66257
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90 KPSSPPBBLKPQCGQKTLRPRFKIIGGBFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 149
 PCWVISATHOFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 IALLKIRSKEGRCAQPSRTIQTICLPSWYNDPQFGTSCEITGFGKENSTDYLYPBQLKWT 180
 210 IALLKIRSKEGRCAQPSRIQTICLPSMYNDPQFGISCEIIGFGKENSIDYLYFBQLKMT 269
 VVKLISHRECQQPHYYGSEVTTKALCAADPQWKTDSCQGDSGGPLVCSLQGRATLTGIVS 240
 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derivs. which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 150 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHND
 1 KPSSPPERLKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 Heinzel-Wieland R;
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
ive 0; Mismatches 0;
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKBENGLAL 276
 330 wGRGCALKDKPGVYTRVSHPLPWIRSHTKEENGLAL 365
 Example 1; Page 10 and Fig 1; 34pp; German.
 Schneider J,
 Bifunctional urokinase variant M16.
 AAR66249 standard; protein; 393 AA
 93DE-04323754
 93DE-04323754
 (revised)
(first entry)
306. .334
366. .372
/label= X1
373. .393
/label= Y1
 Query Match 100.
Best Local Similarity 100.
Matches 276; Conservative
 (CHEF) GRUENENTHAL GMBH.
 Wnendt S,
 to correct PN field.
 WPI; 1995-015191/03.
 Sequence 393 AA;
 Disulfide-bond
 25-MAR-2003
17-AUG-1995
 15-JUL-1993;
 Steffens GJ,
Saunders DJ;
 DE4323754-C1
 15-JUL-1993;
 01-DEC-1994.
 AAR66249;
 61
 121
 181
 270
 Region
 Region
 RESULT 19
 AAR66249
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 149
 120
 209
 180
 269
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 VVKLISHRECQQPHYYGSEVITIKALCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 329
 plasmids - with improved
is, for treating cardiac and
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such derives which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, eag for treatment of arterial occlusions, deep vain thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM field.)
 9
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMT
 210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGSVTYVCGGSLIS
 90 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 Gaps
 . .365
|label= M4
|note= "unglycosylated prourokinase(Ser47-Leu411)"
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 ..
 Length 393;
 Indels
 Query Match 100.0%; Score 1508; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-125; Matches 276; Conservative 0; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 New bifunctional urokinase derivs and related pla fibrinolytic and thrombin inhibiting activities, cerebral infarct, pulmonary embolism, etc.
 Example 1; Page 10 and Fig 1; 34pp; German.
 Location/Qualifiers
 Bifunctional urokinase variant M20
 AAR66253 standard; protein; 393
 urokinase; variant; mutein.
 (revised)
(first entry)
 .85
 WPI; 1995-015191/03
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 393 AA;
 25-MAR-2003
17-AUG-1995
 Synthetic
 AAR66253;
 121
 270
 241
 61
 150
 181
 330
 Key
Region
 RESULT 16
AAR66253
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0, Gaps

Length 393; Indels

```
Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66256 are specific examples of such derive. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, and cerebral infarction and pulmonary deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-WAR-2003 to correct PM field.)
 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac ecerebral infarct, pulmonary embolism, etc.
 /note= "unglycosylated prourokinase(Ser47-Leu411)"
4. .85
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
Saunders DJ;
 Example 1; Page 10 and Fig 1; 34pp; German
 cocation/Qualifiers
 93DE-04323754.
 93DE-04323754
 102. .233
143. .159
151. .222
279. .295
306. .334
306. .334
373. .393
/label= X1
 (CHEF) GRUENENTHAL GMBH
 1. .365
/label= 1
 25. .67
56. .80
 WPI; 1995-015191/03.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 15-JUL-1993;
 15-JUL-1993;
 DE4323754-C1
 01-DEC-1994.
 Synthetic
 Region
 Region
 Region
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ö PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFBVENLILHKDYSADTLAHHND 209 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180 9 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 1 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 0; Gaps 100.0%; Score 1508; DB 2; Length 393; 100.0%; Pred. No. 2.7e-125; ive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 276; Conservative 06 150 121 61 Query Match g ð g ò ð

Sequence 393 AA;

New bifunctional urckinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc. /note= "unglycosylated prourokinase(Ser47-Leu411)" 4 .85 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein. 'n. Heinzel-Wieland WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL Schneider J, Location/Qualifiers Bifunctional urokinase variant M19. Ā AAR66252 standard; protein; 393 93DE-04323754. 93DE-04323754 102. .233 143. .159 1151. .222 247. .295 279. .295 306. .334 /label= X1 /label= X1 /label= X1 . .365 /label= M4 (revised)
(first entry) Steffens GJ, Wnendt S, Saunders DJ; (CHEF ) GRUBNENTHAL GMBH WPI; 1995-015191/03. Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond DE4323754-C1 15-JUL-1993; 15-JUL-1993; 01-DEC-1994. 25-MAR-2003 17-AUG-1995 Synthetic 330 AAR66252; 270 Key Region Region Region RESULT 20 AAR66252 à g

Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R6626 are specific examples of such derives. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, eag for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.) Example 1; Page 10 and Fig 1; 34pp; German.

Sequence 393 AA;

VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240

210 181

g

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209 VVYCLISHRECOOPHYYGSEVTTYMLCAADPOWKTDSCOGDSGGPLVCSLOGRWTLTGIVS 240 9 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 210 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMT 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND Gaps Location/Qualifiers 1. .365 /label M4 /note= "unglycosylated prourokinase(Ser47-Leu411)" fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein. .; 0 Heinzel-Wieland R; 0; Indels Query Match 100.0%; Score 1508; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-125; Matches 276; Conservative 0; Mismatches 0; 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276 Wnendt S, Schneider J, Bifunctional urokinase variant M11. AAR66244 standard; protein; 393 93DE-04323754 (revised)
(first entry) 143. .159 151. .222 247. .316 279. .295 306. .334 366. .34 71abel= X1 375. .393 Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond Disulfide-bond DE4323754-C1 15-JUL-1993; 15-JUL-1993; 33 25-MAR-2003 22-AUG-1995 Steffens ( Saunders 1 Synthetic. AAR66244; 90 61 150 121 181 241 Key Region Region Region RESULT 21 AAR66244 B 원 ò d ò g ò 8

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120
 149
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266 are specific examples of such deriver, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-WAR-2003 to correct PM field.)
 90 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 150 PCMVISATHCFIDYPXKEDYIVYLGRSRENSNTQGEMKFEVENLILHKDYSADTLAHND
 181 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 210 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 ...
 100.0%; Score 1500; DB 2; Length 3 100.0%; Pred. No. 2.7e-125; ive 0; Mismatches 0; Indels
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEBNGLAL 365
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Example 1; Page 10 and Fig 1; 34pp; German.
 Location/Qualifiers
 Bifunctional urokinase variant M17.
 AAR66250 standard, protein, 393 AA
 urokinase; variant; mutein.
 (revised)
(first entry)
 Query Match 100.
Best Local Similarity 100.
Matches 276; Conservative
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 393 AA;
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
 25-MAR-2003
17-AUG-1995
 Synthetic
 AAR66250;
 241
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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.

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Chimeric protein contg. plasminogen activating sequence and thrombin-
inhibiting sequence - useful as thrombus-specific thrombolytic agent with
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 330
 Example 1 describes the prodn. of plasmids pSE1 and pSE9 contg. a DNA encoding a chimeric procein with fibrinolytic and thrombin-inhibiting properties. pSE1 encodes the protein given in AAR99597 and pSE9 encodes the protein given in AAR99596
 91 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPXKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 VVKLISHRECQOPHYYGSEVTTKMLCAADPOWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 protein;
 Length 393;
 Thrombin; inhibition; thrombus; thrombolysis; chimeric proiplasminogen activating sequence; fibrinolysis; infarction; angina pectoris; deep vein thrombosis.
 fibrinolysis; infarction;
 Indels
 Heinzel-Wieland
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
iive 0; Mismatches 0;
 276
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKERNGLAL 366
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 plasminogen activating sequence; fibr. angina pectoris; deep vein thrombosis
 Chimeric protein M37 encoded by pSE9.
 ĸ
 Example 1; Page 21-22; 37pp; German.
 Ź
 Janocha
 100.08; Pr.
 393
 94DE-04442665
 standard; protein;
 (first entry)
 Conservative
 (CHEF) GRUENENTHAL GMBH
 Steffens GJ,
 WPI; 1996-269715/28
 Similarity
 Sequence 393 AA;
 rapid action.
 Query Match
Best Local Simil
Matches 276;
 30-NOV-1994;
 05-DEC-1996
 EP714982-A2
 05-JUN-1996
 ຜ
 Synthetic
 151
 121
 181
 271
 241
 AAR99596
 AAR99596;
 61
 211
 Wnendt
 RESULT 24
 AAR99596
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 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 149
 120
 209
 180
 269
 240
 VVKLISHRECQQPHYYGSEVTTKMLCAADDQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 329
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR65244-R6656 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activities or thrombin inhibitors. The proteins are useful as thrombolytic agents, eag for treatment of artexial occlusions, deep vain thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 9
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQPGTSCEITGFGKENSTDYLYPEQLKMT
 210 IALIKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 Gaps
 Thrombin; inhibition; thrombus; thrombolysis; chimeric protein;
 0,
 Length 393;
 Indels
 Heinzel-Wieland
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
ive 0; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKDKFGVYTRVSHFLPWIRSHTKEENGLAL
 Example 1; Page 10 and Fig 1; 34pp; German.
 Schneider J,
 Chimeric protein M38 encoded by pSE1.
 Ā
 standard; protein; 393
 93DE-04323754,
 93DE-04323754
366. .372
/label= X1
373. .393
/label= Y1
 Query Match
Best Local Similarity 100.
Matches 276; Conservative
 (CHEF) GRUENENTHAL GMBH
 ώ,
 WPI; 1995-015191/03
 Sequence 393 AA;
 Steffens GJ,
Saunders DJ;
 15-JUL-1993;
 15-JUL-1993;
 05-DEC-1996
 DE4323754-C1
 01-DEC-1994
 241
 90
 61
 150
 181
 270
 330
 AAR99597
 AAR99597
 Region
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 AAR9959
 RESULT
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240

**%%EXEXEX** 

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Dissminogen-activating amino acid sequence (A) fused at the N- and/or c terminus to a thrombin and/or factor Xa inhibiting amino acid sequence (B) these at the N- and/or c terminus to a thrombin and/or factor Xa inhibiting amino acid sequence (B). Excluded from the claims are (I) where (A) is Ser47 to Leu4II of unglycosylated urokinase linked at the C-terminus to sequences (i) to complycosylated urokinase linked at the C-terminus to sequences (i) to TI-RPSSEFEEFEIDEEK (iii) Where TI= P or V; TZ = L or a bond; T3 = Q or T1 opt. (A) is pref. (pro)urokinase; tissue plasminogen activator (tPA), bat-DA (A) is pref. (pro)urokinase; and/or APSAC (anisolated plasminogen streptokinase activator complex), sep. prourokinase (411 amino acids) or streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen streptokinase) or his sergence or is derived from the human thrombin receptor, antistatin and/or the tick anticoagulant peptide, Most pref. are the 65 amino acid hirudin sequence or one of the six sequences given in AAR99989; to AAR99888, and products were tested in human citrated plasma (5 microg in 200 microl 1:10 diluted plasma). The thrombin time was then 1.2 3, and 1.2 times greater, repectively, than in the absence of the
 IALLKIRSKEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 271 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 330
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 151 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 91 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Proteins with fibrinolytic and anticoagulant activity - useful as
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
ive 0; Mismatches 0;
 331 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Steffens GJ;
 Ą
 Disclosure; Fig 18; 59pp; German.
 AAR66265 standard; protein; 395
 Heinzel-Wieland R,
95EP-00117316
 94DE-04440892
 (revised)
(first entry)
 Query Match 100.
Best Local Similarity 100.
Matches 276; Conservative
 (CHEF) GRUENENTHAL GMBH
 thrombolytic agents.
 WPI; 1996-240720/25
 Sequence 393 AA;
 17-NOV-1994;
 03-NOV-1995;
 25-MAR-2003
17-AUG-1995
 Wnendt S,
 AAR66265;
 61
 181
 241
 121
 RESULT 26
 AAR66265
ID AAR6
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AC AAR6
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 150
 120
 180
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 330
 Chimeric protein contg. plasminogen activating sequence and thrombin-
inhibiting sequence - useful as thrombus-specific thrombolytic agent with
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 240
 thrombolytic; plasminogen; urokinase;
 9
 Example 1 describes the prodn. of plasmids pSE1 and pSE9 contg. a DNA encoding a chimeric protein with fibrinolytic and thrombin-inhibiting properties. pSE1 encodes the protein given in AAR99597 and pSE9 encodes the protein given in AAR99596
 91 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGBMKFEVENLILHKDYSADTLAHHND
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGBMKFBVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 Thrombin, factor Xa, anticoagulant, thrombolytic; plasminogen; u activator; streptokinase; staphylokinase; APSAC; anisolated plasminogen streptokinase activator complex; hirudin; hirullin; antistatin; pWLT27; pWS1; pSE8; pHWS6.
 ö
 Length 393;
 M36: fibrinolytic and anticoagulant activity contg. protein.
 Indels
 Heinzel-Wieland R;
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
cive 0; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 366
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Example 1; Page 19-20; 37pp; German.
 Janocha E,
 AAR99885 standard; peptide; 393 AA
 95EP-00118050
 94DE-04442665
 (first entry)
 Query Match
Best Local Similarity 100.
 (CHEF) GRUENENTHAL GMBH
 Steffens GJ,
 WPI; 1996-269715/28
 Sequence 393 AA;
 rapid action.
 16-NOV-1995;
 10-NOV-1994;
 27-JAN-1997
 EP712934-A2
 22-MAY-1996
 05-JUN-1996
 EP714982-A2
 Synthetic
 Wnendt S,
 271
 61
 151
 121
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 331
 AAR99885,
 AAR99885
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120 210

366

Gaps

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Length 393; Indels

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New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R6626; are specific examples of such derivs. Which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PM file1d.)
 270 VVXLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 329
181 VVKLISHRECQOPHYYGSEVTTKMLCAADPOWKTDSCOGDSGGPLVCSLQGRMTLTGIVS
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 note= "unglycosylated prourokinase (Ser47-Leu411)
 -G##
 Wnendt S, Schneider J, Heinzel-Wieland R;
 276
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 Example 1; Page 11 and Fig 1; 34pp; German.
 Location/Qualifiers
 urokinase variant M29.
 Ą
 AAR66262 standard; protein; 395
 93DE-04323754.
 93DE-04323754
 366. .371
/label= X1
372. .395
/label= Y1
 1. .365
/label= M4
 (revised)
(first entry)
 (CHEF) GRUENENTHAL GMBH
 89
 WPI; 1995-015191/03.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
 Steffens GJ,
Saunders DJ;
 15-JUL-1993;
 Bifunctional
 DE4323754-C1
 15-JUL-1993;
 25-MAR-2003
17-AUG-1995
 01-DEC-1994.
 Synthetic.
 AAR66262;
 241
 Key
Region
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 AAR66262
 RESULT
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 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.
 90 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS 149
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 IALLKIRSKEGRCAOPSRIIOTICLPSMYNDPOFGISCEITGFGKENSTDYLYPEOLKMT 269
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences ARR6544-R66266 are specific examples of such derive, which have both improved fibrinolyric and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolyric agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 150 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 note= "unglycosylated prourokinase (Ser47-Leu411)"
 thrombin inhibition; thrombolytic; anti-thrombotic;
 ;
0
 Length 395;
 Heinzel-Wieland R;
 Indels
 0
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
ive 0; Mismatches 0;
 Example 1; Page 11 and Fig 1; 34pp; German.
 Wnendt S, Schneider J,
 location/Qualifiers
 Bifunctional urokinase variant M32
 93DE-04323754.
 93DE-04323754.
 372. .395
/label= Y1
 1. .365
/label= M4
 fibrinolysis; thrombin ınnı
urokinase; variant; mutein
 366. .371
/label= X1
 Ouery Match
Best Local Similarity 100.
Matches 276; Conservative
 (CHEF) GRUENENTHAL GMBH.
 to correct PN field.
 WPI; 1995-015191/03.
 Sequence 395 AA;
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Steffens GJ,
Saunders DJ;
 DE4323754-C1
 15-JUL-1993;
 15-JUL-1993;
 01-DEC-1994.
 Disulfide-}
Disulfide-}
 121
 Synthetic.
 210
 61
 Key
Region
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150 PCWVISATHCFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHND 209
 210 IALLKIRSKBGRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMT 269
 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 270 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGFLVCSLQGRMTLTGIVS 329
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R6626 are specific examples of such derives which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 improved
cardiac a
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 90 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps

 .365
 /label= M4
 /note= "unglycosylated prourokinase(Ser47-Leu411)"
 .85
 .67
 .80
 .80

 fibrinolysis; thrombín inhibition; thrombolytic; anti-thrombotic;
urokinase; variant; mutein.
 ö
 New bifunctional urokinase derivs and related plasmids - with fibrinolytic and thrombin inhibiting activities, for treating cerebral infarct, pulmonary embolism, etc.
 Length 396;
 Indels
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.7e-125;
ive 0; Mismatches 0;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKOKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 Example 1; Page 10 and Fig 1; 34pp; German
 Location/Qualifiers
 Ą
 Bifunctional urokinase variant M15
 AAR66248 standard; protein; 397
 (revised)
(first entry)
 Conservative
 WPI; 1995-015191/03.
 Query Match
Best Local Similarity
Matches 276; Conserv
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 396 AA
 25-MAR-2003
17-AUG-1995
Saunders DJ;
 Synthetic.
 61
 181
 241
 AAR66248;
 Key
Region
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 269
 KPSSPPBELKFOCGOKTLRPRFKIIGGEFTTIENOPWPAAIYRRHRGGSVTYVCGGSLIS 149
 120
 209
 IALLKIRSKEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 240
 270 VVKLISHRECQQPHYYGSEVTTKALCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 329
 9
 PCW1SATHCF1DYPKKEDY1VYLGRSRLNSNTQGEMKFEVENL1LHKDYSADTLAHND
 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 Gaps
 Location/Qualifiers
1. .365
/label= M4
/note= "unglycosylated prourokinase(Ser47-Leu411)"
 fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic; urokinase; variant; mutein.
 .
0
 Length 395;
 Indels
 Schneider J, Heinzel-Wieland
 Match 100.0%; Score 1508; DB 2; Local Similarity 100.0%; Pred. No. 2.7e-125; es 276; Conservative 0; Mismatches 0;
 330 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 365
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Ą
 Bifunctional urokinase variant M13
 AAR66246 standard; protein; 396
 93DE-04323754.
 366. .377
/label= X1
 378. .396
/label≈ Y1
 (revised)
(first entry)
 CHEF) GRUENENTHAL GMBH
 Wnendt S,
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 395 AA;
 Steffens GJ,
 15-JUL-1993;
 DE4323754-C1
 25-MAR-2003
17-AUG-1995
 01-DEC-1994
 Synthetic
 AAR66246;
 90
 61
 150
 121
 210
 181
 241
 Query Match
 Key
Region
 Region
 Region
 Best Loca
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 AAR66246
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Dymogen AAP50871 is the inactive precursor form of human urokinase. Urokinase zymogen is cleaved into the two-chain form composed of characteristic urokinase H (molecular wt.of 30,000) and L (molecular wt.of 20,000) chains when treated with catalytic amounts of plasmin. The patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a single chain molecular structure, and selective affinity for fibrin. It is a thrombolytic agent which manifests its plasminogen activator activity on cleavage by proteolytic enzymes (e.g. plasmin) and has higher affinity for fibrin than known forms of urokinase
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 102. 126
148. 279
158. 159
/note= "potential cleavage site which generates the two-chain form from the zymogen"
189. 205
197. 268
293. 362
325. 331
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGBFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Thrombolytic agent; plasminogen activator activity; fibrin affinity;
 ò
 Query Match
Best Local Similarity 100.0%; Score 1508; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.8e-125;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
 New urokinase zymogen - useful as thrombolytic agent
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Location/Qualifiers
 Disclosure, Page 12; 30pp; English.
Patent Application No.37119/84)
 Kasai S, Arimura H, Mori K,
 84EP-00306117.
 83JP-00170354
83JP-00195051
 (GREC) GREEN CROSS CORP
 WPI; 1985-106530/18
 Sequence 411 AA;
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Cleavage-site
 Homo sapiens.
 07-SEP-1984;
 13-SEP-1983;
17-OCT-1983;
 02-MAY-1985.
 19
 196
 121
 181
 241
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 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 269
 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 VVKLISHRECQQPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 329
 Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR62244-R66266 are specific examples of such derives, which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, eg. for treatment of arterial occlusions, deep vein thrombolytic agents, and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
 Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese
 New bifunctional urokinase derivs and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac serebral infarct, pulmonary embolism, etc.
 90 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 0;
 100.0%; Score 1508; DB 2; Length 397; larity 100.0%; Pred. No. 2.7e-125; Conservative 0; Mismatches 0; Indels 0;
 Heinzel-Wieland
 Example 1; Page 10 and Fig 1; 34pp; German.
 Schneider J,
 standard; protein; 411
 93DE-04323754
 93DE-04323754
 (first entry)
 279. .295
306. .334
366. .378
/label= X1
379. .397
/label= Y1
 CHEF) GRUENENTHAL GMBH
 Wnendt S,
 WPI; 1995-015191/03
 Best Local Similarity
Matches 276; Conserv
 Sequence 397 AA;
 Disulfide-bond
Disulfide-bond
 30-NOV-1991
 15-JUL-1993;
 15-JUL-1993;
 Steffens GJ,
Saunders DJ;
 DE4323754-C1
 01-DEC-1994
 241
 Query Match
 61
 150
 121
 181
 AAP50871
 AAP50871
 Region
 Region
 AAP50871
ID AAP
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AC AAP
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DT 30-
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 180
 therapy.
 156 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 315
 VVKLISHRECOOPHYYGSEVTTKMLCAADPQWKTDSCOGDSGGPLVCSLQGRMTLTGIVS 240
 316 VVILLISHRECQQPHYYGSEVITIONLOADPQWKTDSCQGDSGGBLVCSLQGRWTLTGIVS 375
 New N-shortened pro:urokinase peptide cpds. with thrombolytic activity and longer in vivo half life, opt. with replacement of arginine-156.
 1 KPSSPPEELKFOCGOKTURPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 136 KPSSPPEELKFÖCGÖKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPBQLKMT
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKWT
 Sequence encoded by entire prourokinase (PKU) gene from PKU-producing tumour cell line ATCC CCL138 clone pUC20.
 New N-shortened pro:urokinase peptide cpds. were prepd. from pUC20. new peptides are useful for treating venous and arterial occlusive diseases. (Updated on 03-OCT-2002 to add missing OS field.)
 Thrombosis; fibrinolytic agent; venous disease; arterial disease
 Length 411;
 Schwarz M;
 Indels
 Query Match
100.0%; Score 1508; DB 1;
Best Local Similarity 100.0%; Pred. No. 2.8e-125;
Matches 276; Conservative 0; Mismatches 0;
 Doerper T,
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
 Example, Fig 2, p 705-8; 21pp; German.
 Baldinger V,
 AAP96146 standard; protein; 411 AA
 88EP-00117186.
 87DE-03735917
 (revised)
(first entry)
 Koerwer W, Kurfurst M,
 WPI; 1989-123847/17.
N-PSDB; AAN91617.
 Sequence 411 AA;
 (BADI) BASF AG.
 15-OCT-1988;
 23-OCT-1987;
 03-OCT-2002
21-JAN-1991
 Unidentified
 26-APR-1989.
 EP312941-A.
 241
 AAP96146;
 196
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 New plasminogen activator variants with additional glycosylation - having increased circulating half life in plasma, used for treating cardiovascular disorders.
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 The new plasminogen activator (PA) variants of the invention are derived from human urokinase, prourokinase or esp. tissue PA (tPA). They are useful for treating cardiovascular discorders such as myocardial infarct or thrombosis. Typical doses are 0.3 mg/kg for infarct and 0.1-0.2 mg/kg for thrombosis. (Updated on 25-MAR-2003 to correct PF field.)
 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 ö
 100.0%; Score 1508; DB 1; Length 411; 100.0%; Pred. No. 2.8e-125; ive 0; Mismatches 0; Indels 0
 Plasminogen activator; urokinase; thrombosis therapy; cardiovascular disorder; myocardial infarct.
 411
 376 WGRGCALXDXPGVYTRVSHPLPWIRSHTKEENGLAL
 label= glycosylation site
 Ą
 Disclosure, Fig 3; 60pp; English.
 AAP91684 standard; protein; 411
 89WO-US001947.
 88US-00196909
 (first entry)
 276; Conservative
 (GETH) GENENTECH INC.
 (revised)
 urokinase.
 Keyt B;
 WPI; 1989-370725/50.
 Query Match
Best Local Similarity
Matches 276; Conserv
 Sequence 411 AA;
 Key
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Modified-bond
 Disulfide-bond
Disulfide-bond
 04-MAY-1989;
 Homo sapiens.
 20-MAY-1988;
 Anderson S,
 30-NOV-1989.
 WO8911531-A.
 25-MAR-2003
13-MAR-1992
 Sequence of
 AAP91684;
 RESULT 31
 PAP91684
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VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 375
256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 315
 precursor-lipid composite - used as thrombolytic agent, having half-life in the blood, enhanced bio:availability and improved
 By forming a precursor-lipid composite, the half-life of this thrombolytic agent in the blood may be increaced, exhibiting improved activity without ahoramal acceleration of fibrinolytic activity. Composit useful as a thrombolytic agent in treatment of cerebral thrombosis, myocardial infarction etc.
 VVKLISHRECQQPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 VVICLISHRECQQPHYYGSEVTTIVMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 0; Gaps
 precursor; fibrinolysis; thrombolytic; cerebral thrombosis;
 Length 411;
 Indels
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.8e-125;
ive 0; Mismatches 0;
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
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 Tamanouchi
 AAR06244 standard; protein; 411
 Claim 3; Fig 1; 11pp; English.
 90EP-00300772
 89JP-00121405
 Urokinase precursor protein.
 (first entry)
 Best Local Similarity 100.
Matches 276; Conservative
 myocardial infarction.
 (GREC) GREEN CROSS
 Matsuda H, Ueda Y,
 WPI; 1990-233117/31
 Sequence 411 AA;
 Homo sapiens
 25-JAN-1990;
 27-JAN-1989;
17-MAY-1989;
 07-DEC-1990
 01-AUG-1990
 EP380334-A.
 Urokinase prolonged pactivity.
 Urokinase
 AAR06244;
 136
 61
 121
 181
 316
 Query Match
 181
 376
 RESULT 34
 AAR06244
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 195
 120
 196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 255
 LALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEIIGFGKENSTDYLYFEQLKMT 180
 240
 316 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCOGDSGGPLVCSLOGRMTLTGIVS 375
 60
 It was extracted from human renal cells and purified using a monoclonal antibody for single-chain prourckinase (scPU) recovered from hybridoma cells created from the fusion of mouse myelmen cells with mouse BALB/c spleen cells which had been preliminarily immunised with scPU. The purified product has a molecular weight of $4,000 in $SDS/polyacrylamide gel electrophoresis. The combined use of scPU and plasminogen at a specific ratio can enhance fibriolytic activity of scPU without causing any systemic fibrinosysis. This enables lowering the dose of scPU which thrombosis and obstructive diseases
 Single-chain prourokinase; fibrinolytic activity enhancer; plasminogen;
 Amino acid sequence of single-chain pro-urokinase extracted from human
 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVI SATHCFI DY PKKEDY I VYLGRSRLNSNTQGEMKFEVENLI LHKDYSADTLAHND
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Fibrinolytic activity enhancer - comprising plasminogen for enhancing activity of single-chain pro-urokinase without causing systemic
 ö
 Length 411;
 Indels
 100.0%; Score 1508; DB 1;
100.0%; Pred. No. 2.8e-125;
live 0; Mismatches 0;
 276
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Disclosure; Page 7; 8pp; English
 AAP93589 standard; protein; 411
 Υ.
 88EP-00116067
 87JP-00248937
 Iga
 (first entry)
 Similarity 100.
 (GREC) GREEN CROSS CORP.
 Tanaka K,
 WPI; 1989-101389/14.
 Sequence 411 AA;
 activity of s.
fibrinolysis.
 Query Match
Best Local Simi
Matches 276;
 Homo sapiens
 29-SEP-1988;
)1-OCT-1987;
 cells.
 19-JUN-1990
 05-APR-1989
 rsukada M,
 thrombosis.
 EP310065-A.
 121
 241
 61
 376
 AAP93589;
 181
 Best Loca
Matches
 renal
 AAP93589
 RESULT
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180 315 240

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120 255

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VVKLISHRECOOPHYYGSEVITKMLCAADPOWKTDSCOGDSGGPLVCSLOGRWTLTGIVS 240
 Modified pro-urokinase has a longer half-life in blood, and disolves thrombin without causing the spontaneous bleeding associated with urokinase. The modification puts an epidermal growth factor domain into the protein, containing the sequence Abn-X-Ser or Abn-X-Thr where X is any residue. Plasmid pHR22 is disclosed as containing the modified
 Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 ï
 Kawabe
 Length 411;
 10. .42
/label= Epidermal growth factor (EGF) domain
 Morita M,
 Score 1508; DB 2;
Pred. No. 2.8e-125;
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKBENGLAL 411
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKBENGLAL 276
 Hirose M,
 20. .31
/label= Second loop
22. .24
/label= Modified site
33. .42
/label= Third loop
 Location/Qualifiers
 10. .19
/label= First loop
 Ą
 Thrombin; fibrin; bleeding; pHR22.
 Disclosure; Fig 1; 27pp; English.
 Amatsuji Y, Kasai S,
 AAR07902 standard; protein; 411
 100.0%;
100.0%;
 89JP-00126434.
 Human pro-urokinase variant
 (first entry)
 (GREC) GREEN CROSS CORP
 WPI; 1990-350147/47.
N-PSDB; AAQ06133.
 Query Match
Best Local Similarity
 Sequence 411 AA;
 18-MAY-1990;
 18-MAY-1989;
 Homo sapiens
 21-FEB-1991
 22-NOV-1990
 Active-site
 Tanabe T,
Arimura H;
 EP398362-A.
 241
 121
 181
 316
 376
 AAR07902
 sednence
 Key
Domain
 Region
 Region
 Region
 RESULT 36
 AAR07902
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 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 195
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 316 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 375
 Modified pro-urokinase has a longer half-life in blood, and disolves thrombin without causing the spontaneous bleeding associated with urokinase. The modification puts an epidermal growth factor domain into the protein, containing the sequence Asn-X-Ser or Asn-X-Thr where X is any residue. Plasmid pHR27 is disclosed as containing the modified
 Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Kawabe H;
 Location/Qualifiers

10. 42
/label= Epidermal growth factor (EGF) domain
10. 19
/label= First loop
20. 31
/label= Second loop
27. 29
/label= Modified site
31. 42
/label= Third loop
 ö
 Length 411;
 Indels
 Morita M,
 100.0%; Score 1508; DB 2;
100.0%; Pred. No. 2.8e-125;
ive 0; Mismatches 0;
 276
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Hirose M,
 AAR07904 standard; protein; 411 AA
 Thrombin; fibrin; bleeding; pHR27.
 Amatsuji Y, Kasai S,
 Disclosure, Fig 1; 27pp; English.
 89JP-00126434.
 90EP-00109473.
 Human pro-urokinase variant
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 276; Conservative
 (GREC) GREEN CROSS CORP
 WPI; 1990-350147/47.
N-PSDB; AAQ06135.
 Sequence 411 AA;
 18-MAY-1990;
 Homo sapiens
 18-MAY-1989;
 21-FEB-1991
 22-NOV-1990
 Active-site
 Tanabe T,
Arimura H;
 EP398362-A.
 61
 241
 AAR07904;
 sequence
 Region
 Region
 Region
 Domain
 RESULT 39
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PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 The sequence is that of a mutant human prourokinase, in which a neutral amino acid in the epidermal growth region has been replaced with a basic amino acid, or an acidic amino acid has been replaced by a non-acidic amino acid. Preferred replacements at 16dly->Lys, 38dly->Lys and 45Asp->Asn. The mutant has an increased hair life in blood as compared to the prior art mutant with a deleted EGF region. It has improved affinity for
 New human pro-urokinase mutants with thrombolytic activity - have a
neutral aminoacid in the epidermal growth factor region replaced with a
basic aminoacid, or an acid residue replaced with a non-acidic residue.
the protein, containing the sequence \mbox{Asn-X-Ser} or \mbox{Asn-X-Thr} where X is any residue. Plasmid \mbox{pHR24} is disclosed as containing the modified
 136 KPSSPPEELKFQCGGKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 VVILISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 196 PCHVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
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La companya de la companya de la companya de la companya de la companya de la companya de la companya de la co
 0
 Indels
 pUK; increased half life; improved fibrin affinity.
 Query Match 100.0%; Score 1508; DB 2; Best Local Similarity 100.0%; Pred. No. 2.8e-125; Matches 0; Mismatches 0;
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Amatsuji Y;
 Claim 1; Page 17-20; 38pp; English.
 Ą
 Tanabe T, Morita M, Hirose M,
 AAR34584 standard; protein; 411
 92EP-00117000.
 91JP-00289257.
 (revised)
(first entry)
 Mutant human prourokinase
 (GREC) GREEN CROSS CORP.
 WPI; 1993-160551/20.
N-PSDB; AAQ41450.
 Sequence 411 AA;
 06-OCT-1992;
 07-OCT-1991;
 Homo sapiens
 25-MAR-2003
14-SEP-1993
 EP541952-A1.
 19-MAY-1993.
 181
 AAR34584;
 121
 241
 61
 sequence
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 888388
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0
 195
 180
 240
 Modified pro-urokinase has a longer half-life in blood, and disolves thrombin without causing the spontaneous bleeding associated with urokinase. The modification puts an epidermal growth factor domain into
 Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIBNQFWFAAIYRHRGGSVTYVCGGSLIS
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKWT
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAOPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 VVKLISHRECQOPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 Kawabe
 .
 Epidermal growth factor (EGF) domain
 Indels
 Morita M,
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
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 Σ
 0; Mismatches
 Hirose
 Modified site
 / Jabel= First loop
20. 31
/ Jabel= Second loop
24. 26 Modified sit
 Location/Qualifiers
 33. .42
/label= Third loop
 Thrombin; fibrin; bleeding; pHR24.
 Amatsuji Y, Kasai S,
 Disclosure, Fig 1, 27pp, English.
 AAR07903 standard; protein; 411
 90EP-00109473.
 89JP-00126434.
 Human pro-urokinase variant.
 GREC) GREEN CROSS CORP
 276; Conservative
 0. .42
label=
 WPI; 1990-350147/47.
 N-PSDB; AAQ06134.
 Homo sapiens
 18-MAY-1990;
 18-MAY-1989;
 21-FEB-1991
 Active-site
 22-NOV-1990
 Tanabe T,
Arimura H;
 EP398362-A
 AAR07903;
 136
 61
 196
 121
 181
 316
 Key
Domain
 Region
 Region
 Region
 Matches
 RESULT 3
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AAY39343;
 181
 241
 Key
Protein
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 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 315
 VVYCLISHRECOOPHYYGSEVITIKYLCAADPOWKIDSCOODSGGPLVCSLOGRMILIGIVS 240
 116 VVKLISHRECQQPHYYGSEVTTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 375
fibrin, and has other features the same as human prourokinase. (Updated on 25-MAR-2003 to correct PN field.)
 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAFHND
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Gaps
 ;
0
 411;
 Length
 Indels
 Query Match 100.0%; Score 1508; DB 2; Best Local Similarity 100.0%; Pred. No. 2.8e-125; Matches 276; Conservative 0; Mismatches 0;
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Pro-urokinase; thrombolysis; fibrin clot lysis.
 293. 362
297. 313
7.note="flexible loop"
325. 341
352. 380
 (NEWE-) NEW ENGLAND DEACONESS HOSPITAL
 AAR62991 standard; protein; 411
 94WO-US007278
 (revised)
(first entry)
 Gurewich
 Key
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Sequence 411 AA;
 Disulfide-bond
Disulfide-bond
 Pro-urokinase
 Homo sapiens.
 28-JUN-1994;
 WO9501427-A1
 02-JUL-1993;
 12-JAN-1995
 AAR62991;
 241
 61
 121
 181
 Liu J,
 RESULT 3
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61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 255
 VVKLISHRECQOPHYYGSEVTTWALCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 240
 116 VVKLISHRECQQPHYYGSEVTTKALCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 375
 AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992.R63108 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and nonspecific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
 33. .42
50. .131
102. .126
135. .136
/note= "Additional cleavage at this site generates low
148. .279
 196 PCWVISATHCFIDYPKKEDYIVYLGRSRINSNTQGBMKFEVENLILHKDYSADTLAHHND
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMT
 1 KPSSPPRELKFOCGOKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 0; Gaps
 cancer;
Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation.
 100.0%; Score 1508; DB 2; Length 411; 100.0%; Pred. No. 2.8e-125; ive 0; Mismatches 0; Indels 0;
 Serine protease; plasminogen; plasmin; activation; matrix; tumour; metastasis; X-ray crystallography; inhibitor.
 1. .158
/label= Mature_urokinase_A_chain
/label= Low_molecular_weight_urokinase
11. .13
/label= Low_molecular_weight_urokinase
11. .19
 276
 376 WGRGCALKDXPGVYTRVSHFLPWIRSHTKEENGLAL 411
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Disclosure; Fig 1; 46pp; English
 AAY39343 standard; protein; 411
 (first entry)
 Query Match 100.
Best Local Similarity 100.
Matches 276; Conservative
 Human pro-urokinase.
 Sequence 411 AA;
 Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Cleavage-site
 Disulfide-bond
 Homo sapiens
 01-DEC-1999
```

158. .159 | note= "Cleavage at this site generates mature urókinase | 1- and B-chains"

59. .411 |abel= Mature\_urokinase\_B\_chain

note= "N-glycosylated"

325. .341 352. .380 405. .406

note= "Links mature urokinase A- and B-chains"

```
Identifying ligands for target biomolecules using X-ray crystallography
 Example 1; Fig 5; 57pp; English.
 Greer J,
 WPI; 1999-571607/48.
 (ABBO) ABBOTT LAB
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
 Cleavage-site
 Modified-site
 Cleavage-site
 Nienaber VL,
 05-MAR-1999;
 W09945379-A2
 06-MAR-1998;
 10-SEP-1999.
 Protein
```

Norbeck DW;

Abad-Zapatero C,

99WO-US004967 98US-00036184

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This sequence represents human pro-urokinase. The mature urokinase consists of an A- and B-chain, linked by a single disulphide bond; and is consists of an A- and B-chain, linked by a single disulphide bond; and is generated by proteolytic cleavage of the peptide bond between Lys 135 and Lys [16 159] Additional cleavage of the peptide bond between Lys 135 and Lys contains an ESF-like domain and a kringle domain, while the B-chain contains the catalytic domain. Urokinase The urokinase A-chain contains the catalytic domain. Urokinase activates plasminogen which, in turn, activates the matrix as serine protease and is strongly associated with tumour cells. Urokinase activates plasminogen which, in turn, activates the matrix matrix and promote tumour contains as effective anticancer that specifically target urokinase may serve as effective anticancer agents. A novel method for identifying such serve as cleaved anticancer agents. A novel method for identifying such ligands used X-ray crystallography to determine if a complex is formed between a ligand and a target biomolecule. However, crystals of a native urokinase/inhibitor complex had poor diffraction quality. Human urokinase constructione engineered so that it would produce crystals with the desired qualities. This engineered urokinase was designated mu-UK
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 195
 196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 255
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 60
 VVKLISHRECQOPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMILIGIVS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHND
 Gaps
 ó
 Query Match 100.0%; Score 1508; DB 2; Length 411; Best Local Similarity 100.0%; Pred. No. 2.8e-125; Matches 276; Conservative 0; Mismatches 0; Indels 0;
 Sequence 411 AA;
 61
 256
 181
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Identifying ligands for target biomolecules using X-ray crystallography.
used for designing ligands with improved biological activity for target
 /note= "Cleavage at this site generates mature urokinas.
A- and B-chains"
 and
 71. 113
102. 126
135. 136
/note= "Additional cleavage at this site generates
molecular weight (LMW) urokinase"
 This sequence represents human pro-urokinase. The mature urokinase consists of an A- and B-chain, linked by a single disulphide bond,
 Serine protease; plasminogen; plasmin; activation; matrix; cancer;
tumour; metastasis; X-ray crystallography; inhibitor.
 148. .279
/note= "Links mature urokinase A- and B-chains"
158. .159
 1. 158 / Albert Mature_urokinase_A_chain
1. 135 / Label Low_molecular_weight_urokinase
11. 19
 Norbeck DW;
241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 159. .411
| Tabel = Mature_urokinase_B_chain
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Vienaber VI., Greer J., Abad-Zapatero C.
 "N-glycosylated"
 AAY42284 standard; protein; 411 AA
 Example 1; Fig 5; 57pp; English.
 99WO-US004518
 98US-00036184
 189. .205
197. .268
293. .362
 01-DEC-1999 (first entry)
 note=
 PI; 1999~551079/46.
 ABBO) ABBOTT LAB.
 Human pro-urokinase
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
 Disulfide-bond
Modified-site
 Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
 Disulfide-bond
 Cleavage-site
 Cleavage-site
 :leavage-site
 409945389-A2
 11-MAR-1999;
 6-MAR-1998;
 Homo sapiens
 10-SEP-1999.
 AAY42284;
 Key
Protein
 Protein
 Protein
 RESULT 41
 AAY42284
ID AAY4
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generated by proteolytic cleavage of the peptide bond between Lys 158 and [16] 159. Additional cleavage of the peptide bond between Lys 115 and Lys [16] generates a low molecular weight urokinase. The urokinase A-chain contains an EGF-like domain and kringle domain, while the B-chain contains the catalytic domain. Urokinase is a serine protease and is strongly associated with tumour cells. Urokinase activates plasminogen which, in turn, activates the matrix metalloproteinases. Plasmin and the metalloproteinases degrade the extraorlular matrix and promote tumour growth and metastasis. Inhibitors that specifically target urokinase must serve as effective anticancer agents. A novel metall of or identifying such between a ligand and a target blomolecule. However, crystals of a native urokinase/finibitor complex had poor diffraction quality. Human urokinase was therefore engineered so that it would produce crystals with the desired qualities. This engineered urokinase was designated mu-UK
 (AAY42285)
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Seguence 411 AA;

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196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 255
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 181 VVKLISHRECQOPHYYGSEVTTRMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 195
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKPEVENLILHKDYSADTLAHHND 120
 256 IALLKIRSKEGRCAQPSRTIGTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 315
 316 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 375
 1 KPSSPPBBLKPQCGQKTLRPRPKIIGGBPTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 60
 0; Gaps
Query Match
100.0%; Score 1508; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.8e-125;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
 241 WGRGCALKDKPGVYTRVSHPLPWIRSHTKEENGLAL 276
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
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Urokinase plasminogen activator (uPA). AAY92836 standard; protein; 411 AA. 29-AUG-2000 (first entry) AAY92836; AAY9283

Homo sapiens.

thrombolytic.

N-terminal; pro-uPA; urokinase plasminogen activator; receptor; uPDR; anti-trancer; anti-metastatic; anti-proliferative; anti-arbascalerotic; anti-thrombotic; anti-angiogenic; anti-inflammatory; anti-arbitic; anti-fibrotic; apoptotic; vasotropic; anti-diabetic; ophthalmological;

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location/Qualifiers
 Disulfide-bond
Disulfide-bond
 bond
 -bond
 Disulfide-bond
Disulfide-bond
 Disulfide-bond
 Disulfide-bond
 Disulfide-bond
 Disulfide-
Disulfide-
 Disulfide-
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The present sequence shows the wild-type urokinase plasminogen activator (UPA). Cyclic peptides based on the amino acids residues 20-30 (the receptor-binding region) of uPA are claimed. These cyclic peptides target the UPA receptor (UPAR). Allowing theirapeutic or diagnostic agents to be receptor-binding region) of uPA are claimed. These cyclic peptides are used, coptionally when linked to a therapeutic agent, to inhibit migration, invasion and proliferation of cells, or angiogenesis, or to induce apoptosis. Particularly they are used, in human or vetrinary medicine, to treat diseases characterized by these processes, e.g. solid tumors, leukaemia or lymphoma (or their metastases); benigh hyperplasia; neovascula cherosolerosis, restenosis; ischaemia, deep vein thrombosis; neovascula cherosolerosis, restenosis; schaemia, deep vein thrombosis; neovascula cherosolerosis, restenosis; ischaemia, deep vein thrombosis; neovascula cherosolerosis; restenosis; ischaemia, deep vein thrombosis; neovascula checosolerosis; ischaemia, deep vein thrombosis; neovascula checosolerosis; ischaemia, deep vein thrombosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula checosolerosis; neovascula
 196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 2
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 🧵
 316 VVKLISHRECQQFHYYGSEVTTKYM.CAADPQWKTDSCQGDGGGFLVCSLQGRWTLTGIVS
 New cyclic peptide, useful for treatment or diagnosis of e.g. tumors sother diseases involving cell proliferation or migration, targets the urokinase plasminogen activator receptor.
 136 KPSSPPEELKFOCGOKTLAPRFKIIGGEFTTIENOPWFAAIYRAHGGSVTYVCGGSLIS
 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMXFEVENLILHKDYSADTLAHHND
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKEMSTDYLYPEQLKMT
 181 VVXLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPBELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 ó
 Query Match
100.0%; Score 1508; DB 3; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.8e-125;
Matches 276; Conservative 0; Mismatches 0; Indels 0
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Disclosure, Fig 1; 93pp; English.
 99WO-US025210,
 98US-00181816,
 (ANGS-) ANGSTROM PHARM INC.
Disulfide-bond 325. .341 Disulfide-bond 352. .380
 Mazar AP, Jones TR;
 WPI; 2000-365605/31.
 Sequence 411 AA;
 WO200026353-A1.
 28-OCT-1999;
 29-0CT-1998;
 11-MAY-2000.
 ##X#X#X#X#X#X#X####X#X####X
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RESULT 43

376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKBENGLAL 411

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(first entry)
 189.
197.
293.
 Sequence 411 AA;
 Key
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Unidentified
 12-JUN-2001
 AAB74797;
 181
 241
 61
 RESULT 44
 AAB74797
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 The present sequence is that of human pro-urokinase plasminogen activator (pro-upA). The invention provides a uPA receptor (uPAR) targeting protein or peptide that is labelled and used in methods of diagnosis and therapy. The labelled protein or peptide preferably has the following properties: it comprises at least 38 amino acid residues, including residues 13-30 of the uPAR binding site of uPA, competes with labelled preparation of a cell or molecule that has a binding site for uPA, has an ICSO value of about 10 nM or less; and is not a fusion protein. Preferred molecules of about 10 nM or less; and is not a fusion protein. Preferred molecules of about 10 nM or less; and is not a fusion protein. Preferred molecules of single chain uPA, tcuPA (inactivated with the suicide inhibitor disopropyl fluorophosphate), the N-terminal ATF fragment (amino acids 1-135 or 1-143) of uPA, or the growth factor domain (residues 4-43). Sultable labels include a radionuclide, a PTF-imageable agent, a fluorescer, a chromogen, a phosphorescer, a chromogen, a phosphorescer, a chromogen, a phosphorescer, a chromogen, a phosphorescer, a chromogen, cell invasion (preferably
 /note= "the ATF domain alternatively comprises residues 1-43"
 102. .126
148. .279
158. .129
/note= "Cleavage at this site results in the formation of
the two-chain active uPA (tcuPA)"
 Novel urokinase plasminogen activator cell surface receptor-targeting protein or peptide, useful for inhibiting anglogenesis or cell migration, invasion or proliferation, is diagnostically or therapeutically labeled.
 Urokinase plasminogen activator; uPA; human; tumour; cell migration; cell invasion; cell proliferation; angiogenesis; apoptosis; antitumour; diagnosis; therapy.
 4. .43
/label= Growth_factor_domain
11. .19
 Human pro-urokinase plasminogen activator.
 Location/Qualifiers
1. .135
/label= ATF
 AAB20489 standard; protein; 411 AA.
 Disclosure, Fig 1, 35pp, English
 27-SEP-2000; 2000WO-US026502,
 (ANGS-) ANGSTROM PHARM INC.
 21-JUN-2001 (first entry)
 Mazar AP, Jones TR;
 WPI; 2001-290611/30.
 Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
 Disulfide-bond
Disulfide-bond
 WO200125410-A2
 Cleavage-site
 Homo sapiens.
 31-OCT-1999;
 12-APR-2001.
 AAB20489;
 Key
Domain
 Domain
 AAB20489
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invasiveness of tumour cells), cell proliferation or angiogenesis, or to diduce apoptosis, preferably in the treatment of a subject having a disease or condition associated with undesized cell magration, invasion, proliferation or angiogenesis (claimed). The protein or peptide is also useful for treating diseases or conditions including primary growth of a solid tumour, leukaemia or Lymphoma, tumour invasion, metastasis, atherosclerosis, myocardial angiogenesis, telangiectasia, corneal disease, rubeosis, movoacular glaucoma, diabetic and other retinopathy, macular degeneration, arthitis, fibrosis, wound healing with scarring and fibrosis peptic ulcers, bone fracture, keloids, or a disorder of vaculogenesis, heematopoiesis, ovulation, menstruation, pregnancy or placentation associated with pathogenic cell invasion or with the protein or peptide probe is internalised by the cells to which it binds, e.g. tumour cells, and is useful for imaging tenhiques in which it reduces the background signal relative to specifically bound probes. This uptake permits clearance of circulating to probe elsewhere in the body increases
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 180
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQPGTSCEITGPGKENSTDYLYPEQLKWT 315
 136 KPSSPPEELKPOCGOKTLRPRFKIIGGEFTTIENOPWFAALYRRHRGGSVTYVCGGSLIS 195
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 VVICLISHRECQOPHYYGSBVTTRWLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Query Match
100.0%; Score 1508; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.8e-125;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps
 Prourokinase; Pro-109; mutagenic; urokinase; zymogen; mutant; lowered fibrinogen dissolving activity; fibrin; E segment; D lowered non-specific fibrin dissolving zymogen activation.
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 411
 Location/Qualifiers
 AAB74797 standard; protein; 411
 Prourokinase protein sequence.
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 The present invention describes a prourokinase mutant comprising the amino acid sequence point mutation at proline 309. The mutation makes the mutant have an intrinsic activity 2.5-20 times lower than that of natural prourokinase, including lowered fibrinogen dissolving activity and lowered non-specific fibrin dissolving zymogen activation. Compared with the natural prourokinase, the fibrin dissolving zymogen activation of the mutant may be promoted by not only the E segment of degraded fibrin but also the D segment. The present sequence represents a wild type prourokinase protein sequence which is used in an example from the present invention. N. B. The sequence in the specification is of poor quality so the sequence given here is of the indexers best interpretation
 195
 120
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 315
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 9
 196 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGSVTYVCGGSLIS
 Gaps
 ö
 100.0%; Score 1508; DB 4; Length 411; 100.0%; Pred. No. 2.8e-125;
 0; Indels
 276
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 376 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 0; Mismatches
 AAE16544 standard; protein; 411 AA.
 Example; Fig 1; 11pp; Chinese.
 10-JUL-2000; 2000CN-00109829.
 10-JUL-2000; 2000CN-00109829
 276; Conservative
 Urokinase zymogen mutant
 WPI; 2001-266614/28.
 Similarity
 Sequence 411 AA;
Disulfide-bond
Disulfide-bond
 Liu J;
 (LIUJ/) LIU J.
 CN1277262-A.
 20-DEC-2000
 AAE16544;
 181
 61
 121
 Query Match
 Local
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Matches
 RESULT 45
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 AAE16544
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The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPh). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microandiopathies, surgically induced thrombotic disorders, angiogenic disorders, upulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, clasorder, male impotence, respiratory disress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder sesonic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (HDA) two chain curokinase (tcuPA) and single chain urokinase (scuPA) protein 195 255 180 315 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120 9 136 KPSSPPEELKFQCGGKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clothing disorder; uterine contraction disorder; respiratory disease; male impotence; adult respiratory distress syndrome; tcuPA; scuPA; two chain urokinase; single chain urokinase. Gaps Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator. ö Length 411; Indels 100.0%; Score 1508; DB 5; 100.0%; Pred. No. 2.8e-125; ive 0; Mismatches 0; 276 411 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL Claim 9; Fig 1C; 117pp; English. 20-JUN-2000; 2000US-0212874P. 13-JUN-2001; 2001WO-US018976. Query Match
Best Local Similarity 100. (UYPE-) UNIV PENNSYLVANIA Cines DB, Higazi AA; WPI; 2002-122240/16. Sequence 411 AA; N-PSDB; AAD27077 WO200197752-A2 Homo sapiens 27-DEC-2001, 241 376 ठ

0

RESULT 46 ADE85977

Human, urokinase-type plasminogen activator; uPA; therapy, hypertension, stroke, hypotension, atherosclerosis, heart attack, thrombotic disorder, microvascular occlusion, angiogenic disorder, pulmonary fibrosis, asthma,

urokinase-type plasminogen activator tcuPA and scuPA protein.

(first entry)

09-APR-2002

Human

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The present sequence is the protein sequence of human mature single chain urokinase plasminogen activatox (scupA). A method of preventing or decreasing the severity of scarring in a subject involves obtaining a pharmaceutical composition comprising (scupA) or a scupA mimetic and administering the pharmaceutical composition to a subject. A method of screening for compounds that prevent scarring involves obtaining scupA or its mimetic, and testing its ability to prevent scarring. The injury is the result of acute/Adult respiratory distress syndrome (ARDS), perminedially irradiation or hyperoxia-induced lung injury, particulate-induced lung injury associated with the man scupA or modified scupA. In a preferred method, testing uses a cultured cell (sepecially a cultured rabbit pleural mesothelial cell or lung fibroblast) or test animal (sepecially a rabbit having tetracycline induced pleural injury). The pharmaceutical composition is directly administered to a site in the subject, intrapleurally or as an aerosol
 120
 240
 195
 255
 180
 256 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 315
 9
 VVKLISHRECQQPHYYGSEVITKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 1ALLKIRSKEGRCAQPSRT1QT1CLPSMYNDPQFGTSCE1TGFGKENSTDYLYPEQLKMT
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 136 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 Human single chain urokinase plasminogen activator mature polypeptide.
 Gabs
 Preventing or decreasing the severity of scarring in a subject by administering a pharmaceutical composition comprising a single chain urokinase plasminogen activator molecule (scuPA) or a scuPA mimetic.
 Human; plasminogen activator; urokinase; scarring; vulnerary; scuPA.
 ;
0
 Length 411;
 Indels
 Query Match 100.0%; Score 1508; DB 7; Best Local Similarity 100.0%; Pred. No. 2.8e-125; Matches 276; Conservative 0; Mismatches 0;
 Disclosure, SEQ ID NO 2; 76pp; English
 standard; protein; 411 AA
 05-APR-2002; 2002US-0370466P.
27-SEP-2002; 2002US-0414202P.
 04-APR-2003; 2003WO-US010323
 (TEXA) UNIV TEXAS SYSTEM
 WPI; 2003-812941/76.
N-PSDB; ADE85976.
 Sequence 411 AA;
 WO2003086278-A2.
 Homo sapiens.
 29-JAN-2004
 23-OCT-2003
 196
 121
 316
 61
 181
 Query Match
Best Local &
 ADE85977;
 ADE85977
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APUK(k,k) is an example of a prourokinase derivative which has increased affinity for blood clots and attacks the components of a thrombus whilst sparing the circulating clotting proteins and platelets. The first 13 N-terminal amino acids replace the first 3 amino acids of natural urokinase. This derivative has a fibrin lysis activity of 9.2 x 10 power4 international units/O.D.280. See also AAQ1022-3 and AAQ10225. (Updated on 25-MAR-2003 to correct PA field.)
 Human prourokinase - like polypeptide(s) with thrombolytic action - have oligopeptide(s) which bind covalently to blood clot (thrombus) by action of Factor XIII.
 146 KPSSPPEELKFQCQQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS
 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMT
 266 IALLKIRSKEGRCAQPSRTIQTICLPSWYNDPQFGTSCEITGFGKENSTDYLYPBQLKWT
 Gaps
 human prourokinase; blood coagulation Factor XIII; thrombolysis.
 0
 Query Match 100.0%; Score 1508; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.9e-125;
Matches 276; Conservative 0; Mismatches 0; Indels 00.
 Kobayashi Y, Watabe K, Mukohara Y, Satoh M, Nakamura H;
WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Human prourokinase derivative APUK (k,k).
 Ą
 Disclosure, Fig 7; 44pp; English.
 AAR10172 standard; protein; 421
 89JP-00150161.
90JP-00123163.
 89JP-00150161
 (revised)
(first entry)
 (NIPS) NIPPON SODA CO.
 WPI; 1991-022232/03.
N-PSDB; AAQ10224.
 13-JUN-1989;
 Homo sapiens
 13-JUN-1989;
 15-MAY-1990;
 25-MAR-2003
21-MAR-1991
 WO9015867-A.
 27-DEC-1990.
 61
 206
 326
 376
 AAR10172;
 AAR10172
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205 120 265 180 325

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120
 275
 The claimed gene product may be expressed in a transformed E.coli host, for the efficient production of high molecular human urckinase. The Neminian of the protein expressed by the transforming plasmid is replaced with a codon frequently used in E.coli. (Updated on 25-MAR-2003 to correct PA field.)
240
 VYKLISHRECQOPHYXGSEVITIKALCAADPQWKTDSCOGDSGGPLVCSLQGRAMILTGIVS 395
 9
 276 IALLKIRSKEGRCAQPSRIGTICLEPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKWT
 1 KPSSPPEBLKFOCGOKTLRPRFKIIGGEFTTIENOPWFAALYRRHRGGSVTYVCGGSLIS
 156 KPSSPPEELKFQCGQXTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 216 PCHVISAIHCFIDYPKKEDYIVXLGRSRLNSNIQGEMKFEVENLILHKDYSADTLAHHND
 121 IALLKIRSKEGRCAQPSRIIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT
 Human urokinase gene - has N-end of aminoacid sequence coded by codon used in Escherichia coli.
VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS
 Gaps
 0
 100.0%; Score 1508; DB 1; Length 431; 100.0%; Pred. No. 3e-125; ive 0; Mismatches 0; Indels 0.
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 431
 Location/Qualifiers
21. .431
 A
 NISSAN CHEM IND LTD.
HODOGAYA CHEM IND CO LTD.
SAGAMI CHEM RES CENTRE.
CENTRAL GLASS CO LTD.
NIPPON SODA CO.
 Disclosure; Fig 2; 19pp; Japanese.
 E.coli; high molecular urokinase
 AAP60783 standard; protein; 431
 85JP-00011032,
 85JP-00011032
 TOYO SODA MFG CO LID
 Query Match 100.
Best Local Similarity 100.
Matches 276; Conservative
 WPI; 1986-254744/39.
 N-PSDB; AAN60703
 Sequence 431 AA;
 Human urokinase.
 JP61181377-A.
 25-JAN-1985;
 Homo sapiens
 25-JAN-1985;
 14-AUG-1986.
 25-MAR-2003
23-OCT-1991
 61
 AAP60783;
 (NISC) N
(HODO) H
(SAGA) S
(CENG) (
(NIPS) N
(TOYJ) T
 181
 336
 241
 396
 Protein
 AAP60783
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 215
 276 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 335
 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120
 9
 The inventors claim a method of producing single-chain pro-urokinase by using as template, mRNA obtd. from cells of an established human kidney-derived cell line. The urokinase is used to treat thrombosis and embolic diseases as well as in the treatment of diseases in combination with
 Sequence encoded by the signal sequence and noncoding region of the pro- {\tt UK} structural gene (Sequence II).
 Enzyme; thrombosis therapy; embolic disease; single-chain pro-urokinase
 Glycosylated single-chain pro-urokinase – prepd. by cultivating animal cells transformed by DNA prepd. from \pi RNA.
 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHGGSVTYVCGGSLIS
 216 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND
 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPRQLKMT
 1 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS
 Ë
 Suyama
 ö
 Query Match 100.0%; Score 1508; DB 1; Length 431; Best Local Similarity 100.0%; Pred. No. 3e-125; Matches 276; Conservative 0; Mismatches 0; Indels 0
 Nishida M,
 421
 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Rimura H,
 1. .20
/label= signal peptide
 Disclosure; Page 8-10; 64pp; English
 location/Qualifiers
 Σ
 /label= A chain
179. 431
/label= B chain
 AAPS0114 standard; protein; 431
 Nagai
 84JP-00037119.
85JP-00017969.
 85EP-00102031
 CROSS CORP.
 Kaneda T,
 WPI; 1985-224693/37.
N-PSDB; AANS0138.
 anticancer agents
 Sequence 431 AA;
 (GREC) GREEN
 Hiramatsu R,
 Homo sapiens.
 3-FEB-1985;
 27-FEB-1984;
 27-SEP-1991
 11-SEP-1985
 EP154272-A.
 156
 61
 AAP50114;
 386
 Peptide
 Domain
 Domain
 RESULT
 AAP501
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 Sequence is modified from the human pro-urokinase with a non-basic residue replacing Lysl35. The product may be expressed from a transformed host such as E.coli, it has long-acting fibrinolytic activity and is stable to proteases such as trypsin, thrombin and plasmin. (Updated on 25-MAR-2003 to correct PA field.)
181 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240
 336 VVKLISHRECQQPHYYGSEVTTKALCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 395
 Human pro-urokinase stable to protease and 135,157-modified - prepd. using transformant e.coli and having long-acting fibrinolytic activity.
 Gaps
 Omori M, Miki T;
 ö
 100.0%; Score 1508; DB 1; Length 431; larity 100.0%; Pred. No. 3e-125; Conservative 0; Mismatches 0; Indels 0
 Fibrinolytic; protease; trypsin; thrombin; plasmin
 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
 Watabe K,
 396 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
 Miyake T, Hibino Y, Kobayashi Y,
Yokoyama M, Matsumoto R;
 Modified human pro-urokinase clone.
 Disclosure, Fig 4; 98pp; Japanese.
 AAP60674 standard; protein; 431 AA
 (SAGA) SAGAMI CHEM RES CENTRE.
(MIYAA) MIYAKE T.
(HODO) HODOGAYA-CHEM CO LTD.
(NIPS) NIPPON SODA CO.
(TOYA) TOYO SODA MIG CO LTD.
(NIPC) NISPON CHEM IND LTD.
(NISC) NISSAN CHEM IND LTD.
(NISC) NISSAN CHEM IND LTD.
(TOYA) TOYO SODA MIG CO LTD.
(TOYA) TOYO SODA MIG CO LTD.
(NIPS) NIPPON SODA CO.
 85JP-00011033.
85JP-00083611.
85JP-00159294.
 86WO-JP000031
 (revised)
(first entry)
 Query Match
Best Local Similarity
Matches 276; Conserval
 WPI; 1986-212124/32.
N-PSDB; AAN60591.
 Sequence 431 AA
 25-JAN-1985;
20-APR-1985;
20-JUL-1985;
 Homo sapiens
 24-JAN-1986;
 25-MAR-2003
16-OCT-1991
 WO8604351-A
 31-JUL-1986
 Miyake T,
 AAP60674;
 50
 AAP60674
ID AAI
 RESULT
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07 61 PGW/18APTD/PURCHYU/GREANING-GWYRENILLHHYDD 120
DD 216 PGW/18APTG/1979FKZD1/V/GREANINSPGGWREFEYRELLHHYDD 275
QY 121 IALLKIESKERRAADESTIGGTG/BRWYROPEGWREFEYRELLHKOYSADTLAHHDD 275
DD 276 IALLKIESKERRAADESTIGGTG/BRWYROPEGWREFEYRENGARF 335
QY 181 VYZLIEHRZOQPHYGSEYTRAK-CAANDWKTOSCOGOSGEPLVGSLOGENTLOTTES
DD 336 WYZLIEHRZOQPHYGSEYTRAK-CAANDWKTOSCOGOSGEPLVGSLOGENTLOTTES
DD 336 WYZLIEHRZOQPHYGSEYTRAK-CAANDWKTOSCOGOSGEPLVGSLOGENTLOTTES
DD 336 WYZLIEHRZOQPHYGSEYTRAK-CAANDWKTOSCOGOSGEPLVGSLOGENTLOTTES
DD 336 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 276
DD 336 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 276
DD 336 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 276
DD 336 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 276
DD 336 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 276
DD 336 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 276
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DD 337 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 277
DD 337 WGRCALKXKGOYTRVSHFLPWISSHTRENGLAL 277
DD 337 WGRCALKXKGOYTROHING MGRCANING WGRCANING ``

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model OM protein - protein search,

May 25, 2004, 14:53:05 ; Search time 50.3138 Seconds (without alignments) 1530.046 Million cell updates/sec Run on:

US-09-880-503-5 1508 1 KPSSPPBELKFQCGQKTLRP.....VSHFLPWIRSHTKEENGLAL 276 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1149313 seqs, 278921704 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_May PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		Appli	App1;	Appli	App1	App.	, Appl	Appl	4, Ap		9, App	21, Appl	4, Ap	75, A	, App	5
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	Description	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence 34,	Sequence 2, Appl	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence 1275, Ap	Sequence	1000
		503-5	503-7	503-3	-821-2	-037-34	-026-34	-421-2	-311-184	-822-161	-671-149	-985-21	-027-414	US-10-295-027-1275	-962-34	***
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	% Query Match Length DB	276	323	411	411	431	431	431	431	431	431	431	431	431	431	,,,,
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	000
	Score	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	000
	Result No.		7	m	4	Ŋ	φ	7	æ	σv	10	11	12	13	14	

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US-10-087-192-5- US-10-193-656-4 US-09-264-4688-1 US-09-880-503-6 US-09-880-503-6 US-10-407-821-3 US-09-264-4688-2 US-09-898-837A- US-09-898-837A- US-09-898-837A- US-10-106-688-6 US-10-106-688-6	US-09-997-003- US-09-987-455- US-09-987-455- US-09-987-457- US-09-987-457- US-09-987-455- US-09-987-455- US-09-987-455- US-09-987-455- US-09-987-455-	US-09-987-455-1 US-09-987-457-1 US-09-987-455-1 US-09-987-455-1 US-09-987-455-1 US-09-987-455-1 US-09-084-491A-3 US-09-084-491A-3 US-09-987-455-1 US-09-987-455-1 US-09-987-455-1 US-09-987-455-1	US-09-987-455-1 US-10-36-101-2 US-09-969-271-7 US-09-974-298-14 US-10-411-037-5 US-10-411-036-2 US-10-413-656-8 US-10-43-656-8 US-10-43-043-701-4 US-10-443-701-4 US-10-441-049-2 US-10-401-049-2	US-09-898-837A US-09-898-837A US-10-172-712- US-10-172-712- US-10-172-712- US-10-172-712- US-10-051-874- US-10-451-1168- US-10-172-782- US-10-170-782- US-10-172-782- US-10-172-782- US-09-961-721-5
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ALIGNMENTS

Sequence 5, Application US/09880503

Sequence No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

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UGS-09-880-503-3
; Sequence 3, Application US/09880503
; Sequence 3, Application US/09880503
; Sequence 3, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: COMPOSITION OF TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; SOFTWARE: PATENT VET: 2.1
; SEQ ID NOS: 18
; SOFTWARE: PATENT VET: 2.1
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US-10-407-821-2

US-10-407-821-2

Sequence 2, Application US/10407821

Publication No. US20030219386A1

GENERAL INFORMATION:

TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED

TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL

TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURALIS IN RABBITS

FILE REFERENCE: UTSN:022US

CURRENT PALICATION NUMBER: US/10/407,821

CURRENT FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: 60/414,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
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IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
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Best Local Similarity 100.0%; Pred. No. 9.9e-146;
Matches 276; Conservative 0; Mismatches 0;
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CRGANISM: Homo sapiens
US-09-880-503-3
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Sequence 7, Application US/09880503

Sequence 7, Application US/09880503

Sequence 7, Application US/09880503

Sequence 8. US-05020131964A1

GENERAL INFORMATION: US-0504

APPLICAMY: ORDER AL-SOOF

TITLE OF INVENTION: TISSUE CONTRACTABILITY

FILE REFERENCE: 9596-331

CURRENT APPLICATION NUMBER: US/09/880,503

CURRENT PILING DATE: 2001-06-13

PRIOR FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 18

SOSTWARE: Patentin Ver. 2.1

SEQ ID NO 7
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  ; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 5556-331
; CURRENT PELLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR PELLOR DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIN Ver. 2.1
; SOFTWARE: PatentIN Ver. 2.1
; SOFTWARE: PATENTIN VER. 2.1
; GORGANISM: HOMO Sapiens
; US-09-880-503-5
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CORGANISM: Homo sapiens
US-09-880-503-7
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Sequence 34, Application US/10411026
| Sequence 34, Application US/10411026
| Publication No. US20040063911A1
| GENERAL INFORMATION:
| APPLICANT: Nose Technologies, Inc.
| APPLICANT: Bayer, Nobert
| APPLICANT: Bayer, Nobert
| APPLICANT: Bayer, Nobert
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| APPLICANT: Abyer, Nobert
| APPLICANT: APPLICATION NUMBER: US 10/328,523 |
| FRIOR PILING DATE: 2001-10-19 |
| FRIOR PILING DATE: 2001-10-19 |
| FRIOR PILING DATE: 2002-06-07 |
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120 PCWVISATHCPIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 275
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Best Local Similarity 100.0%; Score 1508; DB 12; Length 431;
Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
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                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
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; ORGANISM: Homo sapiens
US-10-411-026-34
US-10-411-037-34
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Sequence 34, Application US/10411037

PUBLICARION NO. US20040043446A1

GENERAL INFORMATION:
PAPLICANT: Nece Technologies, Inc.
APPLICANT: Sopt. David
APPLICANT: Copf. David
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Best Local Similarity 100.0%; Pred. No. 9.9e-146;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
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       PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: 60/370,466
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                      ; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-407-821-2
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Sequence 161, Application US/10301822

Sequence 161, Application US/10301822

Publication No. US20030148410A1

GENERAL INFORMATION

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Guillenette, Tracy L.

APPLICANT: Guillenette, Tracy L.

APPLICANT: Guillenette, Subbardi

APPLICANT: Guillenette, Tracy L.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: MATHORS FOR IDENTIFICATIONS, KITS, AND

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION UNMERR: US (1)/301,822

CURRENT APPLICATION NUMBER: US 60/339,971

PRIOR PILING DATE: 2002-01-21

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-05
      APPLICANT: Kanatkar, Shubhangi
APPLICANT: Karen
APPLICANT: Glart, Karen
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Hoersh, Sebastian
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DIDANTIPLICATION, ASSESSMENT, PREVENTION, AND THERAPY
ITILE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/17,311
CURRENT FILING DATE: 2002-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-06-13
PRIOR PLLING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PRESEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
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CRGANISM: Homo sapiens
US-10-171-311-184
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                           216 PCWVISATHCPIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 275
                                                                                                         121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
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Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0;
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PUBLICATION NO. US20020193304A1

GENERAL INFORMATION:
APPLICANT: WADA, NANABU

APPLICANT: WADA, NANABU

TITLE OF INVENTION: ANTI-HIV AGENTS

TITLE OF INVENTION: ANTI-HIV AGENTS

FILE REFERENCE: HAYAK-9

CURRENT APPLICATION NUMBER: US/10/076,421

CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: JP 2001-42655

PRIOR PILING DATE: 2001-06-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PARCHIN UNINER: JP 2001-184284

NUMBER OF SEQ ID NOS: 5

LENGTH: 431

WADE: DATE: ANDI-06-19

LENGTH: 431
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Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-076-421-2
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241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
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Sequence 21, Application US/10131985
Publication No. US20030199440A1
Sequence 21, Application US/10131985
Publication No. US20030199440A1
Septicant: Dack, Wevin N
APPLICANT: Dack, Wevin N
APPLICANT: Path, Paul V
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: McIntosh, Fraser S
APPLICANT: MUSER: US/09/726,295
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 21
LENGTHERS
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GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-985-21
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US-10-295-027-414
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100.0%; Score 1508; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                               Query Match 100.0%; Score 1508; DB 14; Length 431; Best Local Similarity 100.0%; Pred. No. 1e-145; Matches 276; Conservative 0; Mismatches 0; Indels 0;
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WS-10-247-671-149
Sequence 149, Application US/10247671
Sequence 149, Application US/10247671
Sequence 149, Application WS/10247671
Sequence 149, Application WS/10247671
Septicant: Mixita, Thomas
APPLICANT: Mixita, Thomas
APPLICANT: Mixita, Dov
APPLICANT: Raser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REPERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT PILING DATE: 2002-09-18
PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL PROGram
SEQ ID NO 149
LEMMINH: HAI
TYPE: PRI ATSILE ADDRESSED IN TREATED FORM CELLS
CORMARE: PERL PROGram
SEQ ID NO 149
LEMMINH: HOMO SapienS
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NAME/KEY: misc feature
CTHEN OTHER PRORATION: Incyte ID No. US20030194721A1 1453334CD1
US-10-247-671-149
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PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SSOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 431
                                                                                                                              TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-161
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61 PCWVISATHOFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDÝSADTLAHHND 120
120 PCWVISATHOFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKOYSADTLAHHND 275
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                 276 IALLKIRSKEGRCAQPSRIJQTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMT 335
                                                                                                 1 KPSSPPRELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLIS 60
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DENOLITY ST.

ORGANISM: Homo sapiens
5-10-131-985-21

Query Match
Best Local Similarity 100.0%; Score 1508; DB 14; Length 431;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps
121
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216 PCWVISATHCFIDYPXKGDYIVYLGRSRLNSNYQGEWKFEVENLILHKDYSADTLAHHND 275
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APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mark, David H.
APPLICANT: Warson, Susan R.
APPLICANT: Warson, Susan R.
APPLICANT: Bas Biotechnology, Inc.
APPLICANT: Bas biotechnology, Inc.
TITLE OF INVENTION: Methods of Engening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Soreening for Modulators of Cancer
TITLE REPERRNCE: 018501-012500US
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/334,394
PRIOR APPLICATION NUMBER: US 60/334,394
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,211
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PRIOR PILING DATE: 2002-01-08
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Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels
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CORGANISM: Homo sapiens
US-10-295-027-1275
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               APPLICANT: GISH, ALL C.
APPLICANT: GIVEN, RICHARD
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Macker, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 00/663,733
PRIOR APPLICATION NUMBER: US 00/335,049
PRIOR APPLICATION NUMBER: US 60/335,046
PRIOR APPLICATION NUMBER: US 60/335,046
PRIOR APPLICATION NUMBER: US 60/3340,376
PRIOR PILING DATE: 2001-11-12
PRIOR PILING DATE: 2001-11-21
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PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PILING DATE: 2002-01-08
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Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels
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Gish, Kurt C.
Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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ORGANISM: Homo sapiens
US-10-295-027-414
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RESULT 14
US-10-410-962-34
Sequence 34, Application US/10410962
Publication No. US20040077836A1
PUBLICATION No. HOSPANTION:
APPLICANT: Neose Technologies, Inc.

Sequence 1275, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Afar, Natasha

RESULT 13 US-10-295-027-1275

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121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180
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100.0%; Score 1508; DB 16; Length 431;
Best Local Similarity 100.0%; Pred. No. 1e-145;
Matches 276; Conservative 0; Mismatches 0; Indels 0;
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Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REPERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT PILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR PELING DATE: 2000-103-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2010-03-02
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CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PILING DATE: 2001-10-19
PRIOR PLILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PLILORATION NUMBER: US 60/391,777
PRIOR PLILORATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR PLILOR DATE: 2002-06-15
PRIOR PLILOR DATE: 2002-06-16
PRIOR PLILOR DATE: 2002-08-16
PRIOR PLILOR DATE: 2002-08-16
PRIOR PLILOR DATE: 2002-08-16
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PRIOR PLILOR DATE: 2002-08-18

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-594
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Publication No. US20040082026A1
Publication No. US20040082026A1
Publication No. US20040082026A1
APPLICANT: Neces Technologies, Inc.
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: APPLICANT
TITLE OF INVENTION: ALPHA
FILE REFERENCE: 040853-01-5055
                                                         APPLICANT: ZopE, David

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Chen, Xi

APPLICANT: Chen, Xi

APPLICANT: Chen, Xi

APPLICANT: Chen, Xi

APPLICANT: Bowe, Caryn

TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND

TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND

TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND

TITLE OF INVENTION: GRANULOCYTE COLONY

TITLE OF INVENTION: GRANULOCYTE COLONY

TITLE OF INVENTION: GRANULOCYTE COLONY

PRIOR PELING DATE: 2003-04-09

PRIOR PELING DATE: 2001-10-19

PRIOR PELING DATE: 2001-10-19

PRIOR PELING DATE: 2002-06-07

PRIOR PELING DATE: 2002-06-07

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
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SOFWARE: Patentin version 3.2
SEQ ID NO 312
LENGTH: 431
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; ORGANISM: Homo sapiens
US-10-410-962-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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18-08-880-203-2-18DD

336 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 395 396 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 431 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL TYPE: PRT ORGANISM: Homo sapiens Query Match Best Local Similarity Matches 274; Conservat g 원 8 셤 ò ď ठ ò $\stackrel{>}{\delta}$ 셤 ద 215 VVKLISHRECQOPHYYGSEVTTRMLCAADPOWKTDSCQGDSGGFLVCSLQGRMTLTGIVS 240 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 120 276 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 335 180 PCWVISATHCPIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHND 120 281 181 VVKLISHRECQQPHYYGSEVTTYMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240 342 VVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVS 401 221 282 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 341 09 216 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 222 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 1 KPSSPPEELKFOCGOKTLRPRFKIIGGEFTTIENOPWFAAIYRHRGGSVTYVCGGSLIS 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT Gaps . 0 . 0 Query Match 100.0%; Score 1508; DB 12; Length 437; Best Local Similarity 100.0%; Pred. No. 1.1e-145; Matches 276; Conservative 0; Mismatches 0; Indels 0; Length 431; Indels Sequence 4, Application US/10193656

| Publication No. US20030096733A1
| Publication No. US20030096733A1
| Publication No. US2003009673A1
| APPLICANT: W. Tor
| APPLICANT: HOLMAHI, Rikard
| APPLICANT: HOLMAHI, Rikard
| APPLICANT: HOLMAHI, Rikard
| APPLICANT: HOLMAHI, Rikard
| TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ATHRITIS
| FILE REFRENCE: 3810/12577-US3
| CURRENT APPLICATION NUMBER: US/10/193,656
| CURRENT FILING DATE: 2001-07-10
| PRIOR FILING DATE: 2001-07-10
| PRIOR FILING DATE: 2001-07-10
| PRIOR FILING DATE: 2001-07-10
| PRIOR FILING DATE: 2001-07-10
| PRIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: PATCHION VUMBER: US 60/305,182
| SOFTWARE: PATCHION VUMBER: US 60/305,182
| SOFTWARE: PATCHION VUMBER: US 60/305,182
| SOFTWARE: PATCHION VUMBER: US 60/305,182 Query Match 99.8%; Score 1505; DB 14; Best Local Similarity 99.6%; Pred. No. 2.1e-145; Matches 275; Conservative 1; Mismatches 0; 402 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 437 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276 TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
DATABASE ACCESSION NUMBER: GenBank / P00749
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(431)
US-10-193-656-4 LENGTH: 431 181 61 셤 ŏ Q ò g δ g ద d à g ò ઠે ò

181 VVKLISHRECQOPHYYGSEVTTKMLCAADPOWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 240 121 IALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMT 180 61 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 1 KPSSPPBELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 156 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTVVCGGSLIS Gaps 0 Length 431; 2; Indels US-09-244-68B-1

US-09-244-68B-1

Patent No. US20020106775A1

GENERAL INFORMATION:

APPLICANT: Wang, Jieyi

APPLICANT: Wang, Jieyi

APPLICANT: Wang, Jieyi

APPLICANT: Walter, Yack L.

APPLICANT: Walter, Karl A.

APPLICANT: Walter, Karl A.

APPLICANT: Walter, Karl A.

APPLICANT: Walter, Karl A.

APPLICANT: Walter, Karl A.

APPLICANT: Walter, Karl A.

APPLICANT: Walter, Karl A.

APPLICANT: Walter, Karl A.

APPLICANT: Holzman, Thomas F.

ITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE

ITLE REFERENCE: 6310, US. P.

CURRENT APPLICATION NUMBER: US/09/264,468B

CURRENT FILING DATE: 1999-03-06

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastESQ for Windows Version 4.0

SEQ ID NO.

LENGTH: 431 241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEBNGLAL 276 98.8%; Score 1490; DB 9; ilarity 99.3%; Pred. No. 7.3e-144; Conservative 0; Mismatches 2; | CACATOR: Cond Septems | CACATOR: CACA RESULT 19 US-10-282-174-562 ; Sequence 562, Application US/10282174 Page

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RESULT 21
US-10-407-821-3
Sequence 3, Application US/10407821
Sequence 3, Application US/10407821
Sequence 3, Application No. USZ0030219386A1
GENERAL INFORMATION:
APPLICANT: IDELL, STEVEN
TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKED PLEURAL
TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURITS IN RABBITS
CURRENT FILING DATE: 2003-04-04
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/414,202
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
SEQ ID NO 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-10-407-821-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 SKEGRCAQPSKTIQTICLPSMYNDPQPGTSCBITGFGKENSTDYLYPBQLKMTVVKLISH 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 THCFIDYPKKEDYIVYLGRSRINSNIQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR 254
                                        AND METHODS FOR MODULATING MUSCLE CELL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THOFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYREHRGGSVTYVCGGSLISPCWVISAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels 0;
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97.1%; Score 1464; DB 15; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.8e-141;
Matches 268; Conservative 0; Mismatches 0; Indels 00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
97.1%; Score 1465; DB 9; Length 403;
Best Local Similarity 99.6%; Pred. No. 2.5e-141;
Matches 268; Conservative 1; Mismatches 0; Indels
   APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REPERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
FRIOR REPLICATION NUMBER: US 60/212,847
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
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CRGANISM: Homo sapiens
US-09-880-503-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 VVKLISHRECQOPHYYGSEVTIKMLCAADPXWKTDSCQGDSGGPLVCSLQGRMTLTGIVS 395
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Publication No. US20030224380A1
GENERAL INFORMATION:
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Mang, Ain
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Saunders, Aleister J.
APPLICANT: Bertram, Lars
APPLICANT: Bertram, Lars
APPLICANT: Bertram, Lars
APPLICANT: Bertram, Lars
APPLICANT: Bertram, Lars
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Millin, Kristina M.
APPLICANT: Bertram, Lars
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Mallin, Risker, Deborah Lynnson
APPLICANT: Bangson, Andrew Johnson
APPLICANT: Bangson, Andrew Johnson
APPLICANT: Millin, Risker, Deborah Lynnson
APPLICANT: Millin, Risker, Deborah Lynnson
APPLICANT: Bangson, Andrew Johnson
APPLICANT: Bangson, Andrew Johnson
APPLICANT: Bonul 1000
FILE REFERENCE: 37461-3308
CURRENT APPLICATION NUMBER: US 60/338,010
PRIOR FILING DATE: 2001-11-09
PRIOR PLING DATE: 2001-11-09
PRIOR PLING DATE: 2001-11-09
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PRIOR PLING DATE: 2001-11-09
PRIOR PLING DATE: 2001-12-04
PRIOR PLING DATE: 2001-12-04
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PRIOR PLING DATE: 2001-11-09
PRIOR PLING DATE: 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 WGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
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NAME/KEY: VARIANT

LOCATION: 15, 58, 141, 214, 231, 274, 366

OTHER INFORMATION: Xaa = Any Amino Acid
US-10-282-174-562
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US-09-880-503-6
Sequence 6, Application US/09860503
Fracent No. US20020131964A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Ferrandes. Calletine
APPLICANT: Taugles, Land
APPLICANT: Taugles, Lina
APPLICANT: Taugles, Lina
APPLICANT: Taugles Jr. Raymond
APPLICANT: Taugles Jr. Raymond
APPLICANT: Reseals, Luca
APPLICANT: Gerlach, Valerie L
APPLICANT: Gerlach, Valerie L
APPLICANT: Gerlach, Valerie L
APPLICANT: MACDOUGAL!, John R
TITLE OF INVENTION: NOVEL SETNE/THECOING THE SAME
TITLE OF INVENTION: NUMBER: US/09/898,837A
CURRENT FILING DATE: 2001-07-03
FRIOR PAPLICATION NUMBER: U.S.S.N. 60/165,986
PRIOR PAPLICATION NUMBER: U.S.S.N. 60/194,839
PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
PRIOR PLING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ALPSMYNDPQFGTSCEITGFGKEQSTDYLYPPQLKMTVVKLISHRECQQPHYYGSEVTTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 MLCAADPOWKTDSCOGDSGGPLVCSLOGRMTLIGIVSWGRGCALKDKPGVYTRVSHFLPW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 CLPSMYNDPOFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGSSLISPCWVISATHCFIDYPKKEDYIVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDVIVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels 0; Gaps
          APPLICANT: Walter, Karl A.
APPLICANT: Walter, Karl A.
APPLICANT: Severin, Jean M.
APPLICANT: Severin, Jean M.
APPLICANT: Galji, Rohinton
APPLICANT: Johnson Jr., Rohert W.
APPLICANT: Holzman, Thomas F.
TITLE OF INVENTION: HIGHLY CRYSTALLINE URCKINASE
FILE REFERENCE: 6310.US.Pl
CURRENT APPLICATION NUMBER: US/09/264,468B
CURRENT PILING DATE: 1999-03-05
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 23
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: AMO SAPIERS
TYPE: FRT
CORGANISM: Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.4%; Score 1333; DB 9;
99.2%; Pred. No. 4.3e-128;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann, John L.
Burgess, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 244; Conserva
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US-09-898-837A-47
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Sequence 266, Application US/10360101

Sequence 266, Application US/20360101

Publication No. US20040009550A1

Publication No. US20040009550A1

Publication No. US20040009550A1

APPLICANT: Lechnouts, Cornelis J.

TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way

FILE REPRENCE: 2183-5673

CURRENT APPLICATION WUMBER: US 2003-02-07

PRIOR APPLICATION WUMBER: EP 02077066.8

PRIOR FILING DATE: 2003-05-24

NUMBER OF SEQ ID NOS: 309

SOFFWARE: Patentin version 3.1

SEQ ID NO 266

LENGTH: 445
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                                                                                                                                            180
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                          61 HCFIDYPKKEDYIVYLGRSRLNSNIQGEMKFEVENLLILHKDYSADTLAHNDIALLKIRS 120
                                                                                             KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR 188
                                                                                                                                                                                           ECQOPHYYGSEVTTRMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALK 248
128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KPSSPPEE--LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 KPSSPPEEFTLKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSL
                                                                                                                                  121 KEGRCAQPSRTIQTICLPSMYNDPQPGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR
HCFIDYPKKEDYIVYLGRSRLNSNIQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 MTLIGIVSWGRG--CALKDKPGVYTRVSHFLPWIRSHTKEENGLAL 276
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Pred. No. 4.8e-140;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                            DKPGVYTRVSHFLPWIRSHTKEENGLAL 276
                                                                                                                                                                                                                                                                                                                              241 DKPGVYTRVSHFLPWIRSHTKEENGLAL 268
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, OTHER INFORMATION: sequence of urokinase
US-10-360-101-266
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APPLICANT: Wang, Jieyi APPLICANT: Nienber, Vicki L.
APPLICANT: Henkin, Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Seguence
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Best Local Similarity 96.5%;
Matches 276; Conservative
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US-09-264-468B-2
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US-10-106-698-6266
US-10-106-698-6266
Sequence 6266, Application US/10106698
Sequence 6266, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICATION
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: PCFV0800/26524
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PILING DATE: 1999-01-09
PRIOR PILING DATE: 1999-11-03
PRIOR PILING DATE: 1999-11-03
SEQUENTIAL ONS: 8664
SOFTWARE: Patentin Ver. 3.0
SEQUENTIAL ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND ON SECOND 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 SPCWVASAAHCFIQLPEKENYVVYLGQSKESSYNPGEWKFEVEGLILHBYYREDSLAYHN 276
                                                                                                                                                                                                                                                                                                                                          120 DIALLKIRSKEGRÇAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKM 179
                                                                                                                                                                                                                                                                                                                                                                                             180 TVVKLISHRECQOPHYYGSEVTTKMLCAADPOWKTDSCQGDSGGPLVCSLQGRMTLTGIV 239
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                                                           60 SPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHN
    1 KPSSPPEELKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRHRGGS-VTYVCGGSLI
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Publication No. US20040005579A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/10/264,049
PRIOR APPLICATION NUMBER: PCT/US01/18569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 SWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA 275
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Best Local Similarity 90.9
Matches 140; Conservative
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CRGANISM: Homo sapiens
US-10-106-698-6266
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MOTIS, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT PAPLICATION NUMBER: US/10/087,192
CURRENT PILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-03
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PRIOR FILING DATE: 2001-03-03-03
PRIOR FILING DATE:
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Best Local Similarity 99.6%; Pred. No. 1.5e-126;
Matches 240; Conservative 1; Mismatches 0;
PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
PRIOR FILING DATE: 2000-04-13
PRIOR PILING DATE: 2000-09-15
PRIOR PELING DATE: 2000-09-15
PRIOR PAPLICATION NUMBER: U.S.S.N. 60/181,347
PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
PRIOR APPLICATION NUMBER: U.S.S.N. 60/184,195
PRIOR FILING DATE: 2000-02-09
PRIOR PILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
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PRIOR APPLICATION NUMBER: U.S.N. 09/715,427
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Best Local Similarity 71.0
Matches 196; Conservative
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ORGANISM: Mus musculus
US-10-087-192-591
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APPLICANT: Werner, Rolf-Guenther
HITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 SRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 TSQHLLMRIVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRWTLVGIISWGLG 242
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APPLICANT: Aranya Manosroi
APPLICANT: Jiradaj Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production
TITLE OF INVENTION: DATA-Derived the PA or K2S Molecules
TITLE OF INVENTION: DATA-BETIVE 1050/9/987,455
CURRENT PELING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR APPLICATION NUMBER: 60 00-11-14
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 CG-QKTLRPRFKIIGGEFTTIENOPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREC
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: part of the OTHER INFORMATION: recombinant K2S molecule (modified)
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VGRANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: K2S 260-527
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38.7%; Score 583; DB 10;
Best Local Similarity 44.9%; Pred. No. 3.7e-51;
Matches 119; Conservative 39; Mismatches 97;
                                                              FILE REFERENCE: 0652.2180001
CURRENT APPLICATION NUMBER: US/09/987,457
CURRENT FILING DATE: 2001-11-14
FRIOR APPLICATION NUMBER: 60/268,573
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver: 2.1
SERGTH: 268
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Publication No. US20030049729A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-987-457-17
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                                                                                                                                                                                                                                                                                                                                                                                                         162 KPSSPPBELKFQCGQKTLRPRFKIIGGBFTTIENQPWFAAIYRRHRGGSVTYVCGGSLIS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 PCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHND 281
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; Sequence 39, Application US/09997003
; Publication No. US2030203361A1
; GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
    FILE REFERENCE: PAO.031
; CURRENT APPLICATION NUMBER: US/09/997,003
; CURRENT APPLICATION NUMBER: US/09/997,003
; CURRENT APPLICATION NUMBER: DOCU-11-30
; PRIOR APPLICATION NUMBER: PCT/US00/22157
; PRIOR FILING DATE: 2001-11-30
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-13
; RINGR APPLICATION NUMBER: 60/148,680
; RINGR APPLICATION NUMBER: 60/148,680
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; FROID NOS: 56
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                                                                                                                                                                                                                                                                    DB 15; Length 337; 2.5e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 118;
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                                                                                                                                                                                                                                                                                                                      5; Indels
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Pred. No. 1.9e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 IALLKIRSKEGRCAQHPGLYRPSACPRCITIPSL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IALLKIRSKEGRCAQ-----PSRTIQTICLPSM 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.2%; Scor.
100.0%; Pred. No. 10.
10.0%; Mismatches
                                                                                                                                                                                                                                                                       Score 742; DB Pred. No. 2.5e-3; Mismatches
                               60/209,467
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APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
PRIOR FILING DATE: 2001-06-07
PRIOR PELLING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
LENGTH: 337
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.9%;
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100. Matches 107; Conservative
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US-09-997-003-39
                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-264-049-2927
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Best Local
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Length 268;

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APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 GRCAQPSRTIQTICLPSMYNDPQFGTSCELTGFGKENSTDYLYPEQLKMTWVKLISHREC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 SRCAQESSVVRIVCLPPADLQLPDWTECELSGYGKHBALSPFYSERLKEAHVRLYPSSRC 222
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223 TSQHLLNRTVIDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRWTLVGIISWGLG 282
                                                                                                                                                                                                                                                                                                        APPLICANT: Aradys manostol
APPLICANT: Aradys manostol
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production
CURRENT PELICATION NUMBER: US/09/987,455
CURRENT APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 25
SCHUMBER PATENTION OF: 2.1
SEQ ID NO 17
LING DATE: 2000-11-14
SEQ ID NO 17
LINGTHER SCHUMBER: 2001-10-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 CGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGBRFLCGGILISSCWILSAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 CG-OKTLRPREKIIGGBFTTIENOPWFAAIYRRH-RGGSVTYVCGGSLISPCWVSATHC
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OTHER INFORMATION: Description of Artificial Sequence: K2S 220-527
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38.7%; Score 583; DB 10; Length 30
Best Local Similarity 44.9%; Pred. No. 4.5e-51;
Matches 119; Conservative 39; Mismatches 97; Indels
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Publication No. US20030013150A1
GENERAL INFORMATION:
APPLICANT: Manogroi, Aranya
                                                                                                                                                                                                                       Sequence 17, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
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ORGANISM: Artificial Sequence
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Sequence 16, Application US/09987457

Publication No. US2003001150A1

GENERAL INFORMATION

APPLICANT: Manosroi, Jiradej

APPLICANT: Tayapiwatena, Chatchai

APPLICANT: Tayapiwatena, Chatchai

APPLICANT: Werner, Rolf-Guenther

TITLE OF INVENTION Methods for Large Scale Protein Production in Prokaryotes

TITLE OF INVENTION NUMBER: US/09/987,457

CURRENT FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-02-15

PRIOR FILING DATE: 2001-01-14

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTION UNDER: 2000-11-14

NUMBER OF SEQ ID NOS: 18

LENGTH: 208

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                                                                                                                                                                                                                                                            131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYFFQLKMTVVKLISHREC 190
                                                                                                                                                                                                                                                                                                                                                                                                       QQPHYYGSEVTTKMLCAAD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRG 244
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                                                                                                                                             70
                                                                                                                                                                      13 CG-QKTLRPRFKIIGGEFTTIENQPWPAAIYRRH-RGGSVTYVCGGSLISPCWVISATHC
                                                                                                                                             13 CG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHC
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                                                                                                   97; Indels 10;
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                                                         Length 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: recombinant K2S molecule (modified)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%; Score 583; DB 10;
44.9%; Pred. No. 4.5e-51;
tive 39; Mismatches 97;
                                                       ; Score 583; DB 10;
; Pred. No. 3.7e-51;
39; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALKDKPGVYTRVSHFLPWIRSHTK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCKDVPGVYTKVTNYLDWIRDNMR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                         38.7%;
44.9%;
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                                                         Ouery Match
Best Local Similarity 44.9%
Matches 119; Conservative
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US-09-987-457-16
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Best Local
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SAPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goelz, Friedrich
APPLICANT: Goelz, Friedrich
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryot,
FILE REPERENCE: 655.2.280001
CURRENT APPLICATION NUMBER: 60/268,573
FRICR FILING DATE: 2001-11-14
FRICR FILING DATE: 2001-02-15
FRICR FILING DATE: 2000-11-14
FRICR FILING DATE: 2000-11-14
FRICR FILING DATE: 2001-02-15
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        Best Local Similarity 44.9%; Pred. No. 4.9e-51;
Matches 119; Conservative 39; Mismatches 97; Indels
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ORGANISM: Artificial Sequence
FEAUNISM: Artificial Sequence
FEAUNISM: COHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: recombinant K2S molecule (modified)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 CALKDKPGVYTRVSHFLPWIRSHTK 269
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Sequence 13. Application US/09987457

Publication No. US20030013150A1

GENERAL INFORMATION:
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; Sequence 12. Application US/09987455
; Publication No. US20030049729A1
; GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Georz
APPLICANT: Friedrich Georz
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
TITLE OF INVENTION: DNA-DER: US/09/987,455
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT APPLICATION NUMBER: G0.1-11-14
PRIOR FILING DATE: 2001-01-14
PRIOR FILING DATE: 2001-01-14
; PRIOR FILING DATE: 2001-11-14
; SPRIOR FILING DATE: 2001-11-14
; SPRIOR FILING DATE: 2001-01-13
; SPRIOR DATE: 2001-01-13
; SPRIOR DATE: 2001-01-13
; SPRIOR DATE: 2001-11-14
; SPRIOR PARE: PATENTING DATE: 2001-11-14
; SPRIOR PATENTING DATE: 2001-11-14
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; OTHER INFORMATION: Description of Artificial Sequence: K2S 197-527
US-09-987-455-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: part of
OTHER INFORMATION: recombinant K28 molecule
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Best Local Similarity 44.9%; Pred. No. 4.9e-51;
Matches 119; Conservative 39; Mismatches 97;
FILE REFERENCE: 0652.2180001
CURRENT APPLICATION NUMBER: US/09/987,457
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,573
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
LENGTH: 331
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Length 331

DB 10;

38.7%; Score 583;

Query Match

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APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Mechods for Large Scale Protein Production in Prokaryotes
FILE REFERENCE: 0652.218001
CURRENT APPLICATION NUMBER: US/09/987, 457
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; OTHER INFORMATION: Description of Artificial Sequence: K2S 193-527,
; OTHER INFORMATION: modified
US-09-987-455-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.7%; Score 583; DB 10; Length 335; 44.9%; Pred. No. 5e-51; tive 39; Mismatches 97; Indels 10
                                                                                                                                                                                                                                                 APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Reiddich Goetz
APPLICANT: Rolf-Guenther Werner
ITLE OF INVENTION: Methods for Large Scale Production of
ITLE OF INVENTION: Methods for Large Scale Production of
ITLE OF INVENTION: MAD-Derived tPA or K2S Molecules
FILE REPERBORS: 6652.230001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT APPLICATION NUMBER: 60/268,574
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR APPLICATION NUMBER: GB 0027779.8
PRIOR PILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 335
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                           310 CGQKDVPGVYTKVTNYLDWIRDNMR 334
CALKDKPGVYTRVSHFLPWIRSHTK
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Sequence 12. Application US/09987457

Publication No. US20030013150A1

GENERAL INFORMATION:
                                                                                                                                                      Sequence 14, Application US/09987455
Publication No. US20030049729A1
GENERAL INFORMATION:
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Matches 119; Conservative
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131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPBQLKMTVVKLISHREC 190
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OTHER INFORMATION: modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 339;
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                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: recombinant K2S molecule (modified)
US-09-987-457-12
                                                                                                                                                                                                                                                                                                                                                                                                                                  38.7%; Score 583; DB 10;
44.9%; Pred. No. 5.1e-51;
tive 39; Mismatches 97;
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Pred. No. 5.1e-51;
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Sequence 13, Application US/09987455
Publication No. US20030049729A1
GENERAL INPORMATION:
APPLICANT: Aranya Manosroi
APPLICANT: Charchal Tayaplwatana
APPLICANT: Triadej Manosroi
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Folf-Guenther Wenner
TITLE OF INVENTION: Methods for Large Scale Pro-
FILE REFERENCE: 052.2190011
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT APPLICATION NUMBER: 05/268,574
PRIOR APPLICATION NUMBER: G0/268,574
PRIOR PILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE PATENTIN OF VERSER: GB 0027779.8
SOFTWARE PATENTIN OF VERSER: GB 0027779.8
SOFTWARE PATENTIN OF VERSER: GB 0027779.8
SOFTWARE PATENTIN OF VERSER: GB 0027779.8
SOFTWARE PATENTIN OF VERSER: GB 0027779.8
SOFTWARE PATENTIN OF VERSER: GB 0027779.8
PRIOR APPLICATION NUMBER: 60/268,573
PRIOR FILING DATE: 2001-02-15
PRIOR PEDLICATION NUMBER: GB 00 27 782.2
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 12
LENGIH: 339
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                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 119; Conservative
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APPLICANT: Manosroi, Aranya
APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryote
FILE REFERENCE: 0652,18000,18/09/987,457
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 05/268,573
PRIOR APPLICATION NUMBER: G0/268,573
PRIOR PILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 343
TYPE: DOT
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198 SRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRC
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APPLICANT: Jiradej Manosroi
APPLICANT: Chardel Tayagiwatana
APPLICANT: Chatchai Tayagiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
TITLE OF INVENTION: 0012-119001
CURRENT APPLICATION UNMERS. US/09/987,455
CURRENT FILING DATE: 2001-11-14
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38.7%; Score 583; DB 10;
Best Local Similarity 44.9%; Pred. No. 5.1e-51;
Matches 119; Conservative 39; Mismatches 97;
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Sequence 15, Application US/09987455 Publication No. US20030049729A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Publication No. US20030013150A1

GENERAL INFORMATION:

APPLICANT: Manosroi, Jiradej

APPLICANT: Manosroi, Jiradej

APPLICANT: Tayapiwatana, Chatchai

APPLICANT: Goetz, Friedrich

APPLICANT: Werner, Rolf-Guenther

TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes

FILE REFERENCE: 0652.2180014

CURRENT APPLICATION NUMBER: US/09/987,457
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140 FQERFPPHHLTVILGRTYRVVPGESEQKFEVEKYIVHKEFDDDT---YDNDIALLQLKSDS 197
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194 SRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRC 253
                                                                                                                                               71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
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Best Local Similarity 44.9%; Pred. No. 5.1e-51;
Matches 119; Conservative 39; Mismatches 97;
  Mismatches
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PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: GB 00 27 782.2
PRIOR PILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 14
LENGTH: 343
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 44.9%
Matches 119; Conservative
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APPLICANT: Jizadej Manosroi
APPLICANT: Jizadej Manosroi
APPLICANT: Chardrai Tayapiwatana
APPLICANT: Chardrai Tayapiwatana
APPLICANT: Chardrai Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: MADER: US/09/987,455
CURRENT FILING DATE: 2001-11-14
PRIOR PLICATION NUMBER: 60/268,574
PRIOR PLICATION NUMBER: 60/268,574
PRIOR PLICATION NUMBER: GD 0027779.8
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
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7 OTHER INFORMATION: Description of Artificial Sequence: K28 191-527,
7 OTHER INFORMATION: modified
02-09-987-455-16
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OTHER INFORMATION: Description of Artificial Sequence: K2S 191-527,
OTHER INFORMATION: modified
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38.7%; Score 583; DB 10; Length 343;
Best Local Similarity 44.9%; Pred. No. 5.1e-51;
Matches 119; Conservative 39; Mismatches 97; Indels 10;
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38.7%; Score 583; DB 10; Length 343;
Best Local Similarity 44.9%; Pred. No. 5.1e-51;
Matches 119; Conservative 39; Mismatches 97; Indels 10
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR FLILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: GB 0027779.8
PRIOR FILLING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 15
LENGTH: 343
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Publication No. US20030049729A1
GENERAL INFORMATION:
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ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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                                       71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
                                                            131 GRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPRQLKMTVVKLISHREC 190
                                                                                                                                    191 QOPHYYGSEVITKMLCAAD----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRG 244
                                                                                                                                                                                                                      258 TSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLG 317
80 CGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.7%; Score 583; DB 10; Length 354; 44.9%; Pred. No. 5.4e-51; cive 39; Mismatches 97; Indels 1
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329 CGQKDVPGVYTKVTNYLDWIRDNMR 353

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                                                                                       APPLICANT: Jiradej Manosroi
APPLICANT: Charchai Tayapiwatana
APPLICANT: Charchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Ride-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 052,2190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: K2S 174-527 US-09-987-455-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.7%; Score 583; DB 10;
44.9%; Pred. No. 5.4e-51;
tive 39; Mismatches 97;
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Patent No. US20020061576A1
GENERAL INFORMATION:
APPLICANT: RUBEN, SIEVEN M.
APPLICANT: BANEN, RIBHARD
TITLE OF INVENTION: TISSUE PLASMINOGEN ACT:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 CALKDKPGVYTRVSHFLPWIRSHTK 269
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PRIOR FILLING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: GB 0027779.
PRIOR FILLING DATE: 2000-11-14
Sequence 11, Application US/09987455
Publication No. US20030049729A1
APPLICANT: Aranya Manosroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.99
Matches 119; Conservative
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SOFTWARE: Patentin Ver.
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71 FIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKE 130
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TITLE OF INVENTION: Tissue Plasminogen Activator-Like Protein
FILE REPERENCE: PF370C1
CURRENT APPLICATION NUMBER: US/10/102,704
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/084,491
PRIOR FILING DATE: 1998-05-27
PRIOR APPLICATION NUMBER: 60/048,000
PRIOR PLIING DATE: 1997-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,491A
FILING DATE: 27-MAY-1998
ATTORNEY/ACCTION: 435
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Pred. No. 5.7e-51;
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                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF3.
TELECOMMUNICATION INFORMATION:
TELEFROM: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 3.2
LENGTH: 372
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Best Local Similarity 44.9%;
Matches 119; Conservative 35
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amino acid
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GARRAL INTOLARDAY: Manostoi, Aranya
APPLICANT: Manostoi, Jiradej
APPLICANT: Manostoi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Goetz, Friedrich
APPLICANT: Werhods
TILE OF INVENTION: Methods for Large Scale Protein Production in Prokaryot
TILE OF INVENTION: WINBER: US/09/987,457
CURRENT APPLICATION NUMBER: US/09/987,457
CURRENT APPLICATION NUMBER: 00/268,573
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2001-11-14
FRIOR FILING DATE: 2000-11-14
FRIOR FILING DATE: 2000-11-14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 527
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Publication No. US20030049729A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Wenner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT FILING DATE: 2001-11-14
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38.7%; Score 583; DB 10;
Best Local Similarity 44.9%; Pred. No. 9.1e-51;
Matches 119; Conservative 39; Mismatches 97;
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                                                245 CALKDKPGVYTRVSHFLPWIRSHTK 269
                                                                        US-09-987-457-18
; Sequence 18, Application US/09987457
; Publication No. US20030013150A1
; GENERAL INFORMATION:
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APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: MAN-Derived tPA or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT PAPLICATION NUMBER: U3/09/987,455
CURRENT FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LINGTH: 377
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                                                  Gaps
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Best Local Similarity 44.9%; Pred. No. 5.8e-51;
Matches 119; Conservative 39; Mismatches 97; Indels 10
  ch 38.7%; Score 583; DB 13; Length 372; 1 Similarity 44.9%; Pred. No. 5.7e-51; 119; Conservative 39; Mismatches 97; Indels 10
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Publication No. US20030049729A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-987-455-8
  Query Match
Best Local Si
Matches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 ISQHILINRIVTDIMALCAGDIRSGGPQANLHDACQGDSGGPLVCLNDGRWTLVGIISWGLG 501
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38.7%; Score 583; DB 12; Length 527;
Best Local Similarity 44.9%; Pred. No. 9.1e-51;
Matches 119; Conservative 39; Mismatches 97; Indels 1
                                                                                                                                                                                                                                                          Query Match 38.7%; Score 583; DB 10; Length 527; Best Local Similarity 44.9%; Pred. No. 9.1e-51; Matches 119; Conservative 39; Mismatches 97; Indels 1
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Sequence 1, Application US/10432842

Publication No. US20040071707A1

GENERAL INFORMATION:
APPLICANT: Veronica A. CARROLL
APPLICANT: Adrian L. HARRIS

APPLICANT: ROY BICKNELL
APPLICANT: ROY BICKNELL
APPLICANT: Pat PRICE
TITLE REPRENCE: 117-450 / N.75507A SER

CURRENT APPLICATION NUMBER: US/10/432,842

CURRENT FILING DATE: 2003-09-27

PRIOR APPLICATION NUMBER: PCT/GB01/05244

PRIOR APPLICATION NUMBER: PCT/GB01/05244

PRIOR APPLICATION NUMBER: 2001-11-28

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: MS WORC

SEQ ID NO 1

LENGTH: 527
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: GB 0027779.8
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 19
LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 CALKDKPGVYTRVSHFLPWIRSHTK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: Homo sapiens
                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-987-455-19
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OY 131 GRCAQPERTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHREC 190
Db 382 SRCAGESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVEYPSSRC 441
OY 191 QQPHYYGSBYTTKMLCAAD-----PQWKT-DSCQGDSGGPLVCSLQGRMTLTGIVSWGRG 244
Db 442 TSQHLINRTVTDNMLCAGDTSGGPQANLHDACQGDSGGPLVCLNDGRWTLVGIISWGLG 501
OY 245 CALKDKGVYTRVSHPLPWIRSHTK 269
Db 502 CGQKDVPGVYTKVTNYLDWIRDMNR 526
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Search completed: May 25, 2004, 15:03:44 Job time : 53.3138 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 25, 2004, 14:48:05; Search time 19:1096 Seconds (without alignments) 745.636 Million cell updates/sec Run on:

US-09-880-503-5 Perfect score:

1508 1 KPSSPPBELKFQCGQKTLRP.....VSHFLPWIRSHTKBENGLAL 276 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Issued_Patents_AA:*

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22. /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Appl	Appl	Appl	Appl	Appl	Appli	18, Appl	Appl	Appli	19569	Appli	5188829	Appl	Appli	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appli
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		ΙD	US-08-093-741-83	-80-	-08-560	-08-967-024	-967-024	-08-087	38-286-748B-	3-153-79	US-09-181-816-1	5219569-2	9-10	5188829~1	US-08-560-098A-47	US-09-403-736-2	US-07-942-157A-3	US-08-560-098A-45	ņ	-560	-08-944-	-08-560-098A	-08-811-949-5	ď	-94	-949-3	US-08-811-949-57	-11	US-08-217-618-1
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ALIGNMENTS

US-08-093-741-83

19-08-093-741-83

1 Sequence 83, Application US/08093741

2 Sequence 83, Application US/08093741

3 Patent No. 5681721

3 APPLICANT: STEPPENS, GERD J.

APPLICANT: HEINELDER, JCHANNES

APPLICANT: SCHNEIDER, JCHANNES

APPLICANT: SCHNEIDER, JCHANNES

APPLICANT: SCHNEIDER, JCHANNES

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APPLICANT: SCHNEIDER, JCHANNES

APPLICANT: SCHNEIDER, JCHANNES

APPLICANT: SCHNEIDER, JCHANNES

TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN

TITLE OF INVENTION: INTESTING BFFECT

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:

ADDRESSEE: PV-ORD STEEPT, N. W. Suite 700

CITY: Weshington, D.C.

COUNTRY: U.S.

ZIP: 20005

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 NSQALGLGRHNYCRNPDGDARPWCHVMKDRKLTWEYCDMSPCSTCGLRQYKRPQFRIKGG
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Q28138;

Q1.NOV-1997 (Rel. 35, Last sequence update)

15-WAR-2004 (Rel. 43, Last annotation update)

15-WAR-2009 plasminogen activator precursor (EC 3.4.21.68) (tPA)

(t-pa) (t-plasminogen activator).
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3; Mismatches 150;
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Matches 175; Conser
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MEDINE=2288257; PubMed=12477932;

XI TISSUE=Mammary gland;

XI TISSUE=Mammary gland;

XI Ausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XI Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Didtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Didtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Scheure B.D., Dickson M.C.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Krzywinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N.,

Butterfield Y.S.N.,

Butterfield Y.S.N.,

Butterfield Y.S., Woore R.D.,

Butterfield Y.S.N.,

Butterfiel
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                                                                                                                                                                                                                                                                                                                                                                                     310 HKEFDDDT--YNNDIALLQLKSDSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKH 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 KSSSPFYSEQLKEGHVELYPSSRCAPKFLFNKTVTNNMLCAGDTRSGELYPNVHDACQGD 427
121 PLVQECMYHDCADGKLKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS-VT 178
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-! FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodelling and degratedation, in cell migration and many other physiopathological events.

-! CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
                                                 199 FTSESCSVPVCS----KATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGER
                                                                                                                                                                                                                                                                                                           234 HKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKE
                                                                                                                                                       YVCGGSLISPCWVISATHCFIDYPKKEDYI-----VYLGRSRLNSNTQGEMKFEVENLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 NSTDYLYPEQLKMTVVKLISHRECQOPHYYGSEVTTKMLCAADPQWKT-----DSCQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickles R.J., Darrow A.L., Strickland S., "Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA and its expression during F9 teratocarcinoma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPA_MOUSE STANDARD; PRT; 559 AA.
P11214: Q91VP2;
01-JUL-1989 (Rel. 11, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-Suc-type plagminogen activator precursor (EC 3.4.21.68) (tPA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOGPLVCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSH 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 263:1563-1569(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=88087303; Pubmed=2826484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (t-PA) (t-plasminogen activator)
PLAT.
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TPA MOUSE
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                                                          FURTHER
3 AFTER
             by a disulfide
                                        -!- SUBCELLULAR LOCATION: Secreted, extracellular.
-!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURT.
PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFT.
ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-!- MISCELLANBOUS: Bands to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMARY; SM00020; Tryp. SPC; 1.

PROSITE; P800022; EGF 1; 1.

PROSITE; P801025; EGF 2; 1.

PROSITE; P801025; EGF 2; 1.

PROSITE; P801025; EGF 2; 1.

PROSITE; P801025; FIRRONECTIN 1; 1.

PROSITE; P801012; KRINGLE 1; 2.

PROSITE; P800114; TRYPSIN DOM; 1.

PROSITE; P800114; TRYPSIN HIS; 1.

PROSITE; P8001135; TRYPSIN HIS; 1.

PROSITE; P8001135; TRYPSIN HIS; 1.

PLAGMINOGEN ACTIVATION; HYDRONERS; Serine protease; Glycoprotein; Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Plasma; Kringle; EGF-like domain; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMINOGEN
PLASMINOGEN
             held
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRONECTIN TYPE-I.
               SUBUNIT: Heterodimer of chain A and chain B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-TYPE
TISSUE-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRINGLE 1.
KRINGLE 2.
                                                                                                                                                                                                                                                                                                                                         EMBL, J03520; AAA40470.1; -.
EMBL, BC011256; AAH11256.1; -.
PIR, A29941; A29941.
HSSP, P00750; 1A5H.
MEROPS, S01.232; -.
MEROPS, S01.232; -.
INCEPPO; IPR009003; Cys Ser trypsin.
INCEPPO; IPR006209; EGF_like.
INCEPPO; IPR006209; EGF_like.
INCEPPO; IPR006210; ISGF.
INCEPPO; IPR001254; Peptidase S1.
INCEPPO; IPR001254; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
INCEPPO; IPR001314; Peptidase S1.
PRINTS; PR000131; KINGLE.
PRODOM; PR000189; KRINGLE.
PRODOM; PR000189; KRINGLE.
PRODOM; PR000189; KRINGLE.
PRODOM; PR000180; KRY 2.
SWART; SM00130; KR; 2.
SWART; SM00020; TYYP_SPC; 1.
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plasminogen to form plasmin
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80 HIVPVNSCSEPRCFNGGTCWQAVYFSDF-VCQCPAGYTGKRCEVDTRATCYEGQGVTYRG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOVPSN-CD----CLINGGICVSNKYFSNIHWCNCPKKFGGQHCEIDKSKICYEGNGHFYRG
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37.2%; Score 840.5; DB 1; Length 477;

Best Local Similarity 43.0%; Pred. No. 2.8e-60;

Matches 175; Conservative 56; Mismatches 147; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53616 MW; AA06FD1739C10E5E CRC64;
                                                                                                                                                                                                                       N-LINKED (GLCNAC. ..).
/FIId=CAR_000027.
N-LINKED (GLCNAC. ..).
/FIId=CAR_000028.
                   SIMILARITY.
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     398
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
A Schleuning W.D., Bode W.;

"Catalytic domain structure of vampire bat plasminogen activator: a
"Catalytic domain structure of vampire bat plasminogen activator: a
molecular paradigm for proteolysis without activation cleavage.";

E Biochemistry 36.13483-13493 (1997).

E Biochemistry 36.13483-13493 (1997).

-!- FUNCTION: Probably sesential to support the feeding habits of this exclusively haematophagous animal. Potent thrombolytic agent.

-!- FUNCTION: Probably sesential to support the feeding habits of this plasminogen to form plasmin.

-!- CATALYTIC STORING ACTIVITY: Specific cleavage of Arg-|-Val bond in plasmin.

-!- ENZYME REGULATION: Activity toward plasminogen is stimulated in the krimgle domain apparently mediates fibrin-induced activity.

-!- SUBJUNT: Monomer:

-!- SUBJUNT: Monomer:

-!- SIMILARITY: Contains I EGF-like domain.

-!- SIMILARITY: Contains I Eff-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1.
FIBRONECTIN TYPE-I.
EGF-LIKE.
KRINGLE.
SERING PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                       this
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M63987; AAA31591.1; -

EMBL; M63986; AAA31591.1; -

EMBL; M63986; AAA31591.1; -

EMBL; M63986; AAA31591.1; -

PIR; JGS057; JGS059;

RECPE; JRN006209; EGF_like.

InterPro; IPR006209; EGF_like.

InterPro; IPR006309; EGF_like.

InterPro; IPR006309; EGF_like.

InterPro; IPR006309; EGF_like.

InterPro; IPR006309; EGF_like.

INTERPRO; IPR006309; EGF_like.

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DOMAIN
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253 NSQALGLGRHNYCRNPDGDAKPWCHVWKDRKLTWEYCDMSPCSTCGLRQYKQPQFRIKGG 312
                                                                                                                                                                                                                                                                                                                                           313 LFTDITSHPWQAAIFVKNKRSPGERFLCGGVLISSCWVLSAAHCFVERFPPHHLKVVLGR 372
                                                                                                                                                                                                                                                                                                                                                                                                                            330 KMLCAADP----QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRV 384
                                  34 QCHSVPVRSCSEPRCFNGGTCQQALYFSDF-VCQCPDGFVGKRCDIDTRATCFEGQGITY 132
                                                                                59 RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYV-QV 117
                                                                                                        129 -----CGOKTLR-PRFKIIGG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 SMYNDPQF----GTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTT 329
                                                                                                                                                                                                     193 GKYTTEFCSTPACPKGPTEDCYVGKGVTYRGTHSFTTSKASCLPWNSMILIGKTYTAWRA 252
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LD URTI DESRO

AC 198119;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MRA-2004 (Rel. 43, Last annotation update)

DT 15-MRA-2004 (Rel. 43, Last annotation update)

DT 15-MRA-2004 (Rel. 43, Last annotation update)

DE 3alivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA B salivary plasminogen activate alpha 1)

DE alpha-1).

T-4"s rotundus (Vampire bat).

Thordata, Craniata, Vertebrata, Euteleostomi;
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    3 BLHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY
                                                                                                                                                                                                                                                                                                                      155 EFTTIENOPWFAAIY-RRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGR
                                                                                                                                                                                                                                                                                                                                                                                                       214 SRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRÇAQPSRTIQTICLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donner P.;
"Pleaminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=92019018, PubMed=1937019;

Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,

Alagon A., Donner P., Schleuning W.D.;

The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-1).
Desmodus votundus (Vampire bat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
NCBL_TaxID=9430;
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MEDLINE-931393059; W.D.Med=1109059; Schleuning W.-D., Alagon A., Boldol W., Bringmann P., Petri T., Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                               GL------KPLVQECMV------
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TISSUE=Salivary gland;
MEDLINE=98022741; PubMed=9354616;
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                                            Gaps
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EGGF-LIKE

KRINGLE 1.

KRINGLE 2.

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TISSUE-TYPE PLASMINOGEN ACTIVATOR A
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37.3%; Score 841.5; DB 1; Length 559;
Best Local Similarity 36.5%; Pred, No. 2.8e-60;
Matches 180; Conservative 65; Mismatches 143; Indels 105;
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7DBD3809C1D1C921 CRC64;
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                                                                                                   STRUCTURE BY NMR OF KRINGLE 2.
MEDLINE-90122799; PubMed=2558718;
Bycon 1.-J.,, Kelley R.F., Liinas M.;
Bycon 1.-J.,, Kelley R.F., Liinas M.;
I'M NMR structural characterization of a recombinant kringle 2 domain from human tissue-type plasminogen activator.";
Biochemistry 28:9350-9360(1989).
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STRUCTURE BY NWR OF KRINGLE 2.
MEDLINE-92106329; PubMed-1762144;
MEDLINE-92106329; PubMed-1762144;
MEDLINE-1-J.L., Lilinas M.;
"Solution structure of the tissue-type plasminogen activator kringle
"Solution structure of the tissue-type plasminogen activator kringle
2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE=91200042; PubMed=1901/89;
Byeon I.-J.L., Kelley R.F., Lilnas M.;
"Kringle-2 domain of the tissue-type plasminogen activator. IH-NMR assignments and secondary structure.";
Eur. J. Biochem. 197:155-165(1991).
                           MEDLINE=92118803; Pubmeda1310033; de Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Tulinskly A. Westbrook M.L., Kossiakof A.A.; "Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4-A resolution."; Biochemistry 31:270-279(1992).
                                                                                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                                                             38.0%; Score 858.5; DB 1; Length 562; 37.5%; Pred. No. 1.2e-61; Live 56; Mismatches 152; Indels 97
                    CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
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Matches 183; Conservative
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RAPEDLINE=90130448; PubMed=2105315;

RAPEDLINE=90130448; PubMed=2105315;

RAPEDLINE=90130448; PubMed=2105315;

RAPEDLINE=90130448; PubMed=2105315;

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RAPEDLINE=90130448; PubMed=2105315;

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PROFIN: THE SIRGLE CHAIN, ALMOST FULLY ACTIVE BNZYME, CAN BE FURTHER PROCESSED INTO A TWO-THAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.

SINGSELLAMBOOUS: Bands to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.

SIMILARITY: Contains I EGF-like domain.

SIMILARITY: Contains 1 Eibronectin type I domain.

SIMILARITY: Contains 2 kringle domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rati
                                                                                                                                                                                                                                                                                             (tPA)
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Ny T., Leonardsson G., Hsueh A.J.W.;
"Cloning and characterization of a cDNA for rat tissue-type
                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
11-NOV-1993 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68)
(t-PA) (t-plasminogen activator).
559 AA
PRT;
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EMBL, M31197, AAA42261.1; -.
EMBL, M31185, AAA42261.1; JOINED.
EMBL, M31186; AAA42261.1; JOINED.
EMBL, M31187; AAA42261.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen activator.";
DNA 7:671-677(1988).
STANDARD;
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SEQUENCE FROM N.A.
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JOINED

AAA42261.1; AAA42261.1; AAA42261.1;

AAA42261.1; JOINED AAA42261.1; JOINED

JOINED

AAA42261.1;

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

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SEQUENCE FROM N.A.

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"The structure of the human tissue-type plasminogen activator gene:

"The structure of the human tissue-type plasminogen activator gene:

"The structure of the human tissue-type plasminogen activator gene:

"The structural of thirton and exon structures to functional and

structural domains.";

Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
[2]
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TISSUE=Fetal lung;
MEDLINE=88262579; PubMed=3133640;
Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
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"The human tissue plasminogen activator gene.";
J. Biol. Chem. 261:6972-6985(1986).
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MEDLINE=83169656; PubMed=6572897;
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SEQUENCE OF 31-562 FROM N.A.
MEDLINE-91291340; PubMed-1368681;
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
"Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
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Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
                                                                                                                                                                                                                                                                                                                                                                            the human tissue-type plasminogen g its 5' flanking region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray crystal structure of single-chain human tPA.";
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MalbiNE=28109620; PubMed=6682760;
Walbin P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.;
"Purification and characterization of a melanoma cell plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
MEDLINE-96200985, PubMed-8613982;
Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91159408; PubMed=1900431;
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"Itseue plasminogen activator has an O-linked fucose attached to
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                                                                                                                                                                                                                                                                                                  Thompson D., Tizard R.,
                                        Josephson S.;
"Isolation of cDNA sequences coding for a part of
                                                                                                          plasminogen activator.";
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Fisher R., Waller E.K., Grossi G.,
Schleuning W.-D.,
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MEDLINE=85000468; PubMed=6433976;
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                                                                                                                                                                                                                    SEQUENCE OF 1-36 FROM N.A.
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187 SPCWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHH 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 NDIALLQLKSGSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLK 333
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MEDLINE=2315262; PubMed=6337343;
MEDLINE=2315262; PubMed=6337343;
Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A.,
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Goeddel D.V., Collen D.;
Glondel D.V., Collen D.;
"Cloning and expression of human tissue-type plasminogen activator
CDNA in E. Coli.";
Nature 301:214-221(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
BY SIMILARITY.
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                        699B5E675B162CBF CRC64;
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     Query Match
Best Local Similarity 44.19
Matches 175; Conservative
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R InterPro; IPR009003; Cys Ser_trypsin.

R InterPro; IPR006209; EGF_like.

R InterPro; IPR006210; IEGF.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001214; Peptidase_S1.

R Pfam; PF000051; Kringle; 1.

R Pfam; PF000089; trypsin; 1.

R PROMIS; PR000122; CHYMOTRYPSIN.

R PRINTS; PR00018; KRINGLE.

R SMART; SM0018; KRINGLE.

R SMART; SM0018; EGF; 1.

R PROSITE; PS00020; EGF=1; 1.

R PROSITE; PS00020; EGF=1; 1.

R PROSITE; PS00021; EGF=1; 1.

R PROSITE; PS00021; EGF=2; 1.

R PROSITE; PS00021; EGF=2; 1.

R PROSITE; PS00021; KRINGLE_1; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS00021; KRINGLE_2; 1.

R PROSITE; PS000134; TRYPSIN JES; 1.

R PROSITE; PS000134; TRYPSIN JES; 1.

R PROSITE; PS000134; TRYPSIN JES; 1.

R PROSITE; PS000134; TRYPSIN JES; 1.

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R PROSITE; PS000134; TRYPSIN JES; 1.

R PROSITE; PS000134; TRYPSIN JES; 1.
                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDLINE=93393059; PubWed=1309059; Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T., Schleuning W.-D., Alagon A., Boidol W., Baldus B., Witt W., Donner P.; Paracraschmar J., Haendler B., Langer G., Baldus B., Witt W., Donner P.; Paraminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity."; Pacad. Sci. 67:395-403(1992).
--- FUNCTION: Probably essential to support the feeding habits of this exclusively haematophagous animal. Probable potent thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
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SALIVARY PLASMINOGEN ACTIVATOR BETA.
EGF-LIVE.
KRINGLE.
                              SEQUENCE FROM N.A.

TISSUE=Sallyary gland;

MEDLINE=92039036; PubMed=1937019;

Kraetzschmar J., Handler B., Langer G., Boidol W., Bringmann P.,

Alagon A., Donner P., Schleuning W.D.;

"The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";

Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SUBUNIT: Monomer.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
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CHARGE RELAY SYSTEM (1
CHARGE RELAY SYSTEM (1
CHARGE RELAY SYSTEM (1)
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                                                                                                                                                MERCPE'S GOL-232; -.

RICETPE'S GOL-232; -.

RICETPE'S GOL-232; -.

RICETPE'S IPRO00209; EGF_11ke.

RICETPE'S IPRO00209; EGF_11ke.

RICETPE'S IPRO00201; Kringle.

RICETPE'S IPRO00201; Kringle.

RICETPE'S IPRO00201; Kringle.

RICETPE'S IPRO00201; Kringle.

REPEM: PF00009; EGF; 1.

PFM: PF00009; EGF; 1.

REPEM: PF00009; TRINGLE.

REPEM: PRO0019; KRINGLE.

REPEM: PRO0019; KRINGLE.

REPEM: SMOO19; KRINGLE.

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REPEM: SMOO19; KRINGLE.

REPEM: SMOO19; KRINGLE.

REPEM: SMOO19; KRINGLE.

REPEM: SMOO19; KRINGLE.

REPEM: PRO0118; EGF 2; 1.

REPEM: PROSITE; PS00021; KRINGLE.

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                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- ENZYME REGULATION: Activity toward plasminogen is stimulated in the presence of fibrin I.
-!- DOMAIN: Monomer.
-!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin, and the kringle domain apparently mediates fibrin-induced stimulation of activity.
-!- SIMILARITY: Belongs to peptidase family SI.
-!- SIMILARITY: Contains I EGF-like domain.
-!- SIMILARITY: Contains I fibronectin type-I domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
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                                                              MEDLINE~93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
Biol. Chem. 264:17947-17952(1989).
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EMBL; J05082; AAA31596.1; -.
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121
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PIR; JS0598; JS0598.
HSSP; P98119; 1A5I.
                                            CHARACTERIZATION.
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                                                                                                                                      Conner P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 LKPLVQECMYHDCADGKLKFQCG-QKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGS- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 DYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQPGTSCEITGFGKENS 29±
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ELHQVP----SNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 OCHTVPVKSCSELRČFNGGTCWQAASPSDF-VCOCPKGYTGKQCEVDTHATCYKDQGVTY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 SKFILBFCSVPVCS----KATCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VTYVCGGSLISPCWVISATHCFID-YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHK 23:
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1-FEB-1996 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Saliyary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
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Desmodus rotundus (Vampire bat).
Desmodus rotundus (Vampire bat).
Desmodus rotundus, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
NCBI_TAXID=9430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.5%; Score 868.5; DB 1; Length 477; 43.7%; Pred. No. 1.6e-62; Live 60; Mismatches 148; Indels 21;
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KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53719 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 43.7 tes 178; Conservative
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  417 4
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477 AA;
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28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
(G-plasminogen activator).
Edallus (Chicken).
Edallus (Chicken).
Edaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J0518; AAA49131.1; EMBL; J0518; AAA49131.1; EMBL; J0518; AAA49131.1; EMBL; J05188; AAA49131.1; EMBL; J05188; AAA49131.1; EMBL; J05188; AAA49131.1; EMBL; J05188; AAA49131.1; EMBL; J05188; AAA49131.1; EMBL; J0518; ABSO95; S01.231; EMBRO95; S01.231; EMBRO95; S01.231; EMBRO95; S01.231; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EMBRO95; EM
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CHAIN A (BY SIMILARITY).
GCHAIN B (BY SIMILARITY).
                                                                                                                                                                                                 MEDINES-9101085; Pubmed=2295632;
MEDINES-91010185; Pubmed=2295632;
MESINES-90101085; Pubmed=2295632;
The chicken urokinase-type plasminogen activator gene.";
The chicken urokinase-type plasminogen activator gene.";
J. Balo. Chem. 265:1339-1344[1990],
-1- CATALYTIC ASPENSE TO Peptidase of Arg-|-Val bond in plasminogen to form plasmin.
-1- SIMILARITY: Relongs to peptidase family $1.
-1- SIMILARITY: Contains 1 EGF-1ike domain.
-1- SIMILARITY: Contains 1 kringle domain.
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CONNECTING PEPTIDE.
SERINE PROTEASE.
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                                                                                                                                     Gallus.
NCBI_TaxID=9031;
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188 PCWVISATHCFID----YPKKEDYIVYLGRSRLNSNTQGEMKFEVENLLLHKDYSADTLA 243
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01-FBE-1996 (Rel. 33, last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
28-FBE-2003 (Rel. 41, Last annotation update)
28-Ivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA alpha-2) (BAT-PA) (T-plasminogen activator).
Desmodus rotundus (Vampire bat).
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Desmodontinae; Chiroptera; Microchiroptera; Phyllostomidae;
                                                                                                                                                                                                                                                                                          44.2%; Score 997; DB 1; Length 434;
47.8%; Pred. No. 6.5e-73;
rative 64; Mismatches 122; Indels 18; Gaps
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TISSUB=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Kraerzschmar J., Haendlar B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
"The planshingen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
BY SIMILARITY.

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SY CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

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MEDLINE-90036867; PubMed-2509450;
Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
"Isolation, characterization, and cDNA cloning of a vampire bat salivary plasminogen activator.";
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AC P15638;
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                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (UPA)
PLAU.
                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=817944; PubMed=2985183;
MEDLINE=817944; PubMed=2985183;
Belin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y.,
Reich E., Kocher H.P., Duvoisin R.M.;
"Cloning, nucleotide sequencing and expression of cDNAs encoding
mouse urokinase-type plasminogen activator.";

Bur. J. Blochem. 148:225-232(1985).
402
                         431
360 MTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLA
               389 PTLSGIVSWGSGCAEKNKPGVYTRVSYFLNWIQSHIGEENGLA
                                                                                          433 AA
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INCEPTO; IPR009003; Cys_Ser_trypsin.
INCEPTO; IPR009003; Cys_Ser_trypsin.
INCEPTO; IPR006209; EGF like.
INCEPTO; IPR006210; EGF.
INCEPTO; IPR00823; Pept SIA_uPA.
INCEPTO; IPR00124; Peptidase_S1.
INCEPTO; IPR00134; Peptidase_S1.
INCEPTO; IPR00134; Peptidase_S1A.
PEam; PP00089; trypsin; 1.
PIRSF; PR00722; CHYMOTEXPSIN.
PRINTS; PR00722; CHYMOTEXPSIN.
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SMART; SM00181; EGF; 1.
SMART; SM00130; KR; 1.
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                                                                                         STANDARD;
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HSSP; P00749; 1KDI
MEROPS; S01.231;
                                                                                        UROK MOUSE
P06869;
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CHAIN A (BY SIMILARITY).
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CHAIN B (BY SIMILARITY).
EGF-LIKE.
KRINGLE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
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        PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; FALSE_NEG.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50020; KRINGLE 1; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
PROSITE; PS00135; TRYPSIN_HIS; FALSE_NEG.
PROSITE; PS00135; TRYPSIN_HIS; FALSE_NEG.
PROSITE; PS00135; TRYPSIN_SER, 1.
Plasminogen activation; Hydrolaee; Serine protease; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                      72.1%; Score 1626.5; DB 1; Length 70.2%; Pred. No. 1.4e-123; ive 50; Mismatches 61; Indels
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(Rel. 14, Last sequence update)
                                                                                                                          EGF-like domain; Zymogen; Signal 20 POTENTIAL.
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 SM00020; Tryp SPc; 1.
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les 283; Conservative
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 GKENSTDYLYPEQLMMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGG
                                                                                LILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGISCEITGF
                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 24, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
                                                                                                                                                                                                                                                                                                                   STRAIN=Fischer 344;

MEDLINE-22233409; PubMed=1568219;

Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,

Kefford R.F.;

Transcriptional and posttranscriptional activation of urokinase

plasminogen activator gene expression in metastatic tumor cells.";

Cancer Res. 52:2489-2496(1992).
                                                                                                           403
                                                                                                                      PLVCTIQGRLTLTGIVSWGRDCAMKYKPGVYTRVSKFLPWINTHTRGEINLVL 433
                                                                                                          PLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEENGLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR009003; Cys_Ser_tryps
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR008293; Pept_SlA_uPA.
InterPro; IPR001254; Peptidase_Sl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X63434; CAA45028.1; -. EMBL; X65651; CAA46601.1; -. PIR; S24604; S18932. HSSP; P00749; IKDU.
                                                                                                                                                                               STANDARD;
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VCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 HDCADGKLK-----FQCGQKTLRPRFKIIGGEFTTIENQPWFAALYRRHRGGS-VTY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
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POTEMULAL.

UROKINASB-TYPE PLASMINOGEN ACTIVATOR.
CHAIN A (BY SIMILARITY).
CHAIN B (BY SIMILARITY).

EGF-LIKE.
CONNECTING PEPTIDE.
SERINE PROTEASE.
BY SIMILARITY.
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llarity 72.2%; Pred. No. 5.6e-126;
Conservative 45; Mismatches 58;
InterPro; IPR001314; Peptidase_S1A
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modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).

EMBL; L03546; AAA51419.1; -.
EMBL; X65801; CAA59796.1; -.
PIR; JN0560; JN0560.
HASSP; 800749; ILWW.
MEROPS; 801.231; -.

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440
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                                                                                        OPWFAALYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQ 221
                                                                                                                                                                                                   320
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                                                                         -----KLKFQCGQKTLRPRFKIIGGEFTTIEN 161
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                                         RGKANTNTGGR PCLPWNSATVLLNTYHAHRPDALQLGLGKHNYCRNPDNQRRPWCYVQVG
                                                                                                                                          QPWFAAIYRRHRGGSVTYVCGGSLISPCWVSATHCFINYQQKEDYIVYLGRQTLHSSTH
                                                                                                                                                                                                                                                                                          321 GASCEIVGFGKEDPSDYLYPEQLKMTVVKLVSHRECOOPHYYGSEVTTKMLCAADPQWKT
                                                                                                                                                                           GEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQF
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                         RGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG
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 SHELHQESGASNCGCLNGGKCVSYKYFSNIQRCSCPKKFQGEHCEIDTSQTCFEGNGHSY
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UROK BOVIN
STANDARD; PRT; 433 AA.
UROK BOVIN
OSSE9209, 2028209;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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MEDLINB=932161119; PubMed=8385052;
Kraetzschmar J., Haendler B., Kojima S., Rifkin D.B.,
Schleuning W.-D.;
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                                                                                                                                                  DR InterPro; 128009003; Cye_Ser_trypsin.

DR InterPro; 128009003; Cye_Ser_trypsin.

DR InterPro; 128006209; EGF_like.

DR InterPro; 12800012; Kringle.

DR InterPro; 12800124; Peptidase_S1.

DR InterPro; 12800124; Peptidase_S1.

DR Pfam; PF000651; Kringle; 1.

DR Pfam; PF000651; Kringle; 1.

DR PRINTS; PR00122; CHYMOTEXPSIN.

DR PRINTS; PR00109; Kringle; 1.

DR PRNTS; PR00109; Kringle; 1.

DR PRNTS; PR00109; Kringle; 1.

DR PROSITE; PS00020; Tryp_SPC; 1.

DR PROSITE; PS00020; Tryp_SPC; 1.

DR PROSITE; PS00020; EGF_1; 1.

DR PROSITE; PS00020; EGF_1; 1.

DR PROSITE; PS00021; KRINGLE 2; FALSE_NEG.

DR PROSITE; PS00021; KRINGLE 2; I.

DR PROSITE; PS00021; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

RATIGNE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

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KRINGLE

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CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

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CHAIN A (BY SIMILARITY).
CHAIN B (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney;
Ravn P., Berglund L., Petersen T.E.;
"Cloning and characterization of the bovine plasminogen activators uPA and tPA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and tPA.";
Int. Darity U. 5:605-617(1995).
-!-CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- INDUCTION: By retinoic acid.
-!- SIMILARITY: Delongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bovine urokinase-type plasminogen activator and its receptor: cloning and induction by retinoic acid.";
Gene 125:177-183(1993).
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R MERCPE'S SOLISIF. -

R InterPro; IPR006209; EGF like.

R InterPro; IPR006209; EGF like.

R InterPro; IPR000201; Kringla.

R InterPro; IPR001254; Peptidase S1.

R InterPro; IPR001254; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R INTE; PR00722; CHYMOTRENIN.

R PR00722; CHYMOTRENIN.

R RRINTS; PR00725; CHYMOTRENIN.

R RRINTS; PR000136; KRINGLE.

R ROSITE; PS000020; KRY SEC: 1.

R ROSITE; PS000020; TryP SEC: 1.

R ROSITE; PS000021; RRINGLE S1.

R ROSITE; PS000021; RRINGLE S1.

R ROSITE; PS000021; RRINGLE S1.

R ROSITE; PS000021; RRINGLE S1.

R ROSITE; PS000021; RRINGLE S1.

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Q -> H (IN REF. 1; CAA26511).
A -> GS (IN REF. 1; CAA25806).
EB32FCRF501321EE CRC64;
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81.0%; Score 1827.5; DB 1;
Best Local Similarity 78.1%; Pred. No. 9.9e-140;
Matches 329; Conservative 32; Mismatches 41; I
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-!- SIMILARITY: Belongs to peptidase family -!- SIMILARITY: Contains 1 EGF-like domain. -!- SIMILARITY: Contains 1 kringle domain.
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442 AA;
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MEDLINE=85087954; Pearson D., Altus M.S., Reich E.;
Nagamine Y., Pearson D., Altus M.S., Reich E.;
"cDNA and gene nucleotide sequence of porcine plasminogen activator.";
Nucleic Acids Res. 12:9525-9541(1984).
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (UPA)
PLAU.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPLVCSIQGHVTLTGIVSWGRGCALKDKPGVYTRVSRFLPWIHSHTRBQNGLAL
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-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                     92.6%; Score 2090; DB 1; Length 433; 90.6%; Pred. No. 7.3e-161; Live 17; Mismatches 10; Indels 12
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433 AA;
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TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            292
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                                                                                                                                                                                                                                                                                                                                                                                                                    SNEIHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRG 80
of two chains, A and B. The high molecular mass form contains a long chain A. Cleavage occurs after residue 155 in the low molecular mass form to yield a short Al Chain.

PHARMACENTICAL: Available under the name Abbokinase (Abbott). Used in Pulmonary Embolism (PE) to initiates fibrinolysis.

SIMILARITY: Belongs to peptidase family S1.

SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 LHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGK
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1016227;
1016227;
101627190 (Rel. 14, Created)
101-APR-1990 (Rel. 14, Last sequence update)
101-APR-1990 (Rel. 14, Last annotation update)
10164/10189-1799 plasminogen activator precursor (EC 3.4.21.73) (uPA)
(U-plasminogen activator).
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                                                                                                                                                                                                                                                                                                                                                      99.2%; Score 2240; DB 1; Length 431; 97.8%; Pred. No. 6.2e-173; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                  EMBL, AF37730; AAK53822.1; --
EMBL, BC011375; AAH13575.1; --
EMBL, K03226; AAC97138.1; --
EMBL, K02286; AAAC1252.1; --
EMBL, A21571; CAA01559.1; --
EMBL, A21571; CAA0159.1; --
PIR, A00931; UKHU.
PDB; 1KDU; 31-OCT-93.
                                                                                                                                                                                           EMBL, X02419, CAA26268.1; -...
EMBL, M15476, AAA61253.1; -...
EMBL, D00244, BAA01175.1; -...
EMBL, D1143; BAA0119.1; -...
EMBL, X02760; CAA26535.1; -...
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MEDLINE=97218551; PubMed=9065988;
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                     238 NSWFCVGFLEGGKDSCQRDSGGPVVCNGQ----LQGVVSWGHGCAWKNRPGVYTKVYNYV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 CGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISAT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 HCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 KEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 P----AQYITRISPVCLASSNEALTEGLICVTTGWGRLSGVGNVTPAHLQQVALPLVTVN 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 OCRQ--YWGSSITDSMICAGGA--GASSCQGDSGGPLVCQKGNTWVLIGIVSWGTKNCNV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chymotrypsin-like proteinase (EC 3.4.21.-) CTRL-1 - human chymotrypsin-like proteinase (EC 3.4.21.-) CTRL-1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) Cort. C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 22-Jun-1999 C;Accession: 138136 # S; Solheim J; Kristensen, T; Kolsto, A.B.; Prydz, H. Hum. MOl. Genet. 2, 1589-1595, 1993 A;Title: A tight cluster of five unrelated human genes on chromosome 16q22.1. A;Reference number: 138135; MUID:94093544; PMID:8268911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
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                                                                                                                                                               209 VYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: 138136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-264 <RES>
A;Cross-references: EMBL:X71874; NID:g406226; PIDN:CAA50710.1; PID:g406228
                                                   150 KIIGGEFTTIENQ-PWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYI
                                                                                                                                                                                                                                                                                                                                 182 TISLPTA--PPAAGTECLISGWGNTLSFGADYPDELKCLDAPVLTQAECKAS--YPGKIT
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Indels
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A;Introns: 18/1; 52/3; 79/2; 106/3; 167/1; 211/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolasin; trypsin homology
F;34-257/Domain: trypsin homology <TRY>
F;75,121,214/Active site: His, Asp, Ser #status predicted
87;
Mismatches
38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:CTRL
A;Cross-references: GDB:204061
Conservative
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les 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 DWIK 297
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92;
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Best Local S:
Matches 90
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Matches
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A;Reference number: A90958; MUID:87217962; PMID:3646943
A;Accession: A26823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: S33496
R;Wiegand, U.; Corbach, S.; Minn, A.; Kang, J.; Mueller-Hill, B.
submitted to the EMBL Data Library, March 1993
A;Description: Identification, cloning and characterization of a cDNA encoding a human A;Reference number: S33496
A;Accession: S33496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --VSLIDKIQLGCLPAAGTILPNNYVCYVTGWGR-LQTNGASPDILQQQQLLVVDYATCS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 KPGWWGSTVKTNMICAGG-DGIISSCNGDSGGPLNCQGANGQWQVHGIVSFGSSLGCNYY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 IDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 RCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 QPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVC-SLQGRMTLTGIVSWGR--GCALK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 CGQKTLRPRF-KIIGGBFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trypsin (EC 3.4.21.4) IV form a - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 15-Aug-1997
                                                N; Alternate names: pancreatopeptidase E
C; Species: Sus scrofa domestica (domestic pig)
C; Accession: A26823
C; Accession: A26823
R; Kawashima, I; Tani, T.; Shimoda, K.; Takiguchi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gabs
                                                                                                                                                                                                                                                                                                   A.Molecule type: mRNA
A.Residues: 1-269 «KAM»
A.Residues: 1-269 «KAM»
A.Residues: 1-269 «KAM»

A.Cross-references: GB:N16651; NID:g164441; PIDN:AAA31027.1; PID:g164442
C;Superfamily: trypsin; trypsin homology
C;Reywords: hydrolase; serine proteinase
F:1-6/Domain: signal sequence #status predicted «SIG»
F:17-28/Domain: propeptide #status predicted «PRO»
F:29-269/Product: elastase II #status predicted «NAT»
F:29-265/Domain: trypsin homology TRY»
F:73,121,216/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
16.8%; Score 380; DB 2; Length 269;
Best Local Similarity 34.1%; Pred. No. 3.6e-22;
Matches 88; Conservative 50; Mismatches 106; Indels
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A;Cross-references: GDB:335300
A;Map position: 7435-7435
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;81-296/Domain: trypsin homology <TRY>
F;120,164,257/Active site: His, Asp, Ser #status predicted
                           - pig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 DKPGVYTRVSHFLPWIRS 393
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37.7%;
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C;Genetics:
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-304 <WIE>
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A;Gene: GDB:HGF
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                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-728 <MIY>
A; Residues: 1-728 <MIY>
A; Residues: 1-728 <MIX>
A; Cross-references: GBH M29145; NID: g184041; PIDN: AAA52650.1; PID: g306846
B; R; Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A; Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy A; Reference number: A39006; MUID: 91110540; PMID: 1824873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A39006
;Molecule type: mRNA;
;Residues: 1-161,167-728 <RUB>
;Residues: 1-161,167-728 <RUB>
;Cross-references: GB:M55379
;Experimental source: embryonic lung
;Experimental source: embryonic lung
;Experimental source: commun. 75, 660-667, 1991
jochem. Biophys. Res. Commun. 75, 660-667, 1991
;Title: Identification of the N-terminal residue of the heavy chain of both native and ;Reference number: PH0114; MUID:91207365; PMID:1826837
;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.; Jochem. Biophys. Res. Commun. 172, 321-327, 1990
Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor. Reference number: A36677; MUID:91025062; PMID:2148836
Accession: B36677
Molecule type: RNA
Residues: 1-728 <883>
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: 1-288, "ET' < HAR>
A,Residues: 1-288, "ET' < HAR>
A,Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Blochem: 197, 15-22, 1991
                                                                                                                                                            Cross-references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032
                                                                                                                                                                                                                                                                                                                                                                                                      Status: not compared with conceptual translation
                                                                                                                                                                                                 Molecule type: mRNA;
Residues: 1-167,167-728 <SB4>
Cross-references: EMBL:X16323
Experimental source: leukocyte
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A,Status: preliminary
A,Molecule type: mRNA
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A;Map position: 7421.1-7421.1
A;Drtons: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 69/: A;Drtons: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 69/: C;Complex: disulfide-bonded heterodimer of chains derived from the same precur: C;Function:
A;Doscription: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Kgywords: alternative splicing; glycoprotein; growth factor; heterodimer; kr; F;1-31494,495-728/Product: hepatocyte growth factor #status experimental <AGN-F;2494/Domain: kringle homology <AR1-F;2494/Domain: kringle homology <AR2-F;2105-389/Domain: kringle homology <AR3-F;31-288/Domain: kringle homology <AR3-F;31-288/Domain: kringle homology <AR3-F;31-288/Domain: kringle homology <AR3-F;320-389/Domain: kri
A;Cross-references: EMBL.X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
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A;Title: Tumor cytotoxic factor/hepatccyte growth factor from human fibroblast. A;Reference number: 152253; MUID:92062058; PMID:1835383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 IGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKE--DYIV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 HEHDMTPENFKCKDLRENYC-RNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 GNGHFYRGKASTDIMGRPCLPWNSAIVLQQIYHAH---RSDALQLGLGKHNYCRNP-DNR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- MVHDCADGKLKFQCGQKTLRPRFKI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NELHQVPSNCDC--LNGGTCVSNKYFSNIHWC-----NCPKKFGGQ--HCEIDKSKTCYE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 GNGKNYMGNLSQTRSGLTCSMWDKN---MEDLHRHIFWEPDASKL---NENYCRNPDDDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 YLGRSRLNSNTQGEMK--FEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 TTKWLCAADPQWKTDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHP
                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
*Molecule type: mRNA
A;Residues: 161-166 <SHI>
A;Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g237997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 728;
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16.9%; Score 382; DB 1; Length 720
Best Local Similarity 26.9%; Pred. No. 7.4e-22;
Matches 114; Conservative 62; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 RRPWCYVQVGLKPL----VQEC----
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Gaps

22;

72

253

313

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AAHCGV----KTSDVVVAGEFDQGSDEENIQVLKIAQVFKNPKFNMFTV--RNDITLLKL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: JHO579
A,Molecule type: DNA
A,Residues: 1-728 <5EK>
A,Molecule type: DNA
A,Residues: 1-728 <5EK>
A,Cross-references: DDBJ:D90318
A,Note: the authors translated the codon GAA for residue 662 as Gly
A,Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to J7EID, March 1991
A,Bescription: Organization of the human hepatocyte growth factor-encoding gen
A,Reference number: JU0333
A,Accession: JU0333
A,Molecule type: DNA
A,Residues: 1-481, RT', 484-728 <5E2>
R;Weidner: K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.;
R;Weidner: K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.;
R;Weidner: K.M.; Arakaki, V.S.A. 88, 7001-7005; 1991
A;Title: Evidence for the identity of human scatter factor and human hepatocyt
A;Reference number: A41140; MUID:91334393; PMID:1831266
A;Accession: Mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon mexicon m
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A;Title: Organization of the human hepatocyte growth factor-encoding gene. A;Reference number: JH0579; MUID:91340155; PMID:1831432
J. Biol. Chem. 259, 14265-14270, 1984
A,Tille: Isolation and sequence of a rat chymotrypsin B gene.
A,Reference number: A22658, MUID:85054881; PMID:6209274
A,Reference number: A22658, MUID:85054881; PMID:6209274
A,Rocession: A22658
A,Rocession: A22658
A,Rocidues: 1-263 «BEL»
A,Cross-references: GB:K02298; NID:g203653; PIDN:AAA98732.1; PID:g203654
C,Genetics: 18/1; 52/3; 79/2; 105/3; 166/1; 210/3
A,Introns: 18/1; 52/3; 79/2; 105/3; 166/1; 210/3
C,Superfamily: trypsin; trypsin homology
C,Keywords: hydrolase; pancreas; prodicted «SIG»
F,1-18/Domain: signal sequence #status predicted «SIG»
F,1-18/Domain: trypsin B #status predicted «MAT»
F,34-256/Domain: trypsin homology «TRY»
F,34-256/Domain: trypsin homology «TRY»
F,34-256/Domain: trypsin homology «TRY»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 FQCGQKTLRPRF----KIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 ATHCFIDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-728 <WEI>
A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSTPAVYSRVTALMPWVQ 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33...
Best & 87; Conservative
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A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
B;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
B;Introns: 24/1; 79/3; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 24/2; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig. 10-175/Domain: Edr. homology < EG2>
Fig. 10-175/Domain: Edr. homology < EG2>
Fig. 10-175/Domain: Edr. homology < EG2>
Fig. 10-175/Domain: activation peptide #status experimental < APT>
Fig. 10-211/Domain: activation peptide #status experimental < APT>
Fig. 10-211/Domain: activation peptide #status experimental experimental rypsin homology < TRY>
Fig. 49, 56, 58, 61, 62, 67, 68, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental Fig. 60, 101-120, 112-131, 140-151, 147-160, 162-175, 183-319, 238-254, 373-387, 398-426/D Fig. 60, 112/Disulfide bonds: #status predicted acid (App) #status experimental Fig. 19, 20, 355/Fainding site: carbohydrate (Apr.) (covalent) #status experimental Fig. 12-12/Cleavage site: Arg. Leu (thrombin) #status experimental Fig. 12-12/Cleavage site: Arg. Leu (thrombin) #status predicted Fig. 12-12/Cleavage site: Asp. Ser #status predicted Fig. 13, 299, 402/Active site: His, Asp. Ser #status predicted Fig. 13, 299, 402/Active site: Asp. (covalent) (partial) #status atypical
                                            A.Contents: annotation, beta-hydroxyaspartic acid
C.Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also forcomment: Protein C is synthesized in the liver as a single chain precursor, which is obin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
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N;Alternate names: chymotrypsinogen B
C;Species: Rattus norvegicus (Norway rat)
C;pacies: Rattus norvegicus (Norway rat)
C;pacession: A2.658
C;Accession: A2.658
R;Bell, G.I.; Quinto, C.; Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter,
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.larity 28.2%; Pred. No. 3.8e-22;
Conservative 50; Mismatches 147; Indels 1
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              number: A44606; MUID:92184750; PMID:1544894
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bin, which cleaves a dodecapeptide from the
C.Genetics:
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A.Gene: GDB:PROC
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A; Residues: '0', 107-461 <FOS2>
A; Residues: '0', 107-461 <FOS2>
A; Residues: '0', 107-461 <FOS2>
R; Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzky, J.; Crabtree, G.R.;
Nucleic Acids Res. 13, 5233-5247, 1985
A; Title: The structure and evolution of a 461 amino acid human protein C precu
A; Reference number: A23789; MUID:85269639; PMID:2991859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 NDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFG---KENSTDYLYPE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 CKVVESSD-----C--TTKINARIVGGINSSLGEWPWQVSL--QVKLVSQNHMCGGSI
                                                                                                                                                                                                                                                                                                                                                                                                     186 ISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 IGROWILTAAHCFDGIPYPDVWRIYGGILNLSEITNKTPPSSIKELIHQKYKMSEGSY-
                                                                                                                                                                                                        126 CMVHDCADGKLKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 QLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTL
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A, Molecule type: DNA
A, Residues: 1-461 < F001>
A, Residues: 1-461 < F001>
A, Cross-references: GB:M11228, NID:g190333, PIDN:AAA60166.1; PID:g190334
A, From Community, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
B, Proc., Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A, Fitle: Evolution and organization of the human protein C gene.
A, Reference number: A25426; MUID:86120978; PMID:3511471
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A.Mosledule trype: DNA
A.Residules: 1-445,'L',446-461 <PLU>
A.Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
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Residues: 1-461 <BEC>
;Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
                                                                                                    25;
Length 638;
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rroc. Natl. Acad. Sdi. U.S.A. 81, 4766-4770, 1984
rroc. yfftle: Characterization of a cDNA coding for human protein C.
;Reference number: A21781; MUID:84272714; PMID:6589623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 TGIVSWGRGCALKDKPGVYTRVSHPLPWIRSHTKEENGLAL
          Query Match 17.1%; Score 386.5; DB 1; Best Local Similarity 31.7%; Pred. No. 2.9e-22; Matches 89; Conservative 58; Mismatches 109.
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F;210-109/Domain: apple repeat <API>
F;10-109/Domain: apple repeat <API>
F;210-289/Domain: apple repeat <API>
F;210-289/Domain: apple repeat <API>
F;21-380/Domain: apple repeat <API>
F;21-380/Domain: apple repeat <API
F;31-380/Domain: apple repeat <API
F;31-380/Product: plasma Kallikrein light chain #status experimental <NAII>
F;31-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F;396/Binding site: carbohydrate (Asn) (covalent) #status predicted F;396/Binding site: carbohydrate (Asn) (covalent) #status predicted F;396/Binding site: Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 17638 ~SEI>

>Cross-references: GBN30282; NID:g205010; PIDN:AAA41463.1; PID:g205011

>NOTE: part of this sequence, including the amino ends of both the heavy and light chai

>Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, N.G.

Jochim. Biophys. Acta 999, 103-110, 1988

Jittle: Rat plasma kallikrein: purification, NH(2)-terminal sequencing and development

>Reference number: S06851; MUID:90089457; PMID:2597701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 20.45;391-413 <PAQ>
A; Residues: 20.45;391-413 <PAQ>
B; Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, R.; Lazur
DNA Cell Biol. 8, 563-574, 1989
A; Title: The cDNA structure of rat plasma kallikrein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: coagulation factor XI; trypsin homology (Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflationselventin: signal sequence #status predicted <SIG>
120-39/Product: plasma kallikrein heavy chain #status experimental <WAII>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.; Rougeon, F.; Lazur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;Cross-references: GB:M58590; NID:g206721; PIDN:AAA42069.1; PID:g206722;;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex ';Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a lare linked by one or more disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasma kallikrain (BC 3.4.21.34) precursor - rat
NiAlternate names: Fletcher factor; kininogenin; serum kallikrein
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Sep.1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C.Accession: A39180; A3320; 56851; I53041; 806852
R.Beaubien, G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay, M.; Chretien, M.; Seidah, I A;Telfe: Gene structure and chromosomal localization of plasma kallikrein.
A;Reference number: A39180; MUID:91129236; PMID:1993180
                                                                                                                                                                                   337 KDACKGDSGGPHATRFRGTWFLTGVVSWGEGCAAAGHFGIYTRVSRYTAWLRQLMGHPPS 396
     SGWGQLLERG---VTARKLMVVLVPRLLTQDCLQQSRQRPG--GPVVTDNMFCAGYSDGS 336
                                                                                                    TDSCQGDSGGPLVCSLQGRWTLTGIVSWGRGCALKDKFGVYTRVSHFLPWIR---SHTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Accession: A33180
A)Accession: DNA
A)Accession: DNA
A)Accession: Boar
A)Coss-references: GB:J05315
A)Coss-references: GB:J05315
A)Coss-references: GB:J05315
B)Coss-references: GB:J05315
B)Coss-references: GB:J05315
B)Coss-references: GB:J05316
B)Coss-references: GB:J05316
B)Coss-reference number: A33320; MUD:90091743; PMID:2598771
A)Accession: A33320
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A; Mocleaule type: protein
A; Residues: 58-62, 7X., 64-68 ~MCM>
A; Mocleaule type: protein
A; Mocleaule type: protein
A; Mocleaule type: protein
A; Mother the residue designated 'X' was determined to be hydroxyaspartic acid
R; Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.;
J. Biochem. 104, 867-869, 1988
A; Title: A new trisaccharide sugar chain linked to a serine residue in bovine b of
A; Title: A new trisaccharide sugar chain linked to a serine residue in bovine b of
A; Reference number: A44566, MUID:89213999; PMID:3149637
A; Contents: annotation
A; Mote: structure and location of covalently bound carbohydrate
C; Function:
A; Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor X in the presence of calcium and tissue factor X in A; Pathway: blood coagulation factor X; EGF homology; Gla domain homology; Trypsin
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology acid.
C; Superfamily: coagulation factor VIII a light chain #status experimental acid.
F; 1-152/Product: coagulation factor VIII a heavy chain #status experimental acid.
F; 1-152/Product: coagulation factor VIII heavy chain #status experimental acid.
F; 1-152/Product: coagulation factor VIII heavy chain #status experimental
F; 1-152, 10-16, 10, 20, 25, 26, 29, 34, 35/Modified site: gamma-carbohydrate (Ser) (covalent) #status experimental
F; 1-152, 10-16, 10, 20, 25, 26, 29, 34, 35/Modified site: carbohydrate (Ser) (covalent) #status experimental
F; 103, 242, 344, Active site: Arg-Is (coagulation factor XIIa) #status experimental
F; 103, 242, 344, Active site: Arg-Is (coagulation factor XIIa) #status experimental
F; 103, 242, 344, Active site: Arg-Is (coagulation factor XIIa) #status experimental
F; 103, 242, 344, Active site: His, Arg-Gly (coagulation factor XIIa) #status experimental
                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Mesidues: 1-407 < TAK;
R; Mesidues: 1-407 < TAK;
R; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochen. Biophys. Res. Commun. 115, 8-14, 1983
A; Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent
A; Reference number: A20274; MUID:83308813; PMID:6688526
A; Accession: C20274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                           sequence.
                   coagulation factor VIIa (EC 3.4.21.21) - bovine Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Dos primigenius taurus (cattle)
Ciscession: A31979; C20274
Ritakeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga J. Biol. Chem. 263, 14868-14877, 1988
A; Title: Bovine factor VII. Its purification and complete amino acid sequence A; Reference number: A31979; MUID:89008362; PMID:3049594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLPWNSATVLQQTYHAHRSDALQLGLGKHNYC-RNPDNRRRPWCYVQVGLKPLVQECMVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSK--TCYEGNGHFYRGKASTDTMGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chymotrypsin (EC 3.4.21.1) 2 precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 27-ul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C;Accession: A21195
R;Pinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7490, 1983
A;Title: Identification of cDNA clones encoding secretory isoenzyme forms: sequence dete
A;Reference number: A21195; MUID:84170253; PMID:6584866
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                                                                                                                                                           150 KIIGGEFITIENO-PWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYI 208
                                                                                                                                                                                                                                                                          268
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                                                                                                                                                                                             209 VYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQ
                                                                                                                                                                                                                                                                                                                                                                        269 TICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                        125 TLLLPSAC - ASAGTECLISGWGNTLSSGVNYPDLLQCLVAPLLSHADCEAS - YPGOIT
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-23 < PIN.
A; Cross-references: GB: KO1173; NID:g163945; PIDN:AAA30841.1; PID:g163946
C; Superfamily: trypsin; trypsin homology
C; Keyworsa: hydrolase; protein digestion; serine proteinase
F; 34-256, Domain: trypsin homology < TRY>
F; 75, 120, 213/Active site: His, Asp, Ser #status predicted
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                                                           DB 2; Length 247;
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F;63,107,200/Active site: His, Asp, Ser #status predicted
                                                                                                        83;
                                                   17.3%; Score 390.5; DB 38.1%; Pred. No. 5e-23; ive 41; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKDKPGVYTRVSHFLPWIR 392
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                                                                         Local Similarions

193; Conservative
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                                                   Query Match
Best Local S:
Matches 93
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A;Reference number: A93755
A;Reference number: A93755
A;Contents: annotation; revisions
B;Contents: annotation; revisions
A;Contents: annotation; revisions
A;Contents: annotation; revisions
A;Contents: annotation; revisions
A;Reference number: A00550; MUID:75146445; PMID:1092332
A;Contents: annotation; revisions
A;Reference number: A00550; MUID:75146445; PMID:1092332
A;Contents: annotation; revisions
A;Reference number: A00550; MUID:75146445; PMID:1092332
A;Contents: annotation; revisions
A;Reference number: A9254; MUID:76072097; PMID:512
A;Contents: annotation; X-ray crystallography; binding sites for calcium, sub: A;Reference number: A92554; MUID:76072097; PMID:512
A;Contents: annotation; X-ray crystallography; binding sites for calcium, sub: A;Contents: annotation; X-ray crystallography; binding sites for calcium, sc;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.
C;Comment: Autocatalytic cleavage after Lips-6 leads to beta-trypsin by releas; a spseudotrypsin. A cleavage may also occur after Arg-105.
C;Guperfamily: trypsinogen gangeriamidigation; serine proteinase; zymogen: F;1-229/Product: trypsinogen #status experimental cZYM.
F;1-229/Product: trypsinogen #status experimental cZYM.
F;1-200/product: trypsinogen #status experimental cZYM.
F;1-200/product: trypsinogen #status experimental cZYM.
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F)7-222/Domain: trypsin homology <TRY>
F)7-131,132-229/Product: alpha-trypsin #status experimental <MPT>
F)7-131,132-229/Product: alpha-trypsin #status experimental
F)6-7/Clasavage site: Lys-11e (enteropeptidase) #status experimental
F)13-143,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental
F)6,90,183/Active site: His, Asp, Ser #status experimental
F)8,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status experimental
F)131-132/Cleavage site: Lys-Ser (autolytic) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for bovine pancreatic
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C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 KIVGGYTCGANTVPYQVSL-----KSGYHFCGGSLINSQWVVSAAHCY----KSGIQV
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A;Notecule type: mRNA
A;Residues: 1-247 cHUB-
A;Residues: 1-247 cHUB-
A;Residues: 1-247 cHUB-
A;Cross-references: EMBL:X54703; NID:g829; PIDN:CAA38513.1; PID:g830
C;Superfamily: trypsin; prypsin homology
C;Superfamily: trypsin; trypsin digestion; serine proteinase
F;24-239/Domain: trypsin homology <TRY>
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17.5%; Score 394.5; DB 1; Length 229;
Best Local Similarity 37.4%; Pred. No. 2.2e-23;
Matches 91; Conservative 41; Mismatches 86; Indels 25
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R;le Huerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.;
Eur. J. Biochem. 193, 767-773, 1990
A;Title: Isolation and nuclectide sequence of cDNA clone
A;Reference number: S13813; MUID:91065383; PMID:1701147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 WIR 392
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                                                                                                                                                                                                                                                        trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2.P29) - chicken

N.Alternate names: trypsinogen II
C;Species: Gallus gallus (chicken)
C;Date: 23-Aug.1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
C;Accession: $55066; $72347
R;Wang, K.; Gan, L.; Lee, I.; Hood, L.
B;Ochem. J. 307, 471-479, 1995
A;Title: Isolation and characterization of the chicken trypsinogen gene family.
A;Reference number: $55066
A;Molecule type: mRNA
A;Residues: 1-248 <WMNL
A;Residues: 1-248 <WMNL
A;Residues: 1-248 <WMNL
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NiContains: trypsingerius taurus (cattle)
Species: Bos primigenius taurus (cattle)
Cidacesion: Apollo4; Mequence revision 28-Feb-1986 #text_change 18-Jul-1997
Cidacesion: Apollo4; Mol96; S08774
R.Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
Bliochem. Biophys. Res. Commun. 24, 346-352, 1966
A;ritle: Covalent structure of bovine trypsingen. The position of the remain A;ritle: Covalent A;Reference number: A90164; MUD:67168848; PMID:5967094
A;Accession: A90164; MUD:67168848; PMID:5967094
A;Residues: 1-57, 'C',59-67,'O',69-150,'N',152-176,'N',178-229 cMIK>
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38.7%; Pred. No. 2e-23;
cive 40; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor - bovine
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Best Local Similarity 38.7<sup>3</sup>
Matches 94; Conservative
390 WIRSHT 395
                                                                           848 WIKEQT 853
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A; Map position: basolateral cell surface C; Superfamily: membrane-bound arginine-specific serine C; Reywords: protein Ainerian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 397; DB 2
Pred. No. 6e-23;
9; Mismatches 1
                                                              401
                                                                                                   412
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28.2%; Pre-
                                                              FLPW----IRSHTKEENGL
                                                                                   A, Contents: Small intestine
A, Accession: JC7775
A, Molecule type: mRNA
A, Residues: 1-855 < SAT>
A, Cross-references: DDBJ:AB037898
C; Comment: This enzyme, an epithel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 28.2 Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: protein digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
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C.Species: Sattus norvegicus (Norway rat)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C.Accession: 83377; 832013
B.Cochim. Biophys. Acta 1173, 350-352, 1993
A.Fitle: Clohing and sequence analysis of rat hepsin, a cell surface serine proteinase. A.Reference number: S33777; WUID:93305733; PMID:8318546
A.Accession: S33777
A.Accession: S33777
A.Fitle: Pre-liminary
A.Residues: 1-416 <FAR>
F;127,308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status experimental F;128-347,340-345/Disaulfide bonds: #status predicted F;390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted F;390-391/Aleavage site: Arg-Ile (coagulation factor XIIa) #status predicted
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                                                                                                                                                                                                                                                                                                                                     316
                                                                                                                                                                                                                                                                                                                                                                                                              COOPHYYGSEVITIMICAADPQWKTDSCOODSGGPLVCSLOGRMTLTGIVSWGRGCALKD 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLCAADPQWKTDSCQGDSGGPLVC----SLQGRMTLTGIVSWGRGCALKDKPGVYTRVSH 386
                                                                                                                                                                        144 TLRPRFKIIGGEFTTIENOPWFAAIY-----RRHRGGSVTYVCGGSLISPCWVISATHCF
                                                                                                                                                                                                     TIKTSTRIVGGINSSWGEWPWQVSLQVKLTAQRH-----LCGGSLIGHQWVLTAAHCF
                                                                                                                                                                                                                                                                                                                                 RCAQPSRTIQTICLPSMYNDPQFGTSCELTGFG--KENSTDYLYPEQLKMTVVKLISHRE
                                                                                                                                                                                                                                                                                                                                                        --LNYTEFQKPICLPSKGDTSTIYINCWVTGWGFSKEKGE---IQNILQKVNIPLVTNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCVDEGGL-PLAQRLLDVISVCDCPRGRFLTATCQDCGRRKL-PVDRIVGGQDSSLGRWP
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                                                                                                                                                                                                                                                       IDYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 WCYVQVGLKPLVQECM----VHDCADGKLKF----QCGQKTLRPRFKIIGGEFTTIENOP
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G.Superfamily: hepsin; trypsin homology
C.Steywords: hydrolase; liver; serine proteinase; transmembrane protein
F;22-44/Domain: transmembrane #status predicted <TMN>
F;162-399/Domain: trypsin homology <TMX>
F;187-293.299/Domain: trypsin homology <TMX>
F;187-203.290-356,321-337,48-380/Disulfide bonds: #status predicted
F;202,256,352/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                               17.8%; Score 402; DB 1; Length 638; larity 33.1%; Pred. No. 1.8e-23; Conservative 56; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 401; DB 1; Length 416;
Pred. No. 1.3e-23;
5; Mismatches 103; Indels
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Best Local Similarity 34.2%; Pre Matches 109; Conservative 55;
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                                                                                                                Similarity
                                                                                                                                    88;
                                                                                           Query Match
Best Local S
Matches 88
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: TSNA
A;Molecule type: TSNA
A;Molecule type: TSNA
A;Molecule type: TSNA
A;Molecule type: TSNA
A;Experimental source: Strain Male, 7-week-old
A;Experimental source: Strain Male, 7-week-old
A;Experimental source: Strain Male, 7-week-old
A;Experimental source: Strain Male, 7-week-old
A;Experimental source: Strain Male, 7-week-old
A;Title: A role for membrane-type serine protease (MT-SPI) in intestinal epithe
A;Reference number: JC7775; PMID:11573963
                                                                                                                                                                                                                                                                               membrane-bound arginine-specific serine proteinase precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Dec-20131, Sequence_revision 14-Dec-2001 #text_change 03-Feb-2003
C;Accession: 0C7731, GC7778
R;Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; .
J. Biochem. 130, 425-430, 2001
A;Title: Characterization of a membrane-bound arginine-specific serine protease
A;Reference number: JC7731; MUID:21421307; PMID:11530019
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BGEWPWQVSLHALGOG----HLCGASLISPDWLVSAAHCFQDETIFKYSDHTMWTAFLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 679 LDQSKRSASGVQEHKLKRIITHPSFNDFTFDY--DIALLELE----KPAEYSTVVRPICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         535 GKCLPQSQQC---NGKDDCGDGSDEA---SCDNVNAVSCTKYTYRC-----QNGL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 IBNOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFID----YPKKEDYIVYLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 RSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CNCPKKFGGQHCE-
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A,Residues: 20-27;40-46, 'X', 48, 'H';50, 'X', 52-70, 'H';75-76, 'X', 78-80;103-113;13

260-283, 'X', 285;287-291, 'X', 293-295;314-317, 'X', 319-320;321-324; 'X', 739-333;3

2525;338-551;562, 'X', 564-567;573, 'X', 575-576;578-583, 'X', 585;592-604 <ACM>
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent C;Comment: The zymogen is activated by factor XIIa, which cleaves the molecule are linked by one or more disulfide bonds. XIIa, which cleaves the molecule C;Comment: The enzyme cleaves Lys-Kg and Arg-Ser bonds. It activates, in a relingen and may also play a role in the renin-angiotensin system by converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
391-621/Domain: trypsin homology <TRY>
21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,3
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yResidues: 1-638 -CHD3
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yResidues: 1-638 -CHD3
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yResidues: 1-638 -CHD3
yResidues: 1-638 -CHD3
yReference number: 337939, MUID:91152016; PMID:1998666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 GWG---NTQY-YGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGGIDACQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NiAlternate names: Kininogenin; plasma prekallikrein
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession: M00921; A37939
                                                                                                                                                                                                                            |:: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
                                                                                                                                                                                                                                                                                                                                                                                                     233 LHKDY----SADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEIT
                                                                                                                                                                    122 LVQECMVHDCADGK----LKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSV
                                                                                                                                                                                                                                                                                                                                        178 TYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGE-----MKFEVENLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 YHGGYLPFRDPNSEENSNDIALVHLSSP----LPLTEYIQPVCLPAAGQALVDGKICTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFGKENSTDYLYPBQ----LKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 GDSGGPLVC----SLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPW----IRSHTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 GDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFREWIFQAIKTHS-E
                                                                                         Gaps
                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease
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Title: Human plasma prekallikrein, a zymogen to a serine; Reference number: A00921; MUID:86243359; PMID:3521732
                                     7.2e-24;
ches 98;
                                     34.9%; Pred. No. 7.2e ive 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: GDB:KLK3
;Gross-references: GDB:127575; OMIM:229000
                                Best Local Similarity 34.9:
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 ENGL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 ASGM 413
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A; Accession: A36557
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A; Molecule the sequence including the amino ends of both the heavy and light chai
C; Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
C; Comment: This protein, southesized in the liver, circulates as a noncovalent complex w
C; Comment: This protein, sould activated by factor XIIa, which cleaves the molecule into a li
are linked by one or more disulfide bonds.
C; Superfamily: coagulation factor XI; trypsin homology
C; Keywords: blood coagulation factor XI; trypsin homology
C; Keywords: blood coagulation factor XI; trypsin homology
C; Keywords: blood coagulation factor XIIa
F; 20-199/Domain: apple repeat cAP1>
F; 20-109/Domain: apple repeat cAP2>
F; 200-289/Domain: apple repeat cAP3>
F; 291-380/Domain: apple repeat cAP4>
F; 291-380/Domain: apple repeat cAP4>
F; 291-380/Domain: apple repeat cAP4>
F; 291-280/duct: plasma kallikrein light chain #status experimental cLCH>
F; 391-621/Domain: trypsin homology cTRY>
F; 21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F; 21-104,47-37,51-57,111-194,337-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F; 21-104,47-37,51-57,111-194,39-6,144-148,578/homin predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKLVDSPD-----C---TTKINARIVGGTNASLGEWPWQVSL--QVKLVSQTHLCGGSI 423
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Ricession: SOR (man)
Ricession: Rowel trypsin-like serine protease (hepsin) with a putative trans Air Reference number: SOR (man)
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Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 CMVHDCADGKLKFQCGQKTLRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFG---KENSTDYLYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 ISPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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;Gros-references: GDB:135685; OMIM:142440

;Map position: 19411-19413.2

;Superfamily: hepsin; trypsin homology

;Keywords: hydrolase; liver; serine proteinase; transmembrane protein

;23-465/Domain: transmembrane #status predicted <TWN>

;163-400/Domain: trypsin homology <TRY>

;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted

;203,257,353/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cykeywords: glycoprotein; Mydrolase; serine proteinase; transmembrane protein Cykeywords: glycoprotein; sequence #status predicted <SIG> F1.32/Domain: signal sequence #status predicted <MIG> F3.344, A3.43, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44, A3.44,
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prostasin (EC 3.4.21.-) precursor - human
C;Species: Homo sapiens (man)
C;Dates: 24-May-1996 #text_change 21-Apr-2003
C;Dates: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003
C;Accession: A57014; A5866
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
J. Biol. Chem. 270, 13483-13489, 1995
A;Title: Molecular cloning, tissue-specific expression, and cellular localization of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
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A;Status: translated from GB/EMBL/DDBJ
A;Roidcus translated from GB/EMBL/DDBJ
A;Roidcus 1-343 < KBS.
A;Roidcus 1-343 < KBS.
A;Cross-references: GB:L41351; NID:g862304; PIDN:AAC41759.1; PID:g862305
A;Experimental source: prostate
A;Experimental source: prostate
A;Experimental source: prostate
B;Yu, J.X.; Chao, L.; Chao, J.
J. B;Ol. Chem. 269, 18843-18848, 1994
A;Title: prostanin is a novel human serine proteinase from seminal fluid. A;Reference number: A54866; MUID:94308140; PMID:8034638
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A)Cross-references: GDB:676446; OMIM:600823
A)Map position: 16pll.2-16pll.2
C)Superfamily: trypsin, trypsin homology
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Matches 100; Conservative
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R.Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong J. Biol. Chem. 270, 24004-24009, 1995
A.Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot A.Reference number: 146259; MuID:96025778; PMID:7592597
A.Accession: 146260
A.Accession: 146260
A.Molecule type: mRNA
A.Residues: 1-810 cLaw>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
          265 RTIQTICLESMYNDPQ-FGTSCELTGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYY
                                                                                                                                                                                                                                                             27 NIHW--CNCPKKFGGQHCEIDKS------KTCYEGNGHFYRGKASTDTMGRPCL
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C;Superfamily: plasmin; kringle homology; plasminogen-related protein j
C;Keywords: hydrolase; serine proteinase
C;Keywords: hydrolase; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology «PLPH»
F;185-181/Domain: kringle homology «KR2»
F;275-352/Domain: kringle homology «KR2»
F;379-466/Domain: kringle homology «KR3»
F;379-466/Domain: kringle homology «KR3»
F;882-803/Domain: trypsin homology «KR5»
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Db 1068 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHQHRRTPENHPNDDLTMNYCRNPDA 1122	OV 143 KTLRPRFKIIGGEFTTIENOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI 199
Qy 108 RRRPWCYVQVGLKPLVQECMVHDCADGKLKFQCGQ 142	: : :
Db 1123 DTGPWCFTMDPSVRREYCNLTRCSDTEGTVVTPPTVIPVPSLEAPSEQASSSPDCGK 1179	Qy 200 DYPKKEDYIVYLGRSRINSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGR 259
CY 143 KILRPRFKIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFI 199	Db 271 RSSRPSTYKVVLGTHHBLRLAAGAQQIDVSKLFLEPSRADIALLKLSS 318
Db 1180 PQVEPKKCPGSIVGGCVAHPHSWPWQVSLRTRFGKHFCGGTLISPEWVITAACCLE 1235	じりー
200 DYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHNDIALLKIRSK :: :	Db 319PAIITQNVIPACLPPADYVVANWABCFVTGMGBTQDSSNAGVLKEAQLPVIENKV 372
1236 TFSRPSFYKVILGAHQEVNLESHVQEIEVSRLFLEPIGADIALLKL 1	
OY 257 EGRCAQPSRIQTICLEPSMYNDPQFGISCEITGFGKENSTDYLYPEQLKMTVVKLI 312	374 CNRYEYLNGRVKSTEL
313 SHREÇQOPHYYGSEVITYMLÇAADPOWKTDSÇÇÇBSGGFLYCSL	OY 3// NEVERTREEN 391 DD 434 KPGVYVVSFINMI 448
Db 1335 ENTVCHYEFINGRVKSTELCAGHLAGGTDRCQGDNGGPVYCFDKDKXILRGITSWGPGC 1394	
Oy 373 ALKDKPGVYTRVSHFLPWI 391	NESULI 31 NESULI 31 Prain-amerific earine profesinace (RC 2 4 21 -) - mouse
Db 1395 ACPNKPGVYVRVSSFVTW1 1413	C;Species: Mus musculus (house mouse) C;Date: 24-Jan-1998 #sequence revision 13-Mar-1998 #text change 31-Mar-2000
RESULT 30	C;Accession: JC5759 R;Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.; Tsujimura, A.; Yame chi, l
A61545 plasmin (EC 3.4.21.7) precursor - horse (fragments)	Biochem. Biophys. Res. Commun. 239, 386-392, 1997 A;Title: Molecular cloning of a novel brain-specific serine protease with a k? gle-l
N;Alternate names: plasminogen N;Contains: miniplasminogen	
C;Species: Equus caballus (domestic horse) C;Date: 28-Oct-1994 #sequence revision 01-Nov-1996 #text change 18-Jul-1997	A; Molecule type: mRNA A; Residues: 1-761 < YAM>
)	A.Cross-references: DDBJ:D89871 A.Experimental source: brain
Enzyme 40, 63-69, 1988 A.Title: Structural aspects of the plasminoden of various enecies	
A; Reference number: A61545, MUID:89005015, PMID:3168975 A; Accession: A61545	C)Acywolus: glycoglocall; hydrolase; scille plocallase F;85157/Domain: Kringle-like #status predicted <kri> F:161-264/Domain: scavenger recentor cveteine-rich domain homology <src7></src7></kri>
A;Molecule type: protein A;Residues: 1-33;34-117 <sch></sch>	Fil6-266,273-372,386-486/Domain: scavenger receptor cysteine-rich #status pre sted . F:513-516/Domain: furin binding #status predicted <frb></frb>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E. Protein Seq. Data Anal. 4, 69-74, 1991	F;517-755/Domain: trypsin homology <trv>F:93.521.569/Binding site: carbohydrate (Asn) (covalent) #status predicted</trv>
A;Title: Complete amino acid sequence of equine miniplasminogen. A;Reference number: S17527; MUID:92052077; PMID:1946332	F;562,612,711/Active site: His, Asp, Ser #status predicted
A;Accession: S17527 A;Molecule type: protein A:Residine: 118-455 , SC7.	19.2%; Score 434; DB 2; Length 761; ilarity 29.0%; Pred, No. 7.1e-26; Conf. No. 7.1e-26;
ed protein precu	יומרכוופט בנסי כטומפרביעמרביעם מסי שומרכוופט בנסי דווממנט סכי, כמנים מסיי ממנים מסיי ממנים מסיי ממנים מסיי ממנים
C) NEYWOLUS: ILLILINGIAELS; GLYCOPICCEIN; NYGROIASE; KIINGIE; PLASMA; SETINE Proteinase; Z F;1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <pro></pro>	28 IHWCNCEKKRGGRH-CEIDKEKICK-EGNGH
F;1-35/Domain: activation peptide (fragment) #status experimental <apt> F;34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <mat></mat></apt>	346 VSFIQCSRRQWGRHDCSHREDVGLTCYPDSDGHRLSPGFPIRLVDGENKKEGRVEVFVNG
F;37-114/Domain: kringle homology <kr4> F;118-455/Product: miniplasminogen #status experimental <min></min></kr4>	
F;126-205/Domain: kringle homology <kr5> F;226-455/Domain: plasmin chain B #status experimental <bch></bch></kr5>	DD 406 OWGTICDDGWTDKHAAVICRQLGYKGPARARTMAYFGEGKGPIHMDNVKCTGNEKALADC 465
F;226-448/Domain: trypsin homology <try> F;267,310,405/Active site: His, Asp, Ser #status predicted</try>	92 LOLGLGKANYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCADGKLKRQCGQKTLR :: : : : : : : : :
Query Match 20.0%; Score 451.5; DB 2; Length 455;	466 VKQDIGRHN-CRHSEDAGVICDYLEKKASSSGNKEMLSSGGGLRLLH
Hest Local Similarity 32.5%; Pred. No. 1.88-27; Matches 122; Conservative 45; Mismatches 169; Indels 39; Gaps 12;	OY 147 PRRK-IIGGEFTTIENOPFRAAIYRRHRGGSVTYVCGGSIISPCWVISATHCFIDY-PKK 204
Qy 27 NIHWCNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHA 86 Db 103 SYWRFCNIRKCSFTVORBSERDOMIGIGKGVGKKATTVTGERGABADPHP 157	
87 HRSDALQLGLGKHNYCRNPD-NRRRPWCYVQVGLKPLVQECWVHDCADGKLKFQCGQ 1	Db 572 RSYAVRVGDYHTLVPEEFEQEIGVQQIVIHRNYRPDRSDYDIALVRLQGPGEQCARLS 629

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apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
(Species: Macaca mulatra (rhesus macaque)
(Species: Macaca mulatra (rhesus macaque)
(Spate: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
(SAccession: A32869; A30848
(R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
A;Title: Chem. 264, S957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of syn.
A;Reference number: A32869; MUID:89174660; PMID:2925643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4394 SHVQ---EIEVSRLFLEPTQA-----DIALLKL----SRPAVITDKVMPACLPS--- 4435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4281 PDGDINGPWCYT-MNPRKLFDYCDIPLCASS--SFDCGKPQVEPKKCPGSIVGGCVAHPH 4337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4228 CMFGNGKGYRGKKATTVTGTPCQEW-----AAQEPHRHSTFIPGTNKWAGLEKNYCRN 4280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 PD-NRRRPWCYVQVGLKPLVQECMYHDCADGKLKFQCGQKTLRPR---FKIIGGEFTTIE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 NOPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSR---LN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 SNIQGEMKFEVENLILHKDYSADILAHHNDIALLKIRSKEGRCAQPSRIIQTICLPSMYN 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 DPQF----GISCELIGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 CYEGNGHFYRGKASTDIMGRPCLPWNSATVLQQTYHAHRSDALQLGLGK-----HNYCRN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: applipoprotein(a); kringle homology; trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F;S0-127/Domain: kringle homology <KRl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4484 AEHLARGIDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYARVSRFVIWI 4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 AADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A; Residues: 1-1420 < TOM>
A; Cross-references: GB:J04635; NID: 9342072; PIDN:AAA36833,1; PID: 9342073
                                                                                                                                                                                                                                                                                                                                                                                                                                                               603
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 4548;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 1.9e-28;
Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.1%; Score 477; DB 2;
llarity 34.0%; Pred. No. 6.4e-29;
Conservative 43; Mismatches 137,
                                                                                                                                                                                                                                                                                                                                                                                                   Score 478;
Pred. No. 1
                                                                                                                       KR32>
                                                                                                                                                                                  < KR34>
                                                                                                                                                                                                                    < KR35>
                                                                                                                                                                                                                                                 < KR36>
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F,506-583/Domain: kringle homology <KR5
F,620-69/Domain: kringle homology <KR5
F,726-803/Domain: kringle homology <KR6
F,726-803/Domain: kringle homology <KR8
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                                                                                                                                              F;3676-3753/Domain: kringle homology
F;3782-3859/Domain: kringle homology
F;386-3973/Domain: kringle homology
F;4104-4201/Domain: kringle homology
F;428-4201/Domain: kringle homology
F;428-4307/Domain: kringle homology
F;428-457/Domain: trypsin homology
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                                                                                         nomology
                                                                                                                          nomology
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                                                                                                                                                                                                                                                                                                                                                                                                   21.2%;
36.0%;
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                                                                                                                       kringle
kringle
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Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                        F;3334-3411/Domain: K
F;348-3525/Domain: K
F;362-3639/Domain: K
F;3676-3753/Domain: K
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                                                                                                                                    A;Cross-references: GB:L07899; NID:g867973; PID:g967974
R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacco Proc. Natl. Acad. Sci. U.S.A. 89, 11884-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipopr A;Reference number: A47233; MUD:93087573; PMID:1454851
A;Accession: 160906
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lochemistry 31, 3113-3118, 1992
Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wi
Reference number: 152415; MUID:92207924; PMID:1554698
Accession: 152415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Gene: GDB:LPA
A):Cross-references: GDB:120699, OMIM:152200
A):Map posttion: 6q56-6q27
A;Note: several genes closely linked on chromosome 6 are identical in the first coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: apolipoprotein(a); kringle homology; trypsin homology; keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase; 1:1-9/Domain: signal sequence #status predicted <SIG>
20-4548/Product: apolipoprotein(a) #status experimental <MAT>
20-4548/Product: apolipoprotein(a) #status experimental <MAT>
                                              Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues; 1-16 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ:
Molecule type: DNA
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;Cross-references: GB:M86877; NID:g178780; PIDN:AAB49909.1; PID:g553185;Note: apo(a) gene 1 (nomenclature of reference 152415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-16 <RE4>
; Cross-references: GB:M86878; NID:g178782; PIDN:AAA51749.1; PID:g553186
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Gross-references: GB:M90078; NID:g178786; PIDN:AAA35547.1; PID:g553188

Note: apo(a) gene 1 (nomenclature of reference 152415)

Accession: A47233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB:M90079; NID:g178784; PIDN:AAA35546.1; PID:g553187
Reference number: A47277; MUID:93165698; PMID:7679504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ:
Molecule type: DNA
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Molecule type: DNA
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F;256-333/Domain: Kringle homology «KR2»
F;370-447/Domain: Kringle homology «KR4»
F;484-561/Domain: Kringle homology «KR5»
F;598-675/Domain: Kringle homology «KR6»
F;712-708/Domain: Kringle homology «KR8»
F;956-903/Domain: Kringle homology «KR8»
F;940-1017/Domain: Kringle homology «KR8»
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2-359, 3-342 	WF 165 	SC 344 	.000 less, M.; St inogen	PID:9 620 C.G.; wh, R is how ogous 2-314, ',316 K.; & wartz, the r ated r
<pre></pre>	CGQKTLRPRFKIIGGEPTTIENOPWF : : :	GSEVTTKALCAADPOWKII	_change_08-Dec-415, I65286 i.; Chen, B.Y.; nologous to plas	PIDN:CAA29618.1; PID: 1, Q.T.; MAILEr, C.G.; 1) shows that it is ho 196,'DKG',200;292-314 /sow, B.R.; Meer, K.; ne and members of the
Fil04-583/Domain: plasmin chain A #status experimental <ach> Fil10-880/Domain: kringle homology <kr1> Fil10-880/Domain: kringle homology <kr2> Fil10-880/Domain: kringle homology <kr3> Fil284-461/Domain: kringle homology <kr3> Fil284-81/Domain: kringle homology <kr3> Fil284-81/Domain: kringle homology <kr3> Fil284-805/Domain: kringle homology <kr3> Fil284-805/Domain: kringle homology <kr3> Fil284-805/Domain: plasmin chain B #status experimental <bch> Fil284-805/Domain: plasmin chain B #status experimental <bch- #status="" <ar3="" <fil284-805="" b="" bristone="" chain="" domain:="" experimental="" fil284-805="" homology="" plasmin="" predicted="" trypsin=""> Covalent) #status experimental <fil284-805 #status="" b="" chain="" conservekastdtmgrpclpwnsatvlqqtmahrrsdalqlglgkhnycrnpd-nr="" domain:="" fil088-123,="" fil088-1234-1205-1205-1205-1205-1205-1205-1205-1205<="" fil284-805="" jachycrastdtmgrpclpwnsatvlqqtmahrrsdalqlglggkhnycrnpd-nr="" plasmin="" predicted="" td=""><td>G-E-H X</td><td>EITGFGKENSIDYLYPE-QLKWTVVKLISHRECQOPHYGGSEVTTKMLCAADPQWKTDS </td><td>ispecies: Homo sapiens (man) jate: 30-Jun-1989 #text_chi jate: 30-Jun-1989 #text_chi jacession: 180657; A28017; A427277; 160906; A47233; 152415, McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; (ature 330, 132-137, 1987 jattle: cDNA sequence of human apolipoprotein(a) is homolog jReference number: 800657; MUID:88039109; PMID:3670400 jAccession: 800657 MOIGCULE type: mRNA</td><td>A; Residues: 1-4548 cMCL. A; Residues: 1-4548 cMCL. A; Residues: 1-4548 cMCL. A; Cross-references: GB:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g A; Cross-references: GB:X06290; EMBL:X0696; NID:g28619; PIDN:CAA29618.1; PID:g R; Eaton, D.L.; Flead: G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; A; Title: Partial amino acid sequence of apolipoprotein(a) shows:that it is home A; Reference number: A28017; MUID:87204109; PMID:3472206 A; Rccession: A28017 A; Molecule type: protein A; Residues: 20-21, P:23-34;177-179, N', 181-186, T', 188-196, 'DKG', 200; 292-314, X', 4396-4401 cEnt> X', 4396-4401 cEnt> R; Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; E.Proc. Natl. Acad. Sci. U.S.A. 90, 1869-1373, 1993 A; Title: S' control regions of the apolipoprotein(a) gene and members of the residual aminosity of the residual apolity of the residual aminosity</td></fil284-805></bch-></bch></kr3></kr3></kr3></kr3></kr3></kr3></kr2></kr1></ach>	G-E-H X	EITGFGKENSIDYLYPE-QLKWTVVKLISHRECQOPHYGGSEVTTKMLCAADPQWKTDS	ispecies: Homo sapiens (man) jate: 30-Jun-1989 #text_chi jate: 30-Jun-1989 #text_chi jacession: 180657; A28017; A427277; 160906; A47233; 152415, McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; (ature 330, 132-137, 1987 jattle: cDNA sequence of human apolipoprotein(a) is homolog jReference number: 800657; MUID:88039109; PMID:3670400 jAccession: 800657 MOIGCULE type: mRNA	A; Residues: 1-4548 cMCL. A; Residues: 1-4548 cMCL. A; Residues: 1-4548 cMCL. A; Cross-references: GB:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g A; Cross-references: GB:X06290; EMBL:X0696; NID:g28619; PIDN:CAA29618.1; PID:g R; Eaton, D.L.; Flead: G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; A; Title: Partial amino acid sequence of apolipoprotein(a) shows:that it is home A; Reference number: A28017; MUID:87204109; PMID:3472206 A; Rccession: A28017 A; Molecule type: protein A; Residues: 20-21, P:23-34;177-179, N', 181-186, T', 188-196, 'DKG', 200; 292-314, X', 4396-4401 cEnt> X', 4396-4401 cEnt> R; Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; E.Proc. Natl. Acad. Sci. U.S.A. 90, 1869-1373, 1993 A; Title: S' control regions of the apolipoprotein(a) gene and members of the residual aminosity of the residual apolity of the residual aminosity
n chain A #status e homology <rr1- #="" #status="" (asn)="" (cc="" (ser)="" 21.5%;="" 35.4%;="" 42;="" 48="" <rr3-="" <rr4-="" asp,="" ative="" b="" c)="" chain="" drastdymgrpclpms="" drydrate="" e="" e:="" grastdtmgrpclpms="" grasttvagvpcqewaaq<="" his,="" homology="" misma="" n="" n-11,1199-183,192-="" nisma="" pred.="" score="" ser="" td=""><td>LKPLVQECMVHDCADGKLK </td><td>SEGENSTDYLYPE-QLKMTVVV </td><td>(man) uence revision 3 017; A47277; I66 n, J.E.; Kuang, f. human apolipog 57; MUID:8803916</td><td>CL> B.X06290; EMBL.X06696; NID:9286 G.M.; Kohr, W.J.; McLean, J.W. U.S.A. 84, 3224-3228, 1987 b acid sequence of apolipoprote 28017; MUID:87204109; PMID:3472 ein ,23-34;177-179,'N',181-186,'T', J.G.; Lindahl, G.E.; Liu, A.C. U.S.A. 90, 1369-1373, 1993 egions of the apolipoprotein(a)</td></rr1->	LKPLVQECMVHDCADGKLK	SEGENSTDYLYPE-QLKMTVVV	(man) uence revision 3 017; A47277; I66 n, J.E.; Kuang, f. human apolipog 57; MUID:8803916	CL> B.X06290; EMBL.X06696; NID:9286 G.M.; Kohr, W.J.; McLean, J.W. U.S.A. 84, 3224-3228, 1987 b acid sequence of apolipoprote 28017; MUID:87204109; PMID:3472 ein ,23-34;177-179,'N',181-186,'T', J.G.; Lindahl, G.E.; Liu, A.C. U.S.A. 90, 1369-1373, 1993 egions of the apolipoprotein(a)
F;104-583,584-812/Product: plasmin #status experimental F;104-583/Domain: kringle homology <rr1> F;182-269/Domain: kringle homology <rr2> F;282-359/Domain: kringle homology <rr2> F;282-359/Domain: kringle homology <rr3> F;284-312/Domain: kringle homology <rr3> F;384-461/Domain: kringle homology <rr3> F;384-805/Domain: kringle homology <rr4> F;584-805/Domain: trypsin homology <rr5> F;584-805/Domain: trypsin homology <rr5> F;56-80,60-68,110-188 131-171,159-183,192-269,195-323,213 F;56-80,60-68,110-188 131-171,159-183,192-269,195-323,213 F;315/Binding site: carbohydrate (Ser) (covalent) #status F;365/Binding site: carbohydrate (Ser) (covalent) #status F;624,667,762/Active site: His, Asp, Ser #status predicte F;624,667,762/Active site: His, Asp, Ser #status predict F;624,667,762/Active site: His, Asp, Ser #status predict F;624,667,762/Active site: His, Asp, Ser #status predict F;624,667,762/Active site: His, Asp, Ser #status F;624,667,762/Active site: His, Asp, Ser #status F;764,667,762/Active site: His, Asp, Ser #status F;765/Binding<br <="" td=""/><td>109 RRPMCYVQVGLKP 543 NGPWCYTMNPRKP 166 AAIYRRHRGGSVT :: 599 VSLRRSSR 226 FEVENLILHKDYS 654 IPVSRLFREDSQA</td><td>Oy 286 EITGFGKENST Db 702 YITGWGETGGT OY 345 QGDSGGPLVCS Db 759 QGDSGGPLVCF RESULT 28 S00657 S00657 N'ALLETTALE 10(a) (EC 3.4.21.</td><td>B: Homo sapiens 30-Jun-1989 #seq ion: S00657; #seq ion: S01657; #seq ion: S0185 #sequence o nce number: S006 ion: S00657</td><td>es: 1-4448 «MCL» references: GB.X06290; EMBI D.L.; Fless, G.M.; Kohr, W Ll. Acad. Sci. U.S.A. 84, 3 Partial amino acid sequent nce number: A28017; MUID:87 ion: A28017 ion: A28017 be: Jorctein es: 20-21, 'P', 23-34;177-175 4401 < EATS L). Clarke, U.G.; Lindahl L). Acad. Sci. U.S.A. 90, 11 Acad. Sci. U.S.A. 90, 55; control regions of the</td></br></br></br></br></br></br></br></br></br></br></br></br></rr5></rr5></rr4></rr3></rr3></rr3></rr2></rr2></rr1>	109 RRPMCYVQVGLKP 543 NGPWCYTMNPRKP 166 AAIYRRHRGGSVT :: 599 VSLRRSSR 226 FEVENLILHKDYS 654 IPVSRLFREDSQA	Oy 286 EITGFGKENST Db 702 YITGWGETGGT OY 345 QGDSGGPLVCS Db 759 QGDSGGPLVCF RESULT 28 S00657 S00657 N'ALLETTALE 10(a) (EC 3.4.21.	B: Homo sapiens 30-Jun-1989 #seq ion: S00657; #seq ion: S01657; #seq ion: S0185 #sequence o nce number: S006 ion: S00657	es: 1-4448 «MCL» references: GB.X06290; EMBI D.L.; Fless, G.M.; Kohr, W Ll. Acad. Sci. U.S.A. 84, 3 Partial amino acid sequent nce number: A28017; MUID:87 ion: A28017 ion: A28017 be: Jorctein es: 20-21, 'P', 23-34;177-175 4401 < EATS L). Clarke, U.G.; Lindahl L). Acad. Sci. U.S.A. 90, 11 Acad. Sci. U.S.A. 90, 55; control regions of the
F:104-583 F:1104-583 F:1104-583 F:122-269 F:284-851 F:284-851 F:584-805 F:56-80,60 F:56-80 F	8 8 8 8 8	O O O O KW 82	C;Specie C;Date: C;Accen R;McLean Nature 3 A;Tile: A;Referei A;Access	
NG 536 P 594 P 594 NG 551 NG 651 NG 695 NG 753	666	33 kmpfer, U.; Rick vith human plasem	for human and	nents of human, factor in a va plasminogen act ecursor homology cringle, plasma,
CADGKLKFQCGQKTIRPRFKIIGGEFTTIENQP	thange 18-Jun-19	19.1; PID:949496 idator sselet, S.J.; Ka nn. Comparison w	eic acid coding 1, PID:g163552	ninal CNBr fragminal CNBr fragminal a proteclytic urokinase-type tted protein preplase; kidney; k
NRRRPWCYVQVGLKPLVQECMYHDCADGKLKFQCGQKTLRPRFKIIGGEFTTIENQP	hpr-1995 #text_c 7 7.E. 44 of the bovine F	12; PIDN:CAA5593 tt-8 is the init ler, G.A.K.; Ros vvine plasminoge PMID:3846532 'L',556-812 <sc. 'r.<="" td=""><td>Ty deoxyribonucl PMID:6148961 PMID:A48361 PHID:A4A30714.</td><td>re of the N-tern PMID: 7238497 cd clots; acts e cativates the clasminogen-relation of the coprocein; hydrodicted csig.</td></sc.>	Ty deoxyribonucl PMID:6148961 PMID:A48361 PHID:A4A30714.	re of the N-tern PMID: 7238497 cd clots; acts e cativates the clasminogen-relation of the coprocein; hydrodicted csig.
NRRRPWCYVQVGLKPLVQECMYHDCADGKLKFQCGQKTLRFR-	reor - bovine gen aurus (cattle) Le revision 28, 7 158961, 80373 6. Detersen, Library, May 19 characterizatin	402; NID:g4949; ther Met-1 or Met. 78, 1985 1 sequence of bo MUID:85203906; MUID:8523906; 115,'H',517-554,	1984 Mulo:85023311; B/EMBL/DDBJ -812 < MAL> 35; NID:9163551 -6.; Schaller,	70, 1981 primary structur MUID:81212097; s fibrin of bloc n follicle; also ngle homology; nce #status prec
	3.4.21.7) precu: names: plasmino; os prinigenius ep-1987 #sequen 545046, A25835 L., Andersen, M the EMBL Data 1 n: Cloning and number: \$45046 S45046	ype: mRNA rences: EBREL:X7: al source: live: s uncertain whe s. uncertain whe d.; Moser, P.W. hem. 149, 267-2 hem. 149, 267-2 hem. 149, 267-2 A25835; A25835; A25835 protein YPe: protein ype: protein	23, 4243-4250, mumber: 142961 145961 anslated from Glype: mRNA 706-743, K,745 R.A.; Lerch, 1	Eur. J. Biochem. 114, 465-470, 1981 A.Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma A.Acession: 803735, MUID:81212097; PMID:7238497 A.Acession: 803736 A.Acession: 803736 A.Mocial type: protein A.Residues: 27-83 cBRU> C.Function: A.Residues: 27-83 cBRU> C.Function: A.Besidues: 27-83 cBRU> C.Function: A.Besidues: 27-83 cBRU> C.Function: A.Besidues: 27-83 cBRU> C.Function: A.Besidues: 27-83 cBRU> C.Function: A.Besidues: 27-83 cBRU> C.Function: A.Besidues: 27-83 cBRU> C.Function: A.Besidues: 27-83 cBRU> C.Function: A.Besidues: 4.Besidues claim follicle: also activates the urokinase-type plasminogen ns the walls of the graafian follicle: also activates the urokinase-type plasminogen C.Superfamily: plasmin, kringle homology; plasminogen-related protein precursor homol C.Superfamily: signal sequence #status predicted cSIG> F.1-26/Domain: signal sequence #status predicted cSIG>
0.9y 10.7 0.9y 10.7 0.9y 1.64 0.9y 2.24 0.9y 2.24 0.9y 2.24 0.9y 2.24 0.9y 2.24 0.9y 2.24 0.9y 2.24 0.9y 2.24	RESULT 27 PLBO PLBO NALemate C; Species: B C; Date: 30-8 C; Accession: R; Berglund, submitted to A; Descriptio A; Reference A; Accession:	A, Molecule t A, Residues: A, Cross the A, Note: it i B, Schaller, B, Challer, B, Title: Com A, Reference A, Accession: A, Residues: A, Residues: R, Malinowski	Blochemistry A,Title: Cha A,Reference A,Accession: A,Status: tr A,Molecule tr A,Residues: A,Cross-refe R,Brunisholz	Bur J. Bioc A;Tile: Con A;Reference A;Accession: A;Residuels C;Function: C;Fun